

(32) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT C

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number
WO 01/57272 A2

(51) International Patent Classification⁷: **C12Q 1/68**

94043 (US). **RANK, David, R.** [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

(21) International Application Number: PCT/US01/00663

(22) International Filing Date: 30 January 2001 (30.01.2001)

(74) Agent: **RONNING, Royal, N., Jr.**; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

(81) Designated States (*national*): AE, AG, AI., AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): **MOLECULAR DYNAMICS, INC.** [—/US]; 928 East Arques Avenue, Sunnyvale, CA 94086 (US).

Published:

— without international search report and to be republished upon receipt of that report

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **PENN, Sharron, G.** [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). **HANZEL, David, K.** [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). **CHEN, Wensheng** [CN/US]; 210 Easy Street #25, Mountain View, CA

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

WO 01/57272 A2



HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file pto_PLACENTA.txt, created 24
25 January 2001, having 26,548,337 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

placenta and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches – and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species – there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

 Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25 Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,
30 particularly those with polygenic etiology.

Summary of the Invention

35 The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least
25 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof 35 wherein said probe hybridizes at high stringency to a

nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human
10 placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for
15 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

20

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

10 As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

25 As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a
5 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a
10 portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a
15 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF
20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another
25 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit
30 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

35 As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual
5 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

10

Brief Description of the Drawings

The present invention is further illustrated with
15 reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and
20 associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional
25 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of
30 ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described,
35 of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray.
The graph shows the number of sequence-verified products
that were either not expressed ("0"), expressed in one or
more but not all tested tissues ("1" - "9"), or expressed
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
expression of verified sequences that showed expression
with signal intensity greater than 3 in at least one
tissue, with: FIG. 7A showing the expression as measured by
10 microarray hybridization in each of the 10 measured
tissues, and the expression as measured "bioinformatically"
by query of EST, NR and SwissProt databases; with FIG. 7B
showing the legend for display of physical expression
(ratio) in FIG. 7A; and with FIG. 7C showing the legend for
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3
signal intensity for arrayed sequences that were identical
to sequences in existing EST, NR and SwissProt databases or
that were dissimilar (unknown), where black denotes the
20 signal intensity for all sequence-verified products with a
BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30})
("unknown") and a dotted line denotes sequence-verified
spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases
25,000 to 130,000), containing the carbamyl phosphate
synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

35 FIG. 1 is a flow chart illustrating in broad

outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained
5 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence
10 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A
15 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

20 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can
25 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part
30 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100
35 in the present invention include GenBank, and particularly

include several divisions thereof, including the
htgs(draft), NT (nucleotide, command line), and NR
(nonredundant) divisions. GenBank is produced by the
National Institutes of Health and is maintained by the
5 National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
eukaryotic organisms will also prove useful as genomic
10 sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
are predicted to have a biological function as specified by
15 the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
regulating message degradation after transcription into
20 mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

The particular genomic sequence to be input into
25 process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
given genomic region. In such case, the input often will
30 be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
experimental confirmation is identified. Experimental
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
this latter case therefore process 300 can output the
5 entirety of the input sequence.

The subset of sequences output from process 300
is then used in process 400 for experimental verification
and characterization of the function predicted in
process 200, which experimental verification can, and often
10 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the
functional information obtained in the physical and/or
bioinformatic assays of process 400. Such annotation can
be done using any technique that usefully relates the
15 functional information to the sequence, as, for example, by
incorporating the functional data into the sequence data
record itself, by linking records in a hierarchical or
relational database, by linking to external databases, by a
combination thereof, or by other means well known within
20 the database arts. The data can even be submitted for
incorporation into databases maintained by others, such as
GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation
can be input into process 500 from external sources 600.

25 The annotated data is then displayed in process
800, either before, concomitantly with, or after optional
storage 700 on nontransient media, such as magnetic disk,
optical disc, magneto-optical disk, flash memory, or the
like.

30 FIG. 1 shows that the experimental data output
from process 400 can be used in each preceding step of
process 10: e.g., facilitating identification of functional
sequences in process 200, facilitating identification of an
experimentally suitable subset thereof in process 300, and
35 facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, 5 as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the 10 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously 15 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily 20 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other 25 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity 30 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) 35 ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query
20 can be generated that takes into account the initial
negative result.

When query 20 returns sequence meeting the query
5 criteria, the returned sequence is then passed to optional
preprocessing 24, suitable and specific for the desired
analytical approach and the particular analytical methods
thereof to be used in process 25.

Preprocessing 24 can include processes suitable
10 for many approaches and methods thereof, as well as
processes specifically suited for the intended subsequent
analysis.

Preprocessing 24 suitable for most approaches and
methods will include elimination of sequence irrelevant to,
15 or that would interfere with, the subsequent analysis.
Such sequence includes repetitive sequence, such as Alu
repeats and LINE elements, vector sequence, artificial
sequence, such as artificial polylinkers, and the like.
Such removal can readily be performed by identification and
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the
genomic sequence returned by query 20 with public or
private databases containing known repetitive sequence,
vector sequence, artificial sequence, and other artifactual
25 sequence. Such comparison can readily be done using
programs well known in the art, such as CROSS_MATCH, or by
proprietary sequence comparison programs the engineering of
which is well within the skill in the art.

Alternatively, or in addition, undesirable,
30 including artifactual, sequence can be identified
algorithmically without comparison to external databases
and thereafter removed. For example, synthetic polylinker
sequence can be identified by an algorithm that identifies
a significantly higher than average density of known
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,

where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible
5 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving
10 hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such
15 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process
20 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in
25 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the
30 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression
35 of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the
10 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with
15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer
25 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify
30 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it
5 has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10 The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic
15 sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased
20 commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves
25 to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later
30 sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least
35 about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays

typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"
35 libraries targeted at a particular biological question,

R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure
5 expression only of those genes found in EST libraries,
shown herein to represent only a fraction of expressed
genes. Furthermore, such libraries - and thus microarrays
based thereupon - are biased by the tissue or cell type of
message origin, by the expression levels of the respective
10 genes within the tissues, and by the ability of the message
successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the
methods of the present invention enable sequences that do
not appear in EST or other expression databases to be
15 determined - subsequently arrayed for expression
measurements could not, therefore, have been represented as
probes on an EST microarray. And as further demonstrated
in the examples, *infra*, the remaining population of genes
identified from genomic sequence by the methods of the
20 present invention - that is, the one third of sequences
that had previously been accessioned in EST or other
expression databases - are biased toward genes with higher
expression levels.

Representation of a message in an EST and/or cDNA
25 library depends upon the successful reverse transcription,
optionally but typically with subsequent successful
cloning, of the message. This introduces substantial bias
into the population of probes available for arraying in EST
microarrays.

30 In contrast, neither reverse transcription nor
cloning is required to produce the probes arrayed on the
genome-derived single exon microarrays of the present
invention. And although the ultimate deposition of a probe
on the genome-derived single exon microarray of the present
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
20 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the
30 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-
30 spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression
20 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound

noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or

approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

- 5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

- 10 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

- Alternatively, or in addition, the color, hue, 15 density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be 20 indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

- As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, 30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

- Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show
5 predictions of a plurality of different functions.
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity
5 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links
10 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be
15 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical
20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of
25 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of
30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to
35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to
5 indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user
10 interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data
15 from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the
20 physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence
25 that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to
30 rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes
5 and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis,
10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought
15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease,
20 neurodegenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

25 A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all
30 such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, it is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may
35 be detected in placenta.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
5 46(3):425-8 (1999)), in drug discovery screens (see, for
example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
10 Expression Profile Analysis of Human Breast Cancer
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
15 appreciated that even those probes that show no change in
expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
20 failure of the agent to change a gene's expression level is
evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
25 lead compound discovery or in subsequent screening of lead
compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

30 WO 99/58720 provides methods for quantifying the
relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);

5 Schena *et al.*

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5 Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase
35 hybridization, however — that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as
5 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes
10 of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one
15 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more
20 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand
25 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art
30 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to
35 provide single-stranded nucleic acid probes that have

sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 13,233 - 26,232. Such amino acid sequences are set out in SEQ ID NOS: 26,233 - 38,837. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5 After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic
15 DNA.

 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

 The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

 ORFs predicted by any two of the three programs
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single
35 gene if fewer than 7 exons were found within the 25 kb

window.

PCR

The largest ORF from each gene bin that did not
5 span repetitive sequence was then chosen for amplification,
as were all consensus ORFs longer than 500 bp. This method
approximated one exon per gene; however, a number of genes
were found to be represented by multiple elements.

Previously, we had determined that DNA fragments
10 fewer than 250 bp in length do not bind well to the amino-
modified glass surface of the slides used as support
substrate for construction of microarrays; therefore,
amplicons were designed in the present experiments to
approximate 500 bp in length.

15 Accordingly, after selecting the largest ORF per
gene bin, a 500 bp fragment of sequence centered on the ORF
was passed to the primer picking software, PRIMER3
(available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first
20 additional sequence was commonly added to each ORF-unique
5' primer, and a second, different, additional sequence was
commonly added to each ORF-unique 3' primer, to permit
subsequent reamplification of the amplicon using a single
set of "universal" 5' and 3' primers, thus immortalizing
25 the amplicon. The addition of universal priming sequences
also facilitates sequence verification, and can be used to
add a cloning site should some ORFs be found to warrant
further study.

The ORFs were then PCR amplified from genomic
30 DNA, verified on agarose gels, and sequenced using the
universal primers to validate the identity of the amplicon
to be spotted in the microarray.

Primers were supplied by Operon Technologies
(Alameda, CA). PCR amplification was performed by standard
35 techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median
15 size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe
30 sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were

then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

Exon Microarrays

The two genome-derived single exon microarrays
5 prepared according to Example 1 were hybridized in a series
of simultaneous two-color fluorescence experiments to (1)
Cy3-labeled cDNA synthesized from message drawn
individually from each of brain, heart, liver, fetal liver,
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100
10 cells, and (2) Cy5-labeled cDNA prepared from message
pooled from all ten tissues and cell types, as a control in
each of the measurements. Hybridization and scanning were
carried out using standard protocols and Molecular Dynamics
equipment.

15 Briefly, mRNA samples were bought from commercial
sources (Clontech, Palo Alto, CA and Amersham Pharmacia
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were
incorporated during separate reverse transcriptions of 1 µg
of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer
20 and 2 µg random 9mer primers as follows. After heating to
70°C, the RNA:primer mixture was snap cooled on ice. After
snap cooling on ice, added to the RNA to the stated final
concentration was: 1X Superscript II buffer, 0.01 M DTT,
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II
enzyme. The reaction was incubated for 2 hours at 42°C.
After 2 hours, the first strand cDNA was isolated by adding
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.
The reaction was then purified using a Qiagen PCR cleanup
30 column, increasing the number of ethanol washes to 5.
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA
corresponding to 50 pmoles of each dye were then dried in a
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; 5 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose 10 expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 15 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 25 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") 30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 35 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates

				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in
30 the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
35 chromosome RNA-binding motif (Chai *et al.*, *Genomics*

49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature
 5 (Fuentes et al., Mol. Genet. 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.
 10 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average
 15 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm
Lung	-4.95 \pm 0.93	-3.75 \pm 0.21
Placenta	-3.56 \pm 0.25	-3.52 \pm 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be
5 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show
10 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes.
15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very
20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following
25 colors indicate a known gene (top to bottom):
red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and
30 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232 . The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give
5 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the
10 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining
15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)
20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
25 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
30 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus
35 presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide
35 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The

peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as
30 the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously
35 been shown to be expressed - the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 13,232) and probe exon (SEQ ID NOs.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring
Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

Page 1 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	6				
912	14087	27162	9.68				
1070	14236		3.01				
1330	14487	27556	10.9				
1645	14787	27882	1.92				
1666	14818	27901	4.94				
1764	14913	28008	1.03				
1788	14937	28030	1.67				
1794	14943	28036	8.63				
1839	15082	28183	1.57				
2034	16175	28285	2.66				
2234	15368	28497	3.39				
2353	15484	28616	2.53				
3255	16429	29447	3.75				
3637	16702	29713	1.48				
3604	16768	29783	10.6				
3651	16814		0.84				
3747	16908	29912	0.98				
4057	17213		0.94				
4314	17457	30446	1.55				
4377	17520	30500	6.88				
4396	17539	30519	0.87				
4396	17539	30520	0.87				
4457	17597		1.69				
4512	17651	30639	0.61				
4958	18088	31094	1.86				
5002	18131		0.6				
5157	18278	31244	5.14				
5166	18290	31255	1.24				
5371	18574	31442	1.78				
5371	18574	31443	1.76				
5636	18735		4.12				
5714	18907		7.26				
5766	18735		3.31				

Page 2 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5858	19048	32354	4.22				
6146	25820	32688	1.61				
6174	19350	32696	1.92				
6548	19708		1.01				
6678	19838	33228	1.25				
6879	19838	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7569	20941	34117	1.18				
7569	20941	34118	1.18				
8251	21333	34851	1.44				
8882	21762	35298	1.14				
9061	22140	35684	0.76				
9061	22140	35685	0.76				
9734	22769	36373	3.82				
9868	23007	36602	0.56				
10096	23124	36725	1.51				
10229	23264	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11280	24346		1.76				
11348	24410	38063	2.79				
11641	24721	38414	1.73				
11749	23835	37561	1.36				
11749	23835	37562	1.36				
11792	24782		2.09				
12057	25038	38746	1.58				
12623	25419		2.06				
12967	25628	31980	1.5				
6177	19853	32700	16.82	9.8E+00 AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18	
8195	21277	34800	1.5	9.8E+00 U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome	
9844	22983	36575	0.48	9.8E+00 Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2	
8944	22983	36576	0.48	9.8E+00 Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2	

Page 3 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10836	23670	37279	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalpr3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalpr1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
10836	23670	37280	0.93	9.6E+00	AF242432.1	NT	Mus musculus Nalpr3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Nalpr1) and general transcription factor 1H1 polypeptide 2 (Gtf2h2) genes, complete cds
2731	15949	25959	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2731	15949	25960	0.97	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M) envelope glycoprotein (E) polyprotein mRNA, partial cds
2990	18168	29182	3.08	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130990.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
7625	20695	34171	0.6	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(5)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-5-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31588	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9830	22685		1	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6160	18336	32681	5.15	8.9E+00	BE871806.1	EST_HUMAN	601851038R1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:3934592 3'
6510	19675	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6510	19675	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
453	13649	26695	1.79	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9654	21097	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21426		0.98	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7501	20576		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8558	21637	35174	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8558	21637	35175	1.42	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700517.1	EST_HUMAN	802128876F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4285508 5'
8953	22032	35573	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35574	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Page 4 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33760	1.07	7.2E+00	BE179090.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7289	20381	33838	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7289	20381	33839	1.22	7.1E+00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9798	22838		9.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11068	24745	38437	2.44	7.1E+00	P05850	SWISSPROT	HYPOPHOSPHATE KINASE (AK)
10187	23224	38818	2.76	7.0E+00	P48810	SWISSPROT	ARGININE KINASE (AK)
11528	24584	38281	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8478	21559	35093	3.17	6.9E+00	P36879	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10569	23584	37200	1.12	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10579	23614	37219	0.6	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
8092	21174	34688	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Scars melanocyte 2N16HM Homo sapiens cDNA clone IMAGE:291860 5'
8092	21174	34689	1.64	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Scars melanocyte 2N16HM Homo sapiens cDNA clone IMAGE:291860 5'
8333	22409		1.62	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEINS VP5 AND VP8
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	HYPOPHOSPHATE KINASE (AK)
5398	18600		0.86	6.8E+00	Q88028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
6875	19834	33223	0.86	6.8E+00	BF672121.1	EST_HUMAN	602152573.F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4293427 5'
9234	28228		0.55	6.8E+00	P51825	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36912	2.14	6.8E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10279	23314	36913	2.14	6.8E+00	Q8ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37496	0.47	6.8E+00	H23330.1	EST_HUMAN	ym60166.s1 Scars infant brain T1B1B Homo sapiens cDNA clone IMAGE:52737 3'
11393	24454		1.48	6.8E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C6C3.05C
9382	22457	36020	7	6.8E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10512	23547	37158	0.52	6.8E+00	BE866001.1	EST_HUMAN	601678435.F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3903969 5'
9843	22982	36574	1.34	6.2E+00	AY010601.1	NT	Schizosaccharomyces commune unknown mRNA
10787	23820	37444	0.7	6.2E+00	6754621	NT	Mus musculus mannose 2, alpha B1 (Man2b1), mRNA
7181	20313	33766	1.6	6.0E+00	BE760163.1	EST_HUMAN	601469031.F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3871303 5'
10021	23059	36655	0.49	6.0E+00	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1165001-1485000 nt, position (617)
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19809	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

Page 5 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11933	24819		3.02	5.9E+00	BE989630.1	EST_HUMAN	601645279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 5'
3613	16777		1.15	5.9E+00	7681567	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20394	33855	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302048.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20803		1.34	5.0E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POL C-TYPE (POL II)
11289	24355	37896	2.03	5.0E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37897	2.03	5.0E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11768	23951	37681	2.52	6.6E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32908	0.74	5.0E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
8982	23021		0.56	5.5E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24087		1.46	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.6E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	35536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7069	20122	35537	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559		1.04	5.4E+00	Q89435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.62	5.4E+00	Q91092	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8999	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8999	22078	35619	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10242	23277	36870	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
10242	23277	36871	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4906	18036	31024	1.47	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6817	19777		0.7	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8270	21352		3.39	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
9184	22832		0.72	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
11928	24914	38616	1.51	5.3E+00	Q27805	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPEPTIDE PRECURSOR
5980	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0891-270400-188-709 HT0891 Homo sapiens cDNA
10583	23618		0.98	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11470	24528		1.93	6.2E+00	Q10138	SWISSPROT	HYPOTHETICAL 81.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
9162	22240	35784	0.94	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
10030	23088	36687	1.33	5.1E+00	P08182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6415	19584	32946	0.74	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10397	23432		0.7	5.0E+00	BF308591.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131508 5'

Page 6 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10845	23879	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24824	38304	7.24	5.0E+00	Z83850.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
10437	23472						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17922		0.78	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8348	21429	34953	12.39	4.8E+00	AF185255.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8738	21817	26550	4.92	4.8E+00	AW750067.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240562.1	EST_HUMAN	PMO-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
301	13517	26550	1.85	4.7E+00	BF240562.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3347	16520	29534	1.02	4.7E+00	AL163280.2	NT	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
7962	21012	34522	0.59	4.6E+00	U87569.1	NT	Homo sapiens chromosome 21 segment HS21C080
9397	22471	36036	1.1	4.6E+00	BE646437.1	EST_HUMAN	Mediaproccoccus jannaschii section 111 of 150 of the complete genome
9397	22471	36037	1.1	4.6E+00	BE646437.1	EST_HUMAN	788g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element;
10800	23835		0.63	4.6E+00	AF240786.1	NT	788g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140 KIAA0645 PROTEIN; contains element PTR5 repetitive element;
7947	20997		0.7	4.5E+00	AF128177.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11804	24892	36593	1.87	4.5E+00	AE001044.1	NT	Issatchenkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
12058	25039	39747	1.53	4.5E+00	BF668941.1	EST_HUMAN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3105	16281	29280	0.84	4.4E+00	BF530893.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3105	16281	29287	0.84	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4216284 5'
8331	19502		1.58	4.4E+00	X13414.1	NT	602072585F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4216284 5'
8245	19419		0.77	4.3E+00	AF059679.1	NT	Murine I gene for MHC class II(Ia) associated invariant chain
7598	20868	34142	2.53	4.3E+00	Y13402.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7792	20948	34341	0.68	4.3E+00	AE001222.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
11101	24174	37809	14.74	4.3E+00	AF240786.1	NT	Treponema pallidum section 38 of 87 of the complete genome
5634	18928		4.1	4.2E+00	P16444	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5711	18904	32199	1.07	4.2E+00	P51826	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-4) (RENAL DIPEPTIDASE) (RDP)
5880	19070		0.71	4.2E+00	O27830	SWISSPROT	LA-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6911	20226	33657	1.87	4.2E+00	P13983	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
							EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

Page 7 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6911	20226	33658	1.87	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22328	35783	5.3	4.2E+00	A1809013.1	EST_HUMAN	w67g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
10122	23160	36756	1.03	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10362	23387		0.47	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT8
7261	20344	33796	0.98	4.1E+00	BE253688.1	EST_HUMAN	60110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7839	20894	34396	7.86	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7860	21010		0.84	4.1E+00	AB041623.1	NT	Palinopeden yessoensis mRNA for calcineurin A, complete cds
7863	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7963	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57603.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
8740	22805	36381	0.81	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22973	36498	2.26	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4333209 5'
10370	23405		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4
10514	23549		0.52	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
11124	24186		2.15	4.1E+00	P08716	SWISSPROT	HYPOTHETICAL PROTEIN HVL1
11214	24283		12.25	4.1E+00	BE886880.1	EST_HUMAN	601607610F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908051 5'
3638	16798		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5675	20130	33546	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5678	20130	33547	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33546	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33547	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7339	20418	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8074	22163	35697	0.49	4.0E+00	Q14157	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10368	23403	37014	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10464	23498	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10464	23499	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37577	1.59	4.0E+00	P14546	SWISSPROT	CYTCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPEPTIDE [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]

Page 8 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.88	4.0E+00	P07594	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS (NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
12133	25113	38917	1.34	4.0E+00	P35611	SWISSPROT	ERYTHROCYTE ADDUCTION ALPHA SUBUNIT
3591	16755	29770	5	3.9E+00	XG4518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4441	17681		0.87	3.9E+00	AF055468.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5775	18967	32270	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5775	18967	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6772	19927	33322	0.93	3.9E+00	AF288209.1	NT	Dicotylellum discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19982	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39286	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
7519	20592	34068	4.26	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4 beta-1) gene, exon 2
8512	21583	35128	2.44	3.9E+00	X65565.1	NT	Xlaevis mRNA for M4 muscularic receptor
11674	23902	37624	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2683	15813		1.53	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6520	19885	33057	1.05	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8827	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9999	23037		0.6	3.8E+00	AJ390361.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7884
12120	25100		11.65	3.8E+00	9631204	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
4128	17282	30277	12.79	3.7E+00	AL161839.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
9378	22454	36017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38450	2.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
12280	25196		1.87	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
608	13795	26814	3.76	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5389	18572	31440	0.78	3.6E+00	BF316310.1	EST_HUMAN	601901866F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4131016 5'
8748	21828	35364	0.86	3.6E+00	D12367.1	EST_HUMAN	HUN000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8749	21828	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUN000TB08 Liver HepG2 cell line. Homo sapiens cDNA clone t808
8847	21826	35464	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome

Page 9 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8847	21928	35495	3.87	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
9864	22804	35498	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9864	22804	35499	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24187		3.21	3.6E+00	M66795.1	NT	Escherichia coli glycerophosphate dehydrogenase (gld) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
3319	19492	29509	1.04	3.5E+00	AF221538.1	NT	Glycoperidium felis heat shock protein 70 (HSP70) gene, partial cds
6123	19302		1	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6341	19511	32868	0.53	3.5E+00	R19745.1	EST_HUMAN	1940c08.r1 Soares infant brain IN1B Homd sapiens cDNA clone IMAGE:34940 5'
8681	21761		0.55	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35551	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
9232	22310	35552	0.99	3.5E+00	AA190998.1	EST_HUMAN	z88b04.s1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
9694	22743	36313	1	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
10739	23772	37383	0.58	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1542	14694	27773	3.81	3.4E+00	AF264577.1	NT	Brassica napus RPB5d mRNA, complete cds
2644	15787	28882	1.07	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7518	20591	34065	2.33	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7880	20692	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955		0.77	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
9274	22350	36901	0.77	3.4E+00	AJ228042.1	NT	Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
9312	22358	35839	0.54	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 8
10471	23508	37119	3.35	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11822	24811	38508	2.06	3.4E+00	L7570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6193	19369	32719	0.97	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6193	19369	32720	0.97	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
8077	21169	34976	1.03	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10681	23715	37321	1.04	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10681	23715	37322	1.04	3.3E+00	AF001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
513	13707	28735	1.79	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene

Page 10 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4136	13707	28735	0.78	3.2E+00	X96422.1	NT	D.reilo zp-50 POU gene
4850	17983	30971	0.95	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5686	18880	32170	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5686	18880	32171	1.16	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	19603	32866	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	19603	32867	1.91	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7781	20837	34330	0.86	3.2E+00	P04276	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7781	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7952	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22308	36369	5.26	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	22795	36369	1.31	3.2E+00	M36383.1	NT	S.cerevisiae threonine deaminase (LVI) gene, complete cds
10345	23380	36991	2.06	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC8 gene for guanylyl cyclase C, complete cds
12219	25169	32503	2.96	3.2E+00	L33838.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5996	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHELTICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7647	20619	34095	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7804	20956		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pale) gene, complete cds
8278	21361	34880	0.51	3.1E+00	P40885	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOETHYRONE DEIODINASE (TYPE 1 5'DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI)
8801	21880	35418	5.14	3.1E+00	P49894	SWISSPROT	TYPE 1 IODOETHYRONE DEIODINASE (TYPE 1 5'DEIODINASE) (DIOI) (TYPE 1 DIO) (5DI)
9459	22575		3.7	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9526	22591	36162	0.55	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10100	23138	36739	0.76	3.1E+00	7524769	NT	Chlorella vulgaris chloroplast, complete genome
10193	23230		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHELTICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10543	23578	37187	4.09	3.1E+00	P49365	SWISSPROT	DEOXYTHYMINE SYNTHASE (DHS)
11751	23937		2.45	3.1E+00	P33516	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11771	24763		2.49	3.1E+00	S56680.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt]
13019	25670		1.17	3.1E+00	U77686.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds

Page 11 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2890	16078	26095	0.95	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18954	31633	1.29	3.0E+00	X53096.1	NT	S. aureus genes encoding Sau86I DNA methyltransferase and Sau86II restriction endonuclease
6686	19844	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6886	19844	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7306	20388		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7348	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.82	3.0E+00	X87838.1	NT	B. rapae DNA for myrosinase
10501	23536	37146	0.56	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE)(ADOMET SYNTHETASE)
11269	24328	37667	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11259	24328	37668	4.96	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11886	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	15208	26324	2.68	2.9E+00	AE002225.2	NT	Chlamydia pneumoniae AR39, section 53 of 84 of the complete genome
7049	20102	33519	1.65	2.9E+00	Z36879.1	NT	F. pingidai gdsPA gene for P-protein of the glycine cleavage system
7360	20439	33889	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33900	4.66	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20684	34160	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	21135	34655	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8052	21135	34656	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE (CONTAINS MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3)
8289	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCI_CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4153059 5'
9438	22512		0.82	2.9E+00	AJ002153.2	NT	Sagittaria edulis gene for seminal vesicle secreted protein semenogelin I
1486	14639	27722	4.77	2.8E+00	AF186396.1	NT	Buxus harlandii malurase K (malK) gene, partial cds; chloroplast gene for chloroplast product
1662	14814		3.14	2.8E+00	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7480	20535	34010	5.05	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9813	22853		0.6	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10928	20535	34010	1.53	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
240	13482	26490	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
240	13482	26491	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5669	18863	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apcA polymorphism Kingle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHSB) gene including complete 5'UTR and complete cds
9168	22248		2.16	2.7E+00	AL118459.1	NT	Boryetia chinensis strain T4 cDNA library under conditions of nitrogen deprivation
9632	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xc88e12x1 NCL CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17793
10718	23751		1.94	2.7E+00	BE083527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4798	17931	30917	5.51	2.6E+00	AF068749.1	NT	CAC-BT0281-03T199-087-h04 BT0281 Homo sapiens cDNA
5685	18859	32143	2.04	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5685	18859	32144	2.04	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5947	19133		2.55	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7727	26220		1.16	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7879	20931		11.26	2.6E+00	AF285052.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
9858	22898	36481	2.85	2.6E+00	AL161540.2	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-83
10583	23598		1.91	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11281	24347	37984	2.2	2.6E+00	AF143675.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12917	26084		3.3	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1492	14643	27726	3.03	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1492	14645	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	19120	32433	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5886	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6868	20020	33429	0.77	2.6E+00	D30052.1	NT	Vibrio cholerae ctxA gene and ctxB gene for cholera toxins, complete cds
7938	20988	34494	1.19	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7995	21034	34547	0.62	2.5E+00	4902802	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9304	22380	35831	1.55	2.5E+00	D50307.1	NT	Rice DNA for adlase C-1, complete cds
10057	23095	36697	0.71	2.5E+00	BE297758.1	EST_HUMAN	801176779F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:3531080 5'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
12216	25167		1.85	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3077	16254	28278	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5072	18158	31134	4.93	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6134	16113	32652	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20811	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20811	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8408	21487		2.8	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8852	21931		1.72	2.4E+00	AW875128.1	EST_HUMAN	RC2.PT0004-031289-011-d05 PT0004 Homo sapiens cDNA
8028	22107	35648	8.99	2.4E+00	P24091	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36876	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36864	2.31	2.4E+00	X62511.1	NT	H.sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P06099	SWISSPROT	XYLULOSE KINASE (XYLULOKINASE)
10528	23563	37169	1.84	2.4E+00	BE326702.1	EST_HUMAN	h63106.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.84	2.4E+00	BE326702.1	EST_HUMAN	h63106.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
11335	24398	38047	1.36	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKO operon and downstream
11940	24720	39413	2.44	2.4E+00	AF158552.2	NT	Fraxia x ananassa cytosolic ascorbate peroxidase (ApxSC) gene. ApxSC-c allele, complete cds
1282	14438	27607	9.98	2.3E+00	Z46724.1	NT	G.domesticus artificial single chain antibody gene [L3]
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5957	19143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYCARBOXYPEPTIDASE
7612	20682	34168	2.75	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Cat++ transporting, ubiquitous (Atp2a3), mRNA
7771	26221		2.37	2.3E+00	P07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
7958	21008	34518	1.28	2.3E+00	X60265.1	NT	M.mazal dnaK and dnaJ genes homologues coding for DnaK and DnaJ
9310	22386	35938	0.52	2.3E+00	5835317	NT	Polyturus ornithinilis mitochondrion, complete genome
9371	22446	36008	1.86	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYL TRANSFERASE (GALACTOSIDE 3-L-FUCOSYL TRANSFERASE)
11041	24120	37763	2.72	2.3E+00	Q07076	SWISSPROT	(FUCOSYL TRANSFERASE 4) (FUCT-IV)
12075	25056	38763	2.14	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
12075	25056	38764	2.14	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12445	25315	32091	7.41	2.3E+00	BE895237.1	EST_HUMAN	601433073F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 5'
4126	17280	30276	1.06	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30553	4.12	2.2E+00	D67071.1	NT	Rat gene for regulacalcin, exon1 (non-coding exon)

Page 14 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4432	17572	30554	4.12	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5458	18658	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5975	19160	32479	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6187	19363	32711	9.39	2.2E+00	BE250383.1	EST_HUMAN	60094340111 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6484	19651	33013	2.87	2.2E+00	Q00336	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18524		3.4	2.2E+00	AA594574.1	EST_HUMAN	nt89502.s1 NCI CGAP Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20545	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	zn9704.11 Stratigene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	zn05g10.r1 Soares_tetal_fetus_N62HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7868	20920	34427	0.86	2.2E+00	P54918	SWISSPROT	ALANINE RACEMASE
8294	21376	34898	0.85	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8294	21376	34897	0.85	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9542	22607		12.49	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9768	26860		2.12	2.2E+00	Q04706	SWISSPROT	TRANSPONSON TY1 PROTEIN A
10259	23294	36890	1.12	2.2E+00	A1260373.1	EST_HUMAN	qm89b03.x1 Soares_placenta_8to9weeks_2NbHP8b9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36891	1.12	2.2E+00	A1260373.1	EST_HUMAN	qm89b03.x1 Soares_placenta_8to9weeks_2NbHP8b9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10673	23707	37315	2.6	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein RGR74 homolog mRNA, complete cds
11728	23912	37536	3.3	2.2E+00	P07811	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	16016	26795	13.2	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449366.1	EST_HUMAN	UIH-B19-akt-e-08-0-UI.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6260	19434		0.97	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6947	20280	33698	3.51	2.1E+00	O70159	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00		NT	Homo sapiens dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYSF) mRNA, and translated products
7191	20056	33466	5.88	2.1E+00	N28575.1	EST_HUMAN	Y08a10.s1 Soares melanocyte 2Nb1M Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M5664
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TF1D (HUMAN);
1223	14393	27444	1.32	2.0E+00	AF180527.1	NT	AU123630 NT2RM2 Homo sapiens cDNA clone NT2RM2000871 5'
1223	14393	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p220kda1 (DOKDEL) mRNA, complete cds
1366	14520	27565	1.37	2.0E+00	AF204927.1	NT	Homo sapiens p220kda1 (DOKDEL) mRNA, complete cds
1606	14758		3.08	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na+K-ATPase beta 1 subunit mRNA, complete cds
2216	16350	28480	7.2	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	15350	28481	7.2	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4216	17365	30353	1.71	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCL_GCAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
4216	17365	30364	1.71	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7722	20786		0.98	2.0E+00	P07566	SWISSPROT	h13c05.x1 NCL_GCAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
8214	21296	34815	4	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
8214	21296	34816	4	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8214	21296	34817	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12815	26022	31670	6.76	2.0E+00		NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
5716	18908	32202	4.28	1.9E+00	6754383	NT	Gallus gallus mitochondrion, complete genome
5715	18908	32203	4.28	1.9E+00	6754380	NT	Mus musculus hsc60l 1,4,5-triphosphate receptor 1 (lbr1), mRNA
6225	19400	32750	1.2	1.9E+00	BE969695.1	EST_HUMAN	Mus musculus hsc60l 1,4,5-triphosphate receptor 1 (lbr1), mRNA
6792	19947		0.82	1.9E+00	AW845688.1	EST_HUMAN	601676636FT NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'
6888	20040		1.91	1.9E+00	Q63627	SWISSPROT	MRO-C10063-071089-002-g02 CT0063 Homo sapiens cDNA
8653	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8653	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8859	21938		3.32	1.9E+00	BF360206.1	EST_HUMAN	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9095	22174		1.86	1.9E+00	O51781	SWISSPROT	CM3-MT0114-010800-323-h12 MT0114 Homo sapiens cDNA
							ARGININE DEMINASE (AD) [ARGININE DIHYDROLASE] (AD)

Page 16 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.8E+00	AA660125.1	EST_HUMAN	ab94a04.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:864574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10790	23823	37447	0.67	1.8E+00	AF248299.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3162	16337	29346	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	29370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	29371	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.8E+00	BF311999.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6528	19692		1.26	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4298272 5'
6879	20031	33441	1.15	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7204	20069	33479	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE- (GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8308	21390	34913	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8308	21390	34914	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9055	22134	35679	2.28	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.78	1.8E+00	R31042.1	EST_HUMAN	yA72508.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9462	22519	36081	0.82	1.8E+00	AW860004.1	EST_HUMAN	QV0-O70030-070300-149-a03 O70030 Homo sapiens cDNA
9886	23034	36826	0.47	1.8E+00	P06828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36994	0.94	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10480	23528		4.71	1.8E+00	AF111849.1	NT	Homo sapiens PRO5530 mRNA, complete cds
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12575	25994		4.97	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12667	28444		6.01	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpct1b) mRNA
13005	25887	31654	1.45	1.8E+00	BF212412.1	EST_HUMAN	60181374F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'
1132	14297	27352	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345	15476	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Page 17 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2446	16573	28702	1.49	1.7E+00	AI141087.1	EST_HUMAN	Q23305.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4581	17718	30701	0.88	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32218	1.73	1.7E+00	BE063546.1	EST_HUMAN	CX40-BT0282-171299-127-e08 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE063546.1	EST_HUMAN	CX40-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6141	19319	32881	3.02	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)
6682	19840	33230	0.87	1.7E+00	P38816	SWISSPROT	(PYRUVATE DEHYDROGENASE (LIPOAMIDE))-PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDP)
7367	20446	33908	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7367	20448	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8222	21304	34825	1.08	1.7E+00	6765713	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Traf1), mRNA
8252	21334	34852	0.81	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Brrd7 Homo sapiens cDNA clone IMAGE:4214669 5'
8739	21818	36352	0.76	1.7E+00	AF246613.1	NT	Hippoglossus hippoglossus Interferon Inducible Mx protein (Mx) mRNA, complete cds
8828	21907		1.63	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8901	21980	35519	0.66	1.7E+00	X68063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8901	21980	35520	0.86	1.7E+00	X68063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35833	1.03	1.7E+00	U19832.1	NT	Rattus norvegicus SA gene, partial cds
9350	25859	35981	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9350	25859	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9808	22846		1	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
10375	23410		0.54	1.7E+00	AW933681.1	EST_HUMAN	EST366761 IMAGE resequences, MAGC Homo sapiens cDNA
10857	23890	37509	0.47	1.7E+00	BE873280.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
10857	23890	37510	0.47	1.7E+00	BE873280.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890484 5'
11886	24884	38582	1.87	1.7E+00	W22424.1	EST_HUMAN	6787 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12523	25356	32066	1.94	1.7E+00	A1678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
2090	15230	28352	19.53	1.6E+00	AF199339.1	NT	MSR1 repetitive element;
2101	15241	28362	4.14	1.6E+00	AF071374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2107	15246	28387	1.28	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2357	15498		0.87	1.6E+00	X88373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
3028	18202	28225	1.22	1.6E+00	W59428.1	EST_HUMAN	B. napus gene encoding endo-polygalacturonase
							z125f01.1 Soares_fetal_heart_NBH118W Homo sapiens cDNA clone IMAGE:341689 5' similar to
							gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);

Page 18 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3857	17017		1.06	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17294		6.05	1.6E+00	BF570077.1	EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17612	30590	1.25	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17612	30591	1.25	1.6E+00	AF155927.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18306	31270	0.59	1.6E+00	AF127897.1	NT	Salmonella enteritidis serovar enteritidis (SBO27) gene, partial cds
5184	18316	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNACIII gene, exon 2
5184	18316	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNACIII gene, exon 2
5948	19134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	19218	32540	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
6598	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-060800-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.6E+00	AW294881.1	EST_HUMAN	U1H-B12-abr-b-04-0-UI s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7364	20472	33938	2.37	1.6E+00	BE907267.1	EST_HUMAN	RC3-CT0415-200700-032-2-10 CT0415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35196	3.3	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35898	0.49	1.6E+00	BE388331.1	EST_HUMAN	601283925F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9659	25957	34615	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9659	25957	34616	1.05	1.6E+00	X52046.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermotoga maritima D-xylose-binding protein (xyf) gene, complete cds
9935	22974	36566	1.49	1.6E+00	T41290.1	EST_HUMAN	ph866_191TV Outward Alu-primered hncDNA library Homo sapiens cDNA
10388	23423	37029	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-060200-100-d07 LT0016 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-060200-100-d07 LT0016 Homo sapiens cDNA
10552	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37726	1.77	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
11082	19218	32540	4.8	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
12006	24991	38695	3.68	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	26275	2.95	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
241	13463	28492	2.44	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
636	13821		1.81	1.6E+00	6752961	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metagidin) (Adam15), mRNA
2481	15608	28732	1.56	1.5E+00	AJ11402.1	NT	Potato virus A RNA complete genome, isolate U
2584	15709	28828	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3208	16608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3462	16628	28649	0.77	1.5E+00	AE001945.1	NT	Deltococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5846	19036	32342	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1;
5846	19036	32343	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1;
6538	19699	33072	2.43	1.5E+00	R17878.1	EST_HUMAN	tp10e02.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 5'
7278	20361	33853	1.68	1.5E+00	BE786396.1	EST_HUMAN	tp10e02.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 5'
7311	20393	33853	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	ak26f10.s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
7768	20826	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	an07b11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to gbs:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN).
8313	21395	34920	0.9	1.5E+00	BE887446.1	EST_HUMAN	gbs:S95936 SEROTRANSFERRIN PRECURSOR (HUMAN).
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
8848	21925	35483	1.09	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
9218	22298		0.48	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9334	22410	35983	0.81	1.5E+00	BF217818.1	EST_HUMAN	601882862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9684	22733	36303	0.85	1.5E+00	R81928.1	EST_HUMAN	yj03f01.f1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9835	22875	36459	1.8	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261099-008-409 CTO192 Homo sapiens cDNA
10064	23102	36705	6.49	1.5E+00	BF376754.1	EST_HUMAN	RCO-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10268	23283		1.86	1.5E+00	BF337874.1	EST_HUMAN	60203577F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37040	2.26	1.5E+00	AA017689.1	EST_HUMAN	zs38g06.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	zs38g06.r1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361308 5'
11684	24683	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hbrt1) Homo sapiens cDNA clone DKFZp547P243 3'
11834	24823		7.68	1.5E+00	X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11829	24915	38617	1.39	1.5E+00	AI400788.1	EST_HUMAN	tp94d09.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
11829	24915	38618	1.39	1.5E+00	AI400788.1	EST_HUMAN	tp94d09.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12616	26095	31662	1.61	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12765	25508		3.92	1.5E+00	AI445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
12888	25589		2.17	1.5E+00	6978492	NT	Rattus norvegicus 5 - Lipoxygenase (ALOX5), mRNA
13220	25784	31888	1.31	1.5E+00	BF223835.1	EST_HUMAN	7q82b06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3'
30	13268	26271	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
30	13268	26272	2.27	1.4E+00	7661686	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.97	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
2411	15541		8.39	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds
2734	15851	28984	1.7	1.4E+00	X74483.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16883		0.79	1.4E+00	5463733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30493	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4370	17513	30494	1.13	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4287556 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5488	18887	31705	1.73	1.4E+00	AW054876.1	EST_HUMAN	w45g07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5645	18839		8.04	1.4E+00	AB032883.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32839	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
8424	28214		3.93	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6581	20189	33614	0.8	1.4E+00	AW83057.1	EST_HUMAN	GM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133269.1	NT	Homo sapiens cavedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7454	20531	34005	1.14	1.4E+00	AW467760.1	EST_HUMAN	ha23f05.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element
7514	20588	34052	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
7514	20588	34053	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
8530	21611		0.72	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8994	22073		5.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9295	22371	35920	1.65	1.4E+00	R20459.1	EST_HUMAN	yg33112.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9308	22472	36038	3.83	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9432	22506	36072	0.95	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4288137 5'
10457	23492	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291098-008-C04 HT0198 Homo sapiens cDNA
10457	23492	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291098-008-C04 HT0198 Homo sapiens cDNA

Page 21 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.96	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23955	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11489	24557	38232	4.52	1.4E+00	AB006862.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11691	24689	38379	3.46	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24689	38380	3.46	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.99	1.4E+00	11545838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen s970-2 (SE70-2), mRNA
684	13775		1.96	1.3E+00	Z73610.1	NT	M. musculo gene encoding 4-Dihydroxyethyl-hispirate dehydrogenase
925	14100	27104	2.79	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative palHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27549	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27550	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14542		0.98	1.3E+00	U61730.2	NT	Cox laetyma-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1641	14783		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2316	19448		2.38	1.3E+00	AB030447.1	NT	Cyrtinus carpio MRPs and MASPs genes for mannose-binding lectin-associated serine protease (MASP)
2615	16739		1.81	1.3E+00	BE968735.2	EST_HUMAN	end MASPs-related protein, complete cds
3005	16180	29201	0.86	1.3E+00	6756521	NT	Mus musculus alpha-spectrin 1, erythroid (Sptn1), mRNA
3886	16849	29857	1.14	1.3E+00	AF010404.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
5631	18626	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOXYGENASE P3 COMPONENT)
5827	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-108 C70289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-108 C70289 Homo sapiens cDNA
6947	19709	33085	1.14	1.3E+00	M33496.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6890	20042		0.71	1.3E+00	Q00166	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
7092	20186	33910	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'
7249	20332	33779	0.96	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pie-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7616	20686	34162	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21576	35112	1.78	1.3E+00	AI009912.1	NT	Sus scrofa plp gene
8642	21722	35259	2.28	1.3E+00	BE963379.2	EST_HUMAN	601657149R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3666195 3'
8758	21837	35378	1.05	1.3E+00	BE974280.1	EST_HUMAN	601660250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21988		1.87	1.3E+00	6910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22069	35609	0.89	1.3E+00	AI927629.1	EST_HUMAN	ws85a07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35978	0.51	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Scores breast 3NbrHst Homo sapiens cDNA clone IMAGE:183076 3'
9347	22423	35977	0.51	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Scores breast 3NbrHst Homo sapiens cDNA clone IMAGE:183076 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S. alba phr-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF089250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	ws03f03.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2628477 3' similar to gb:U31922
9871	22911	36496					TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9871	22911	36496					LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9952	22991	36584	1.65	1.3E+00	O00754	SWISSPROT	ALPHA-MANNOSIDASE (LAMAN)
10031	23069	36668	1.21	1.3E+00	AI927629.1	EST_HUMAN	ws85a07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23069	36668	0.68	1.3E+00	AJ223962.1	NT	Lactobacillus lactis ctenorhis NCDO-inv1 chromosomal inversion junction DNA
10031	23069	36669	0.68	1.3E+00	AJ223962.1	NT	Lactobacillus lactis ctenorhis NCDO-inv1 chromosomal inversion junction DNA
10070	23108	36711	3.93	1.3E+00	BE963379.2	EST_HUMAN	601657149R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3666195 3'
10130	23168		0.57	1.3E+00	AI559644.1	EST_HUMAN	lq77a12.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723
10353	23388	36996	0.5	1.3E+00	AF061251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10353	23388	36997	0.5	1.3E+00	AF061251.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Escherichia coli serotype O157:H7 O antigen gene cluster
10435	23470	37076	1.59	1.3E+00	IM28953.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10811	23844		0.99	1.3E+00	AI163302.2	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10838	23871	37493	0.47	1.3E+00	AI990846.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C102
10851	23894		0.53	1.3E+00	8923637	NT	ws32a10.x1 NCI CGAP_GC08 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
							Q16881 THIOREDOXIN REDUCTASE ;
							Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

Page 23 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37806	0.46	1.3E+00	7948159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37807	0.46	1.3E+00	7948159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10881	23894	37515	0.45	1.3E+00	H42881.1	EST_HUMAN	yo88c03.at Sceres breast 3Nb-HBt Homo sapiens cDNA clone IMAGE:183076 3'
10881	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	yo88c03.at Sceres breast 3Nb-HBt Homo sapiens cDNA clone IMAGE:183076 3'
10832	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11189	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	xp08c03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738868 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11923	24909	38610	2.28	1.3E+00	Z88682.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment
11894	24978		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3-ketacyl-acyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	502023185F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4158462 5'
12707	25688		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	AF187035.1	NT	Stromal lumen cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U38978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxyphenyl dioxygenase (bphCII) gene, complete cds
13231	25981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
667	13653	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	z122a08.s1 Sceres_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:431635 3'
846	14024	27082	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
846	14024	27083	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
846	14024	27084	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
901	14076		1.21	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1187	14348	27407	7.9	1.2E+00	AF080245.2	NT	Eleis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27453	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27454	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2066	15207	28323	1.02	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3179	16354	29339	1.06	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	29421	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	29422	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.57	1.2E+00	P54810	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	28625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16964	28987	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0176-050800-203-g06_1 FT0175 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16605	29625	1.06	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4504	17731		1.91	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4645	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30805	2.03	1.2E+00	AF156485.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T. pinnastrum chloroplast rbcL gene, partial
5554	18751	31788	1.13	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18866	32152	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0161-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.55	1.2E+00	X81879.1	NT	Calicivirus cDNA for orf1, orf2 and orf3
5995	19180	32502	0.77	1.2E+00	AF016032.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6280	19454	32802	2.45	1.2E+00	X74885.1	NT	D.hydrel aryl repeat cluster DNA, fragment D
6342	19512	32869	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6420	19568	32853	1.28	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6420	19569	32954	1.28	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene
6463	19630	32991	36.08	1.2E+00	AA759254.1	EST_HUMAN	af84g12.s1 Scores_testis_NHT Homo sapiens cDNA clone 1322374.3'
							w39b12.s1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273599 3' similar to
6566	19726	33105	0.73	1.2E+00	N83295.1	EST_HUMAN	gb M87935 HUMAAU472 Human carcinoma cell-derived Alu RNA transcript. (RNA); gb:J04970
6630	19780	33178	0.62	1.2E+00	P17671	SWISSPROT	CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6634	19783	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	ECDYSONE-INDUCIBLE PROTEIN E75-A
7055	20108	33924	1.72	1.2E+00	AB028010.1	NT	MR3-ST0161-140200-013-c05 ST0191 Homo sapiens cDNA
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
							Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	zq3805.t1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to
7403	20481		0.71	1.2E+00	AJ271735.1	NT	gb D10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
7542	25847	34092	1.85	1.2E+00	AV734585.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
7628	20883	34385	2.91	1.2E+00	X74207.1	NT	AV734585 cDNA Homo sapiens cDNA clone cDAAFH03 5'
7897	21047	34560	0.6	1.2E+00	BE787646.1	EST_HUMAN	L. lactis pyrD and pyrF genes
8767	21846	35387	3.19	1.2E+00	AB033030.1	NT	601481761F1 NIH_MGC. 68 Homo sapiens cDNA clone IMAGE:3984270 5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA, ALPHA-TREHALOSE PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT
							(TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE
							GLUCOSYLTRANSFERASE)
8863	21842	35477	0.82	1.2E+00	P38427	SWISSPROT	Homo sapiens CGI-30 protein (LOC51611). mRNA
9077	22156		0.7	1.2E+00	7706271	NT	MR2-GT0222-201089-001-e07 GT0222 Homo sapiens cDNA
9226	22304	35847	1.81	1.2E+00	AW37210.1	EST_HUMAN	Yq80a06.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202066 5'
9440	22514	36078	0.61	1.2E+00	H48599.1	EST_HUMAN	

Page 25 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9508	22653	36224	3.79	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HUMHMTA01 Liver HepG2 cell line, Homo sapiens cDNA clone hm01a01
10135	23173	36771	3.6	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10532	23567		0.82	1.2E+00	AB009669.1	NT	Homo sapiens Klotho gene, exon 1
11432	24493	38158	1.69	1.2E+00	M38686.1	NT	Mus musculus Id gene, exon 1
11627	24707	38400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PINO-ST0284-161199-001-d01 ST0284 Homo sapiens cDNA
11666	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37556	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25081	38788	1.68	1.2E+00	M10408.1	NT	Malva mitochondrial F-O-A1Pase proteolipid (subunit 9) gene
12471	25984	31768	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001516.1	NT	Bacillus halodurans genomic DNA, section 9/14
13218	25793		2.66	1.2E+00	AA077609.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
476	13671	26703	1.11	1.1E+00	D86880.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW995383.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575889.1	EST_HUMAN	UHF-BR0-p-aj-f-02-0-UI at NIH_MGC 52 Homo sapiens cDNA clone IMAGE:3074834 3'
2077	16157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29595	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3875	16740	29557	1.02	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3870	16833	29844					wf54h11.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3812	16972	29974	0.99	1.1E+00	AB08360.1	EST_HUMAN	SW.P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3812	16972	29974	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3812	16972	29975	1.16	1.1E+00	AE003886.1	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4054	17210	30220	1.03	1.1E+00	8922841	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4130	17283	30278	0.72	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4331	17474		6.82	1.1E+00	5835331	NT	R. unicomis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5180	18302	31265	2.06	1.1E+00	X78426.1	NT	E. faecalis pfp5 gene
5422	18623	31598	1.49	1.1E+00	6978630	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18924	32218	14.33	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3825635 3'
5760	18942	32243	1.32	1.1E+00	AT138582.1	EST_HUMAN	q885c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736260 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
6404	19573	32935	0.59	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6537	19700	33073	0.72	1.1E+00	R08037.1	EST_HUMAN	ye8903.r1 Soares fetal liver spleen TNF α Homo sapiens cDNA clone IMAGE:124924 5'
6858	20009	33419	0.78	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7447	20524	33997	0.58	1.1E+00	X55981.1	NT	Melze mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.87	1.1E+00	BF683714.1	EST_HUMAN	602138978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20726	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20728	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.35	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11967980	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2), mRNA
8326	21407	34934	3.2	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246828 5'
8416	21497	35029	0.91	1.1E+00	AJ478339.1	EST_HUMAN	hm39ht11.x1 NC1_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160548 3'
8635	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
9015	22094	35634	0.87	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375
9126	22205	35748	0.53	1.1E+00	AJ079946.1	EST_HUMAN	0234405.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080	36348	0.75	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9828	22668	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Smx gene)
9883	22823		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9974	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10038	23078	36676	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10141	23179	36777	4.09	1.1E+00	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10719	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23864	37486	0.56	1.1E+00	AJ878921.1	EST_HUMAN	au51c11.v1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518282 5' similar to gb:D10522
10856	23970	37600	1.97	1.1E+00	11067364	NT	Human mRNA for 80K-L protein, complete cds. (HUMAN); Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
10947	24029		3.14	1.1E+00	AF068942.1	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11343	24408	38055	3.72	1.1E+00	L16877.1	NT	Homo sapiens cytochrome P450C9 (CYP2C9) gene, 5' flank and exon 1
11351	18486		2.74	1.1E+00	8622973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

Page 27 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11388	24427	38083	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11389	24427	38084	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	38409	3.99	1.1E+00	AB09699.1	EST_HUMAN	w78611.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381948 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312		1.82	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12547	26371	32070	3.56	1.1E+00	AF216698.1	NT	Taenia solium Immunogenic protein Ts78 mRNA, partial cds
12689	25980		1.86	1.1E+00	AF234169.1	NT	Dictyostellum discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
116	13347	26374	2.1	1.0E+00	D89425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021684.1	NT	Mareharitia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13781	26800	1.44	1.0E+00	AJ291690.1	NT	Girardinia tigrina mRNA for homeodomain transcription factor (co gene)
594	13877	26910	7.14	1.0E+00	AL193218.2	NT	Homo sapiens chromosome 21 segment HS21C018
596	13879		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti muscle-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V.carbali Algal-CAM mRNA
1795	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	15679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	15679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.95	1.0E+00	AA628453.1	EST_HUMAN	af28908.s1 Soares_t04a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WIP:C42D8.3 CE04204, contains element MER22 MER22 repetitive element;
2640	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2640	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.95	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C9F12.08C IN CHROMOSOME 1
3289	16443	26463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af28908.s1 Soares_t04a_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WIP:C42D8.3 CE04204, contains element MER22 MER22 repetitive element;
3459	16526		0.73	1.0E+00	AF222761.1	NT	Rattus norvegicus neurotrophin U precursor (NtnU) gene, exons 5 and 6
3688	13337		0.75	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.61	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase

Page 28 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4180	17930	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17533		0.72	1.0E+00	8822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31568	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 8
8241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
8248	19422	32768	1.67	1.0E+00	AW452782.1	EST_HUMAN	UIH-B18-abx-d-08-o-UI-s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
8618	19778	33167	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
8871	19830	33219	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PAZG4) gene, exons 2 through 5
8767	19823		1.07	1.0E+00	P46506	SWISSPROT	SFR-11 PROTEIN
6795	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:388382 5'
6795	19950	33350	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:388382 5'
6916	20231	33684	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding veloxopisin
7288	20371	33826	1.15	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7647	20716		9.68	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7889	20941	34447	1.51	1.0E+00	AF192831.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7903	20955	34462	6.02	1.0E+00	AA775191.1	EST_HUMAN	ac79b08.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:888791 3'
8019	21070		0.72	1.0E+00	BF679213.1	EST_HUMAN	802163792F1 NIH_MGC_B3 Homo sapiens cDNA clone IMAGE:4294727 5'
8148	21230	34749	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8148	21230	34750	1.65	1.0E+00	BE868267.1	EST_HUMAN	601443950F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848005 5'
8335	18495		1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21626	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

Page 29 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8672	21762		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21788	35321	0.64	1.0E+00	Q9V6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8708	21788	35322	0.64	1.0E+00	Q9V6T6	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8735	26858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC14-HT0228-181089-011-e06 HT0228 Homo sapiens cDNA
8776	21855	35387	1.15	1.0E+00	U427720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes. >
8922	22001	35640	1.8	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9471	22528	36081	1.95	1.0E+00	BE907592.1	EST_HUMAN	601497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889421 5'
9682	22731	36301	1.62	1.0E+00	6753428	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9682	22731	36302	1.82	1.0E+00	6753428	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9810	22850	36426	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GK Homo sapiens cDNA clone GKCCYA11 5'
9815	22855	36434	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9815	22855	36436	1.32	1.0E+00	U44982.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10318	23353	36981	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBEF) mRNA
10318	23353	36982	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBEF) mRNA
10408	23443	37053	0.69	1.0E+00	A077920.1	EST_HUMAN	cy15d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1965901 3'
10533	23568	37176	3.99	1.0E+00	AV758825.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW004 5'
10694	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428608 5'
10694	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428608 5'
10726	23761	37368	1.22	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37924	1.37	1.0E+00	S90825.1	NT	PBR1-proline-rich protein (ntn3) [human, Genomic, 898 nt]
11342	24405	38054	1.46	1.0E+00	AA701494.1	EST_HUMAN	zh33b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element;
11825	24814		1.62	1.0E+00	L47613.1	NT	Pleca glauca EMB13 mRNA
12328	25238		5.49	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12876	25451		2.67	1.0E+00	AW976184.1	EST_HUMAN	EST388263 MAGE resequences, MAGN Homo sapiens cDNA
3693	16855		1.04	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
6752	18944	32246	9.8	9.9E-01	P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN

Page 30 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5990	19175	32496	0.83	9.9E-01	Q09632	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9461	22518		1.68	9.9E-01	U66667.1	NT	Lycopodium esculentum putative Mt1 copy 1 nematode-resistance gene
8755	22693		2.14	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26763	1.17	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2862	15976		1.29	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3903	17062	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17062	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7623	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7623	20878	34379	1.14	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21995	35534	0.94	9.8E-01	P38662	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23687		1.02	9.8E-01	AA825565.1	EST_HUMAN	cd55404.6t NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110288F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110288F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRT1), CDM protein (CDM), adrenoleukodystrophy protein >
7309	20391	33851	2.73	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.9	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.54	9.7E-01	M80544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35661	0.73	9.7E-01	BE789822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.56	9.7E-01	BF511209.1	EST_HUMAN	U1H.B14-act-e-07-QJL1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25789		3.17	9.7E-01	AL114281.1	NT	Bolitis chereia strain T4 cDNA library under conditions of nitrogen deprivation
4558	17696	30675	0.74	9.6E-01	AF197925.1	NT	Bicinus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17696	30676	0.74	9.6E-01	AF197925.1	NT	Bicinus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.6E-01	AF197925.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5872	19062	32360	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5872	19062	32370	3.51	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6886	20038	33447	0.6	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7612	20588	34059	0.83	9.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8588	21687		1.52	9.6E-01	X98275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
9052	22131	35875	0.92	9.6E-01	B1138.1	NT	Rattus norvegicus (strain R21) Rps2 gene, complete cds
11348	24408	38080	1.42	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein e4 Y isoform gene, complete cds
11808	24788	38496	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	38497	3.91	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
12226	25174		1.31	9.6E-01	11421722	NT	Homo sapiens centromere protein 2 (CEP2), mRNA
12916	26061	31668	1.88	9.6E-01	U91423.1	NT	Sphynx liburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15670	28794	1.81	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
3882	17041	30038	2.1	9.5E-01	BE002340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	9.6E-01	BE002340.1	EST_HUMAN	601675639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35819	0.71	9.5E-01	A1160162.1	EST_HUMAN	q57007.1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9308	22382	35933	1.04	9.5E-01	AW881102.1	EST_HUMAN	RC1-CT0286-241189-011-b02 CT0285 Homo sapiens cDNA
11520	24576	38254	1.56	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37648	1.57	9.6E-01	AW293789.1	EST_HUMAN	UI-H-B12-ahp-4-03-0-JJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16446		5.72	9.4E-01	AF165900.1	NT	Barotalla claudigase RNA polymerase beta subunit (pob) gene, partial cds
3289	19463		2.17	9.4E-01	AF080695.1	NT	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
9068	22146	35682	0.79	9.4E-01	M90724.1	NT	Human Fe-gamma-receptor/IL4 (FCGR2A) gene, exon 4
12498	28343		1.86	9.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3869828 5'
12914	28975		1.4	9.4E-01	11419887	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1769	14919		1.24	9.3E-01	AF242382.1	NT	Homo sapiens phytoacyl-CoA hydroxylase (PHYH) gene, exon 5
2689	18818	28834	3.62	9.3E-01	BE071172.1	EST_HUMAN	RCS-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4148	17298	30289	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4148	17298	30290	0.86	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5709	18802	32197	1.6	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18986	32289	3.48	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7488	20561		1.08	9.3E-01	AF270848.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	9.3E-01	AA847040.1	EST_HUMAN	oe09E03.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
9013	22092		1.1	9.3E-01	AF081981.1	NT	Xenopus laevis CCCH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35780	0.89	9.3E-01	AL161634.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

Page 32 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	25683	31961	2.09	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (IPR2), mRNA
13049	25688		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein pL34 mRNA, complete cds
3311	18484	29505	3.92	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4899	18128		0.61	9.2E-01	BF129973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	18025		1.58	9.2E-01	7103410	NT	Mus musculus scute carrier family 30 (zinc transporter), member 4 (Sc30a4), mRNA
6109	19289	32824	4.97	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3664661 5'
6770	18925	33320	0.65	9.2E-01	M64703.1	NT	N. crassa val1-rRNA synthetase (cyt-20/un-3) gene
9880	22900	36484	0.98	9.2E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22988	36582	1.31	9.2E-01	6671677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10627	23661	37269	1.84	9.2E-01	BF563251.1	EST_HUMAN	7c58e06.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW-NU6M_TRYBB
10883	23967	37696	1.76	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714 5'
1854	14807	27892	1.52	9.1E-01	T96675.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2193	15328		1.49	9.1E-01	8923056	NT	ye52701.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
3275	16449	29468	1.28	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3275	16449	29469	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6298	19469	32824	1.54	9.1E-01	L36033.1	NT	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6935	19794	33183	3.25	9.1E-01	Q61704	SWISSPROT	Human pre-B cell stimulating factor homologous (SDF1b) mRNA, complete cds
7750	20810	34300	17.46	9.1E-01	AA06823.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7916	20967	34473	2.81	9.1E-01	U72993.1	NT	db77g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338882 3'
10379	23414	37023	0.8	9.1E-01	P38432	SWISSPROT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
12595	26054		19.67	9.1E-01	AF050113.1	NT	P80-COLIN
3277	16451	29472	0.8	9.0E-01	7651628	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3439	16807		0.73	9.0E-01	AL161515.2	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4219	17368	30857	0.68	9.0E-01	8622310	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4498	17638	30820	1.43	9.0E-01	AF099810.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
5127	18252	31218	13.05	9.0E-01	AF017729.1	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
7561	20823	34100	0.82	9.0E-01	L42547.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
7579	20651		1.42	9.0E-01	D38621.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
							Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
							Xenopus laevis gene for aldolase, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9540	22614	35183	0.68	9.0E-01	AF068761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
10035	23073	36673	0.48	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; IPHLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5ar) gene, complete cds
5814	18004	32309	2.6	8.9E-01	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6378	19547	32309	1.28	8.9E-01	AF028198.1	NT	Rabbit MHC fragment RLA-DF DNA
6590	25827	33134	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086216 5'
6590	25827	33135	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086216 5'
8821	21701	35237	0.92	8.9E-01	AF250667.1	NT	Olfonase nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
12080	26080	38766	2.72	8.9E-01	AE003944.1	NT	Xylella fastidiosa, section 80 of 229 of the complete genome
12423	26300	37086	4.02	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AF39, section 21 of 94 of the complete genome
4664	17799	30786	2.11	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
5489	18688	31708	0.86	8.8E-01	AF310617.1	NT	Pseudorabies virus Ea glycoprotein M gene, complete cds
7701	20766	34250	0.69	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	26072	38776	7.56	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
12240	26158	36158	2.13	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
477	13672	26704	2	8.7E-01	AF106953.2	NT	Homo sapiens SOST (SOST) gene, partial cds
2475	15602	26727	0.98	8.7E-01	5801893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2838	16115	26127	5.32	8.7E-01	AA698863.1	EST_HUMAN	nm05111.s1 NCL_CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
5120	18245		4.12	8.7E-01	AF121870.1	NT	Pseudomonas aeruginosa lipodermase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
8229	21311	34631	0.66	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9130	22209	35762	0.66	8.7E-01	A1239456.1	EST_HUMAN	q336006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9130	22209	35763	0.66	8.7E-01	A1239456.1	EST_HUMAN	q336006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9839	22978	36569	2.07	8.7E-01	AE004863.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10511	23546	37166	1.08	8.7E-01	BF570199.1	EST_HUMAN	60218541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'

Page 34 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'
11070	24145	37782	5.87	8.7E-01	BF368970.1	EST_HUMAN	QV04-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:4043564 3'
12034	25017	38721	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 G1C Homo sapiens cDNA clone GLOCYG07 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGFBP gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W60089.1	EST_HUMAN	z444603.1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16871	29875	0.95	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3901	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S76772.1	NT	polyprotein (Coxsackie B4 virus CB4, host=mouse, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt)
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Gus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7696	20761		0.94	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 69 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34834	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
8887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12896	25883		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15635		1.46	8.5E-01	AJ011824.1	NT	Arabidopsis thaliana (ecotype Columbia) spl2 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7894	20759	34243	2.36	8.5E-01	BE542812.1	EST_HUMAN	601087107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
8180	21262	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8613	21693	36230	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06801	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35315	0.68	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10558	23593	37198	1.49	8.5E-01	AB006799.1	NT	Cyandium caldarium gene for SlgC, complete cds
10558	23593	37199	1.49	8.5E-01	AB006799.1	NT	Cyandium caldarium gene for SlgC, complete cds
12577	26056		5.28	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30989	0.68	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome

Page 35 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	AF051142.1	NT	Manesira brassicae pheromone binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssal complete genome, segment 5/6
760	13941	26986	2.17	8.3E-01	M89437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and cycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y18177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
6383	18685	31464	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AJ781952.1	EST_HUMAN	nm011212, y5 NCLCGAP_Cos Homo sapiens cDNA clone IMAGE:1078495 9' similar to contains THR.11 THR repetitive element;
10316	23351	36956	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster List1 homolog mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-44 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283408 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	8.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	16249	28368	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2156	16292		1.32	8.2E-01	AF148589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
2744	19861		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0218-161199-031-C08 CT0218 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
4247	17393	30381	0.7	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
5217	18336	31311	1.19	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6781	19836	33332	0.99	8.2E-01	X86283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6781	19836	33333	0.99	8.2E-01	X86283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6913	20228	33661	0.76	8.2E-01	AJ010142.1	NT	Arenaria muscaria mRNA for SCH25 protein
7037	20173	33695	3.19	8.2E-01	AW378433.1	EST_HUMAN	GM4-HT0243-081189-037-e01 HT0243 Homo sapiens cDNA
7419	28844	33966	4.48	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35266	0.55	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23266	36858	0.81	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
10284	23299	36897	1.51	8.2E-01	AF052859.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

Page 38 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10428	23463	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23463	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10596	23631	37239	3.78	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN-BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10598	23631	37240	3.78	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN-BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11942	24928	38631	4.72	8.2E-01	L10127.1	NT	Maduscum contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013	38716	6.12	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87388.1	EST_HUMAN	yw14d02.71 Soares_placenta_8to9weeks_ZNbl-IP8to9W Homo sapiens cDNA clone IMAGE:252185.5'
12607	25408	32046	3.01	8.2E-01	AJ001281.1	NT	similar to gb:M56072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2817	15931		1.38	8.1E-01	AF181839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3547	18712	29723	2.77	8.1E-01	AF050066.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	18712	29724	2.77	8.1E-01	AF050066.1	NT	Homo sapiens MHC class I region
4730	17865	30847	0.63	8.1E-01	4606280	NT	Homo sapiens MHC class I region
5826	19015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6445	18612	32875	0.89	8.1E-01	U16780.1	NT	(MELANOCORTIN-1 RECEPTOR)
6759	18915	33309	2.17	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6759	18915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7681	20746	34227	0.7	8.1E-01	Q47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							CYTOTOCHROME B
8095	21177	34893	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8095	21177	34694	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8808	21887	35428	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8808	21887	35429	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8969	22048	35591	1.14	8.1E-01	AW242647.1	EST_HUMAN	element
10330	23365	36974	0.58	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
10623	23667	37287	0.52	8.1E-01	N84541.1	EST_HUMAN	KX9572F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KX9872 5' similar to EST(C-ONE C-ONE11)
10759	23902		0.54	8.1E-01	AE001226.1	NT	Treponema pallidum section 42 of 87 of the complete genome

Page 37 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24764	38469	2.62	8.1E-01	BE93858.1	EST_HUMAN	RCO-TN0080-220800-025-010 TN0080 Homo sapiens cDNA
11772	24764	38460	2.62	8.1E-01	BE93858.1	EST_HUMAN	RCO-TN0080-220800-025-010 TN0080 Homo sapiens cDNA
12303	26221	32102	2.22	8.1E-01	AE001711.1	NT	Thermoplasma maritima section 23 of 136 of the complete genome
181	13404		2.62	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 16
299	13516	26549	10.2	8.0E-01	AJ132772.1	NT	Bos taurus fib and rlf genes
2093	15233		1.95	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NOI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215031 5'
3146	16322	28334	1.32	8.0E-01	AF127807.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3387	16557	28672	1.29	8.0E-01	AB008163.1	NT	Mus musculus gene for oxiductal glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	X83739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5096	18224	31186	1	8.0E-01		NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21261		2.66	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-006 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3'
10636	23669		0.48	8.0E-01	BE833329.1	EST_HUMAN	QV3-OT0065-280600-250-008 OT0065 Homo sapiens cDNA
10827	23660	37485	0.48	8.0E-01	AB046697.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11198	24267	37902	1.43	8.0E-01	Q82783	SWISSPROT	CREB-BINDING PROTEIN
468	13681	26697	0.75	7.9E-01	D11476.1	NT	Lymantria dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1635	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1897	14839		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	16468	28603	9.03	7.9E-01	AB004816.1	NT	Oryzodagus curticulcus mRNA for mitsugumin26, complete cds
2338	16469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3806	16769	28784	3.57	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4416	17557		0.87	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4734	17669	30862	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4734	17669	30853	0.84	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.68	7.9E-01	Z47210.1	NT	Mus musculus embigin homolog (Drosophila) (Enh), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5235	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.66	7.9E-01	AF139718.1	NT	Chryseomya bezziana peritrophin-48 precursor, gene, complete cds
8476	19642	33003	0.66	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34903	2.66	7.9E-01	X80998.1	NT	P. sativum GR gene
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10255	23290	36687	5.43	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10296	23331	36634	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thiamnose reductase, complete cds
10845	23878	37498	0.81	7.9E-01	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	36218	1.94	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
889	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2349	15480	28612	6.99	7.8E-01	AW959597.1	EST_HUMAN	EST371637 MAGE resequences, MAGF Homo sapiens cDNA
4823	17956	30942	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6194	19370	32721	2.26	7.8E-01	AF116856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-9 PRECURSOR (IL-9) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6591	19751	33136	0.84	7.8E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8688	21788	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	7154405.x1 Soares_NSF_F8_3W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176.3
9434	22508	36074	1.53	7.8E-01	Y10159.1	NT	D discoideum racGAP gene
9533	22598	36170	0.56	7.8E-01	4828873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10328	23364		1.28	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.92	7.8E-01	L29280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACSE5) gene, complete cds
146	13371	26403	5.78	7.7E-01	AF184945.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
744	13925		1.72	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Aelpha) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II>
2776	15692	29003	1.34	7.7E-01	O38916	SWISSPROT	CITRATE SYNTHASE
3438	16806		0.89	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine polypeptide N-acetyl-galactosaminyltransferase 7 (GalNAc-T7) (GALNAc-T7), mRNA
3689	16851	29859	3.66	7.7E-01	AF118085.1	NT	Homo sapiens PRO1976 mRNA, complete cds
4516	17655	30643	3.38	7.7E-01	AF199488.1	NT	Coltux coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17655	30644	3.38	7.7E-01	AF199488.1	NT	Coltux coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5078	18872	32159	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5078	18872	32160	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08600.1	EST_HUMAN	y24902.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127765.3
10049	23087	36689	0.68	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		7.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome

Page 39 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	19399	32748	5.26	7.6E-01	AF069510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6647	19808	33193	0.66	7.6E-01	P31938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6990	18509	31501	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14612.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6990	18509	31526	0.74	7.6E-01	AI253399.1	EST_HUMAN	ac14612.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7198	20081	33472	0.84	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.6E-01	AF148793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; IphLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8318	21400	34824	2.38	7.6E-01	6857782	NT	Mus musculus advinin (Advin-pending), mRNA
8318	21400	34825	2.38	7.6E-01	6857782	NT	Mus musculus advinin (Advin-pending), mRNA
8520	21601	35137	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.6E-01	Q01098	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9167	22246	35789	1.33	7.6E-01	6753577	NT	RECEPTOR SUBTYPE 2C (NR2C) (NMDAR2C)
9478	22536	36100	5.24	7.6E-01	P30372	SWISSPROT	Mus musculus cytochrome P450, 2b8, phenobarbital inducible, type a (Cyp2b8), mRNA
9478	22536	36101	5.24	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.29	7.6E-01	X86347.1	NT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38412	2.29	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24995		2.78	7.6E-01	AL161502.2	NT	H. aspersa mRNA for neurofilament NF70
12203	25157		8.21	7.6E-01	AB020702.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
626	13719		1.31	7.6E-01	AL163301.2	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
597	13787	26807	1.08	7.6E-01	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C101
7690	20755	34240	0.8	7.6E-01	AF062730.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
12621	25354		5.2	7.6E-01	AF163151.2	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
1154	14318	27372	1.61	7.4E-01	AI598146.1	EST_HUMAN	Homo sapiens dentin sialoprotein precursor (DSP) gene, complete cds
2419	15548	28676	0.97	7.4E-01	AB011106.1	NT	tr14b06.x1 NO1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
3820	16980	29983	0.97	7.4E-01	AF112538.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
						NT	Malva pusilla actin (Act1) mRNA, complete cds

Page 40 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30175	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4429	17559	30551	6.12	7.4E-01	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C048
8027	21110	34628	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21989		1.45	7.4E-01	U87860.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9298	22374	35925	6.86	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9357	22432	35990	1.24	7.4E-01	AA187986.1	EST_HUMAN	2p87h01.s1 Stratigene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:625287 3' similar to SW:TCPO_MOUSE P42832 T-COMPLEX PROTEIN 1, THETA SUBUNIT ;
10813	23647	37256	0.7	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1ih), mRNA
12287	25213		1.7	7.4E-01	AI472841.1	EST_HUMAN	1a13h01.x1 NCL_CGAP_Lyn5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		0.73	7.3E-01	AF000062.1	NT	Aeropyrum pernix genomic DNA, section 5/7
4738	17873	30856	0.8	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 62 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288	5.5	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	25841	33771	0.93	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7617	20687	34163	0.69	7.3E-01	Z14133.1	NT	D.melanogaster Cnc mRNA for clathrin heavy chain
7718	20782	34288	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
7718	20782	34289	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFLS_ST Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38448	3.29	7.3E-01	AA678019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFLS_ST Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.86	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (aIF-2a) mRNA, complete cds
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	N.tubaeum NeIF-4A13 mRNA
2532	15957	28781	1.96	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	28323	1.27	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3541	16705	29717	2.36	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp-417-6) gene, vsp-417-6(A)-1 allele, complete cds
3702	18863	29866	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3975	17132	30136	1.57	7.2E-01	BF338350.1	EST_HUMAN	60203559F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18

Page 41 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4882	18022	31007	2.68	7.2E-01	D90314.1	NT	L mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α2)
5225	18347	31318	1.07	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptophysin genes, complete cds; and L-type calcium channel α2)
5308	18425	31398	0.65	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7382	20441	33903	0.59	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8648	21728	35286	1.31	7.2E-01	AF238061.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
9163	22241		0.54	7.2E-01	AF743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10548	23593	37192	2.25	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276381 5'
10877	24058	37690	3.26	7.2E-01	U82823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (Dva) mRNA, complete cds
12737	25488		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
12764	26075		1.46	7.2E-01	Y10188.1	NT	B. thuringiensis PK1 & cap genes, putative
710	13892	28928	11.37	7.1E-01	D21070.1	NT	Rana oatesbelana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3130	16306	28320	16.1	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 16-18
4324	17487	30453	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
4324	17487	30454	3.07	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6069	19251	32579	1.73	7.1E-01	BF681034.1	EST_HUMAN	602165438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6069	19251	32580	1.73	7.1E-01	BF681034.1	EST_HUMAN	602165438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7088	20182	33608	6.48	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoyl-tetrahydropterin synthase (pr) gene, complete cds
8834	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
8834	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-409 BT0567 Homo sapiens cDNA
10059	23097	36700	1.6	7.1E-01	BE904406.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888495 5'
10821	23655	37285	1.1	7.1E-01	M12861.1	NT	Human T-cell receptor gamma-chain J2 gene
12505	25955		2.84	7.1E-01	AA421482.1	EST_HUMAN	z106111.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731108 3'
1257	14415	27479	0.96	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	15647	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	y273e07.s1 Soares multiple sclerosis_2Nbl-MSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element

Page 42 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2521	15647	28771	1.29	7.0E-01	N62412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NbmMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5199	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	19265		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8673	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9517	22582	36150	0.58	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mlIA, mlIR, mlIF, and mlID genes, complete cds
9517	22582	36161	0.58	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mlIA, mlIR, mlIF, and mlID genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13133	25997	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 vifon, complete genome
992	14164	27224	6.3	6.9E-01	U69874.1	NT	Candida albicans equolase epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.9E-01	U69874.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27665	2.91	6.9E-01	AA593530.1	EST_HUMAN	nm2Ba09.e1 NC1_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1095176 3'
3291	18465	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	16698	29707	15.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE782751.1	EST_HUMAN	601465594F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868943 5'
5902	19091	32405	0.82	6.9E-01	AB035662.1	NT	Branchiostoma belcheri BbNA3 mRNA for nucleohord actin, complete cds
6112	19292	32627	0.85	6.9E-01	Y18278.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19666	33029	1.12	6.9E-01	BE266188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7979	21028	34542	0.58	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21250	34769	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9372	22447	36520	0.66	6.9E-01	AF118046.1	NT	Entamoeba dispar calponin transporting ATPase (atpase) gene, partial cds
9898	22936	36521	0.56	6.9E-01	AF206319.1	NT	Musa acuminata pacata lyase 1 (PL1) mRNA, complete cds
9898	22936	36521	0.56	6.9E-01	AF206319.1	NT	Musa acuminata pacata lyase 1 (PL1) mRNA, complete cds
10619	23653	37263	0.78	6.9E-01	BF242367.1	EST_HUMAN	60188080F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11536	24592	38268	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11536	24592	38269	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12146	25949		3.77	6.9E-01	Q99958	SWISSPROT	FORHEAD BOX PROTEIN C2 (FORHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL-14)

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14152	27212	1.94	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2739	15858		1.41	6.8E-01	D00917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2890	14798	27683	1.43	6.8E-01	AA854475.1	EST_HUMAN	gb:U56411.1_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4694	17829	30815	1.32	6.8E-01	J00762.1	NT	Ra(hooded) prolactin gene : exon III and flanks
4980	18109	31085	0.82	6.8E-01	4758621	NT	Homo sapiens hev'n (HEVIN) mRNA
8638	22878	36460	1.06	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23602		5.72	6.8E-01	AA687636.1	EST_HUMAN	nt13907.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:U13548_ma1
11344	24407	38056	2.4	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Siagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11376	24437	38066	1.91	6.8E-01	AF038639.1	NT	Siagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
11376	24437	38067	1.91	6.8E-01	AF038639.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11579	24633	38312	1.57	6.8E-01	AF164151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Anopheles gambiae strain M2 translation initiation factor 4C (T4) (eIF-4C) mRNA, complete cds
11908	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11906	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
300	13525	26559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13580	26598	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1881	13104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451884.1	EST_HUMAN	z12g12.s1 Soares total Tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788310 3' similar to contains element TAR1 repetitive element;
2235	16058	28498	6.16	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Rellet) gene, complete cds, alternatively spliced
3080	16236	28288	5.91	6.7E-01	6578580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30698	0.62	6.7E-01	X74421.1	NT	Stuberium mRNA for glucose-6-phosphate dehydrogenase
5028	18820	31894	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5628	18820	31895	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

Page 44 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	19265	32594	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	19620	32963	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6453	19620	32964	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6754	19910	33304	0.59	6.7E-01	BE86241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6764	19910	33305	0.59	6.7E-01	BE86241.2	EST_HUMAN	601660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.97	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 187 of 529 of the complete genome
7465	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11186	24265	37900	2.06	6.7E-01	BF364649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA
11746	28932	37558	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYL GLUCOSAMINYL-PHOSPHATIDYL INOSITOL BIOSYNTHETIC PROTEIN GPI1
11959	24944	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2570	15695	28819	0.97	6.8E-01	AF075240.1	NT	Homo sapiens SLT1 protein (SLIT2) mRNA, partial cds
2765	15880	26989	1.13	6.8E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	18743	29760	1.16	6.8E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3748	18909	29913	4.58	6.8E-01	Y07699.1	NT	Calicivirus random DNA marker, 282bp
4225	17373		2.48	6.8E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP13) gene, complete cds
6462	19629	32890	3.82	6.8E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klcz2), mRNA
7272	20355	33808	0.82	6.8E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33809	0.82	6.8E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7862	20916	34421	3.7	6.8E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCIGD04 3'
8764	21843	35384	0.59	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9865	22905		2.34	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.8E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
840	13825	28848	2.02	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	28849	2.02	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3519	16685	28698	5.5	6.8E-01	AB041226.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.8E-01	4504632	NT	Homo sapiens interferin 10 receptor, alpha (L10RA) mRNA
4397	17540	30521	7.71	6.8E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18296	31256	2.88	6.8E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

Page 45 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5559	25807	31785	1.86	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
5865	20017	33426	1.3	6.5E-01	D88348.1	NT	(TRANSCRIPTION FACTOR TYE4)
7760	20819	34309	0.74	6.5E-01	X04769.1	NT	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
7848	20901	34404	0.89	6.5E-01	A176882.1	EST_HUMAN	Murine Ig-related lambda(50) gene (exon 1) transcribed selectively in pre-B lymphocytes
10042	23080		0.86	6.5E-01	T78904.1	EST_HUMAN	wc46a02.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE:2321842 3'
10342	23577	37186	2.53	6.5E-01	AF119876.1	NT	yc21b04.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108847 3'
10869	23954	37583	2.55	6.5E-01	H87593.1	EST_HUMAN	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10926	24008	37643	2.98	6.5E-01	AA601287.1	EST_HUMAN	yw1706.r1 Soares_placenta_8to9weeks_2NbpP8a9W Homo sapiens cDNA clone IMAGE:262616 5'
11030	24109		3.38	6.5E-01	AU138078.1	EST_HUMAN	not5c07.s1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
11899	24887	38586	5.43	6.5E-01	AF014115.1	NT	AU138078 PLAGE1 Homo sapiens cDNA clone PLAGE1007810 5'
12666	25386		8.69	6.5E-01	BE465050.1	EST_HUMAN	Plaemodum berghel cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12840	25889		3.63	6.5E-01	Z74145.1	NT	hw74a10.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
262	13481	26513	8.59	6.4E-01	U48848.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
3545	16710	29721	4.42	6.4E-01	U48854.2	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3864	17122	30128	1.46	6.4E-01	AB046827.1	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
4614	17761	30731	0.74	6.4E-01	Y12488.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17761	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus wtn gene
8612	21891	35432	1.58	6.4E-01	AE001247.1	NT	M.musculus wtn gene
10221	23287		0.5	6.4E-01	11418320	NT	Trepnema pallidum section 63 of 87 of the complete genome
10284	23329	36833	7.31	6.4E-01	U82828.1	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10309	23344	36948	1.31	6.4E-01	BF670406.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12693	25461		19.53	6.4E-01	AV759212.1	EST_HUMAN	602150289F1 NIH_JMGC_81 Homo sapiens cDNA clone IMAGE:4281128 5'
447	13643	26682	3.76	6.3E-01	P05228	SWISSPROT	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
548	13741	26765	1.85	6.3E-01	U32689.1	NT	HISTIDINE-RICH PROTEIN PRECURSOR (GLONE PFHRP-III)
2230	15394	28493	3.29	6.3E-01	U81136.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2646	15769	28884	3.65	6.3E-01	U75331.1	NT	Shigella flexneri multi-antigen resistance locus
2646	15769	28885	3.66	6.3E-01	U75331.1	NT	Galus gallus bone morphogenetic protein 1 (BMP-1) mRNA, partial cds
3081	16267		0.93	6.3E-01	Y17275.1	NT	Galus gallus bone morphogenetic protein 1 (BMP-1) mRNA, partial cds
6169	19365	32713	0.84	6.3E-01	BE093906.1	EST_HUMAN	Galus gallus bone morphogenetic protein 1 (BMP-1) mRNA, partial cds
6733	19889	33281	1.01	6.3E-01	L27708.1	NT	Lycopodium esculentum p89a gene, complete CDS
6733	19889	33282	1.01	6.3E-01	L27708.1	NT	PMO-BT0757-010500-002-a03 BT0757 Homo sapiens cDNA
							Streptococcus dysgalactiae (mag) gene, complete cds
							Streptococcus dysgalactiae (mag) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21708		3.44	6.3E-01	BE902044.1	EST_HUMAN	601678899F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958351 5'
9087	22168	35712	0.79	6.3E-01	S62927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9421	22493	38062	0.65	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9620	22675	36245	3.14	6.3E-01	9827521	NT	Varicella virus, complete genome
9620	22675	36246	3.14	6.3E-01	9827521	NT	Varicella virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10641	23675	37285	1.59	6.3E-01	Z73003.1	NT	S cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW795395.1	EST_HUMAN	PMO-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24378	38024	1.78	6.3E-01	AA877715.1	EST_HUMAN	nc08106.st1 NCJ_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK.
11620	24671	38359	6.18	6.3E-01	AI604160.1	EST_HUMAN	QM-BT043-090299-048 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11888	24878	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12086	25066	38772	1.47	6.3E-01	9833361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12358	26257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12582	26029		4.27	6.3E-01	X83528.1	NT	C. limicola pscD gene
5991	19176	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME I
7664	20731		3.59	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7715	25852	34266	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea8 gene, Callitriche, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8497	21578	35114	4.67	6.2E-01	H72255.1	EST_HUMAN	yo01608.st1 Scars fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:213542 3'
9057	22136	35681	0.7	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase
9648	21091	34906	1.47	6.2E-01	BE562887.1	EST_HUMAN	dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9710	22759		2.58	6.2E-01	M24461.1	NT	601338146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3660010 5'
10283	23318	36919	6.83	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10426	23461	37067	0.63	6.2E-01	11420783	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10426	23461	37068	0.63	6.2E-01	11420783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10756	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOLE PROTEINASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

Page 47 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10759	23799	37408	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2483	15595		6.27	6.1E-01	Q678078	NT	Mus musculus secreted acidic cytochrome rich glycoprotein (Spare), mRNA
5653	18847	32129	1.33	6.1E-01	M59940.1	NT	Ceanothus americanus N2 CcMyoD (h1h-1) alternatively spliced genes, complete cds
7008	20145	33664	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20146	33665	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20283	33739	0.67	6.1E-01	AW105653.1	EST_HUMAN	xd60h03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:U12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	20337	33787	0.69	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8955	22074	35612	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8955	22074	35613	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9615	22870	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9615	22870	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36888	1.05	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAC1, section 13 of 529 of the complete genome
10252	23287	36883	0.92	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23665	37489	0.47	6.1E-01	AF025893.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25018	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25018	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13082	25685		1.16	6.1E-01	X95287.1	NT	M. megal orfA, orfB, and orfC of archaeal ABC-transporter system
567	13701	28730	1.76	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
575	13757		4.74	6.0E-01	5802899	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27623	1.83	6.0E-01	AF085263.1	NT	Human respiratory syncytial virus strain CH63-53b attachment protein (G) gene, complete cds
3917	17078	30073	0.87	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.26	6.0E-01	AF058895.1	NT	Homo sapiens Natch3 (NOTCH3) gene, exons 26, 27, and 28
5396	18697	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	U1H.B11-seb-e-10-0-JU1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718618 3'
6669	19828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6800	19855	33355	0.86	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6956	20288	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6955	20288	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20583	34056	6.49	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23066	36664	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23515		1.04	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
10594	23629		0.61	6.0E-01	BE83779.1	EST_HUMAN	RC2-FN0094-190700-017-c08 FN0094 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11846	24835	38529	2.74	6.0E-01	AJ420623.1	EST_HUMAN	h0807.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2095621 3'
12663	25440	32052	2.08	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.46	6.0E-01	AA706087.1	EST_HUMAN	298905.s1 Scores fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12953	25958		1.44	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12998	25933	31768	5.48	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25880		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-H10375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14193	27254	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	16515	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	16515	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17480		3.95	5.9E-01	AF162756.1	NT	Rattus norvegicus cecatin 2 mRNA, partial cds
5289	18407	31574	0.66	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	19754	33140	1.95	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33862	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7566	20628		0.63	5.9E-01	X68801.1	NT	G. gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34795	0.48	5.9E-01	D90811.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8839	21918	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW31/Cx major outer membrane protein (omp1) gene, complete cds
10117	23155		0.64	5.9E-01	P06463	SWISSPROT	EG PROTEIN
10391	23426	37033	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

Page 49 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10908	23991	37624	2.24	5.9E-01	Q8X033	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23999	37632	1.71	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AF1937175.1	EST_HUMAN	PM1-DT0041-180100-002-R03 DT0041 Homo sapiens cDNA
11489	24528	38201	1.98	5.9E-01	AF036426.1	NT	Mus spretus strain SPRET/El CD48 antigen (C448) gene, partial cds
12302	25220	32101	1.78	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.92	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for cordline-5'-phosphate decarboxylase, complete cds
12789	25533		4.82	5.9E-01	P34826	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN L23]
1958	15101	28201	1.26	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.8E-01	BF895738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4078131 5'
4637	17773	30763	3.59	5.8E-01	AB009072.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4917	18047		2.22	5.8E-01	AF110848.1	NT	Megascella scalaris sex-lethal homolog (Meglxl) gene, partial cds, alternatively spliced products
5480	18689		1.02	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5848	18842	32123	0.81	5.8E-01	Q10899	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA* (TFujivara) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32972	0.88	5.8E-01	D60801.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6952	20265		2.37	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	5.8E-01	H41571.1	EST_HUMAN	gb:S78187 M-PPHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34879	0.66	5.8E-01	A1280051.1	EST_HUMAN	q185410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8278	21360	34879	0.66	5.8E-01	A1280051.1	EST_HUMAN	q185410.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34991	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
8395	21496	34992	2.71	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP88
9092	22171	35716	10.4	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9172	22250	35793	1.23	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
9173	22281	35794	0.87	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE TF46F2.2 IN CHROMOSOME X
9785	22835		0.79	5.8E-01	BF031606.1	EST_HUMAN	60155774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
11237	24306	37943	7.28	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11291	24357		3.35	5.8E-01	BF700092.1	EST_HUMAN	60212757F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
11407	24488		1.44	5.8E-01	BF700092.1	EST_HUMAN	60212757F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	5.7E-01	6755253	NT	Mus musculus plasminogen variant translocation 1 (Pvt1), mRNA
3295	16489	29488	1.46	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1A)
3593	16757		2.84	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6485	19852	33014	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454862F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38855590 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Botrytis chereza strain T4 cDNA library under conditions of nitrogen deprivation
7941	20991	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8157	21239		0.55	5.7E-01	AJ251835.1	NT	Mus musculus Koni1, Ltprc3, Mash2, Tapa-1, Tsc4 and Tsc8 genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23838	37481	0.91	5.7E-01	BF540662.1	EST_HUMAN	60206712FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
12255	26192		1.29	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0736-180700-003-e02 HT0736 Homo sapiens cDNA
13025	26675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601654814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16617	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16617	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3989	17146	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
9003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKG Homo sapiens cDNA clone GKCF5F05 5'
9003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKG Homo sapiens cDNA clone GKCF5F05 5'
9575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	25123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601514007FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12272	26204	36382	1.39	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.a1 NCI CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element
12661	17146	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12690	25460		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25759		3.64	5.6E-01	BF573829.1	EST_HUMAN	602132026FT NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8383912	NT	Rattus norvegicus Propenyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2768	16881	28990	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2768	16881	28991	9.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2985	16161	29178	1.17	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3134	16310		1.57	5.5E-01	H46219.1	EST_HUMAN	yo18a10.a1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3306	16480	29501	2.93	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3783	16944	29951	1.34	5.5E-01	P48765	SWISSPROT	FOS-RELATED ANTIGEN-1
5249	18370		1	5.6E-01	AF063866.1	NT	Melanogaster sanguinipes entomopoxvirus, complete genome
5269	18388	31356	1.01	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain BoLA-DIB1 gene, partial cds

Page 51 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7405	20483	33951	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7439	20516		0.74	5.5E-01	AB015596.1	NT	Carassius auratus gene for gonadotropin II beta subunit, complete cds
8878	21798	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0458-170200-090-505 HT0458 Homo sapiens cDNA
9989	23008		0.56	5.5E-01	U88415.1	NT	Crinean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23623	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HFBCQ35
11408	24467	38132	1.64	5.5E-01	BF129607.1	EST_HUMAN	501811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	26404	8.11	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
147	13372	26405	8.11	5.4E-01	7657268	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
598	13788	26808	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1300	14456	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2173	16308		2.8	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2328	16461	28594	2.82	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta cerotene dioxygenase (beta-diox gene)
5774	18966	32269	0.83	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19482	32850	0.93	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE965592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7490	20565	34035	1.98	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7490	20565	34036	1.98	5.4E-01	Z21619.1	NT	S.cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
10195	23232		2.69	5.4E-01	BF572636.1	EST_HUMAN	602076645F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
11334	24387	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11920	24908	39607	2.76	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24908	39608	2.76	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	AI858398.1	EST_HUMAN	w37g04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN);
528	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B), helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2843	15957	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29068	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	16488	29508	3.8	5.3E-01	AF087958.1	NT	Homo sapiens secreted C-type lectin precursor (LIS1) gene, complete cds
4327	17470		1.2	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AI820921.1	EST_HUMAN	z142h12.y5 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.55	5.3E-01	AI820921.1	EST_HUMAN	z142h12.y5 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:740711 5'
5071	18865	32150	0.95	5.3E-01	AA193672.1	EST_HUMAN	z142g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5071	18865	32151	0.95	5.3E-01	AA193672.1	EST_HUMAN	z142g09.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5762	18954	32258	2.32	5.3E-01	BE645620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01950.2	NT	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9156	22234	35779	0.76	5.3E-01	BF433956.1	EST_HUMAN	Roridula georgiana ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast gene for chloroplast product
9156	22234	35780	0.76	5.3E-01	BF433956.1	EST_HUMAN	7e71c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
10416	23451	37056	0.65	5.3E-01	AI854210.1	EST_HUMAN	7e71c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29
11857	24845	38542	5.63	5.3E-01	BE586291.1	EST_HUMAN	repetitive element;
12145	25958		1.73	5.3E-01	AA916053.1	EST_HUMAN	repetitive element;
839	14017	27072	20.65	5.2E-01	L20770.1	NT	w34b02.x1 NCL CGAP_Maf15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20674 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
1190	14352	27410	7.57	5.2E-01	Q9WV30	SWISSPROT	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
1218	14379	27438	3.05	5.2E-01	AF224492.1	NT	cg30a05.s1 NCL CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
1835	15078		3.88	5.2E-01	AL163285.2	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
							Drosophila melanogaster helix-loop-helix mRNA, complete cds
							NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5)(NF-AT5)
							(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
							Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment HS21C085

Page 53 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2213	16347	28478	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	16384	29389	2.1	5.2E-01	U65942.1	NT	Ornithodroma phaeopygia strain S2933 POMP91A and POMP90A precursor, genes, complete cds
3309	16483		1.05	5.2E-01	D73443.1	NT	Azotobacter vinelandii lcd gene for isocitrate dehydrogenase, complete cds
3481	16558		1.61	5.2E-01	AL116780.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	16695	29708	2.01	5.2E-01	AA084165.1	EST_HUMAN	am77605.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:101650.4 3'
3722	16883		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	16885	29891	0.87	5.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
4729	17984	30849	0.81	5.2E-01	6762847	NT	Mus musculus acetylcholine receptor beta (Acb), mRNA
5770	18982	32263	0.92	5.2E-01	AA284261.1	EST_HUMAN	zc4409.77 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone IMAGE:323169 3'
8932	25982	36582	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
8932	25982	36593	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	z405b09.r1 Strabagene muscle 937209 Homo sapiens cDNA clone IMAGE:028793 5'
10233	23288	36868	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	26736		4.93	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13817	26841	2.6	5.1E-01	M56509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
665	13851	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1684	14836	30331	1.02	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	AB58495.1	EST_HUMAN	w36b1.2x1 NCI_QGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17448	30432	2.89	5.1E-01	P86380	SWISSPROT	TRANSCRIPTION REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE091798.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541068.1	EST_HUMAN	601063608F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
6406	19575		0.9	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAU607 5'
7057	20110	33528	1.35	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:146872 3'
8770	21849	35399	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8770	21849	35399	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9886	22926	36510	4.65	5.1E-01	U05412.1	NT	Human regenerating protein (reg) gene, complete cds
9889	22929	36513	3.96	5.1E-01	W22302.1	EST_HUMAN	6851 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94578.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12668	26874		3.49	5.1E-01	BF030207.1	EST_HUMAN	601668693F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3826787 5'

Page 54 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12834	25427		1.31	5.1E-01	BF438982.1	EST_HUMAN	rac51f10.x1 NCJ_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element;
2203	15338	28484	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28485	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (Chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEb), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28472	2.09	5.0E-01	AF009210.1	NT	Buchnera aphidicola genomic fragment containing (Chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEb), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF009210.1	NT	complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3842	17001	30004	0.85	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01	L39483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3977	17134	30137	2.67	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19937		0.82	5.0E-01	BF676199.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34399	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21949	35484	0.66	5.0E-01	BF107848.1	EST_HUMAN	607823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9857	21100	34613	2.73	5.0E-01	BF317212.1	EST_HUMAN	607930387F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
							GLYCOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22884	39445	1.47	5.0E-01	P35573	SWISSPROT	GLYCOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22884	39446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10502	23637		1.23	5.0E-01	BE869218.1	EST_HUMAN	607445024F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3849436 5'
12307	25225		3.84	5.0E-01	AF029215.1	NT	Mus musculus MRO OX-2 antigen homolog gene, exons 2-5, and complete cds
13093	25713		2.25	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
13109	25724		4.71	5.0E-01	O13961	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUI11
812	13991	27045	1.83	4.9E-01	BF571462.1	EST_HUMAN	602075648F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1992	14844	27928	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28198	1.34	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61594	SWISSPROT	FIBRILLIN 1 PRECURSOR

Page 55 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	19337	32682	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	19337	32683	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20980	34156	1.61	4.9E-01	AB040051.1	NT	Oriza sativa subsp. Japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.86	4.9E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9190	22288		1.96	4.9E-01	BF209781.1	EST_HUMAN	601874954F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102803 5'
9369	22484	36028	0.96	4.9E-01	AW339905.1	EST_HUMAN	he80c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2807286 3' similar to TR:086714
9496	26228		2.2	4.9E-01	10846803	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
10524	23559	37166	1.05	4.9E-01	AF053980.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12187	26154		2.61	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13086	26174		4.94	4.9E-01	AA613582.1	EST_HUMAN	ng22611.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144682 3'
13084	25714	31939	1.89	4.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
13181	25769		1.27	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4462	17592		0.69	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5624	18818	31892	9.66	4.8E-01	J02997.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6817	19970	33378	0.89	4.8E-01	U82882.1	NT	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
6927	19980		4.18	4.8E-01	AA659878.1	EST_HUMAN	nu8509.s1 NCI_CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217613
7469	20544		1.83	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (DRS2288E) mRNA
7846	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7938	20989	34487	3.59	4.8E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7938	20988	34498	3.59	4.8E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8089	21171	34686	1.81	4.8E-01	AI820744.1	EST_HUMAN	y77110.y5 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:184798 5' similar to contains element MER6 repetitive element
9446	22592		1.05	4.8E-01	BE155148.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
10212	23248		0.35	4.8E-01	BF568633.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
10968	24047		1.9	4.8E-01	X83602.1	NT	S.cerevisiae ORFs from chromosome X
12279	25208		1.58	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12503	25918		5.78	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3142	16318		0.59	4.7E-01	AF192397.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
6644	19803	33190	8.07	4.7E-01	BF211713.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 6'
7186	20051	33491	0.84	4.7E-01	AI204374.1	EST_HUMAN	qf72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755644 3'

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22352	35904	0.61	4.7E-01	698150.1	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102873.1	NT	Influenza A virus isolate h5N1997 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 9 through 16, and partial cds
11658	24737	38428	1.45	4.7E-01	AW868448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12401	25281		1.84	4.7E-01	BE887783.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'
3837	16997	29899	1.62	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.62	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5335	18732	31747	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5335	18732	31748	0.93	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128472 5'
5588	18783	31628	3.52	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829	3.52	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18857	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601588755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5677	18871	32157	3.62	4.6E-01	A1247679.1	EST_HUMAN	qt59H02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN;
5677	18871	32158	3.62	4.6E-01	A1247679.1	EST_HUMAN	qt59H02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:015338 015338 BUTYROPHILIN;
5685	18879	32169	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5763	18955		0.85	4.6E-01	AF212124.1	NT	Andis schwartzi cytochrome b gene, partial cds; mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PM0-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19555	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from basins 1165761 to 1176238 (section 100 of 148) of the complete genome
6906	20221	33649	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25843	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegavirus e1 protein gene, complete cds
7806	20958	34464	0.78	4.6E-01	AA493577.1	EST_HUMAN	nt04h05.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943363 similar to contains Alu repetitive element; contains element L1 repetitive element;
8515	21626	35131	14.55	4.6E-01	BF697399.1	EST_HUMAN	602130853F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
8948	22025	35565	0.54	4.6E-01	AA93237.1	EST_HUMAN	cc76608.s1 NCI CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:U636341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

Page 57 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	22025	35569	0.54	4.6E-01	AA832237.1	EST_HUMAN	cc76b08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9886	22906	36490	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22906	36491	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
10181	23216	36809	1.15	4.6E-01	AI015634.1	EST_HUMAN	w073e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10181	23216	36810	1.15	4.6E-01	AI015634.1	EST_HUMAN	w073e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11238	24307	37856	2.31	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11248	24317	37857	5.08	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11248	24317	37857	5.08	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.6E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.6E-01	AF019369.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
1980	15103	28203	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
1980	15103	28204	1.15	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2833	16110	29124	4.83	4.5E-01	AA677086.1	EST_HUMAN	z155d02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3390	16552	29565	0.66	4.6E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2865280 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3390	16552	29566	0.66	4.6E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2865280 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3393	16563	29578	4.46	4.5E-01	Q05763	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3485	18332	29851	1.51	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4139	17261	30329	1.18	4.6E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN
4188	17336	30329	1.02	4.5E-01	A1708908.1	EST_HUMAN	as66d09.x1 Barstead cDNA HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
4292	18478	31161	4.71	4.6E-01	AW873495.1	EST_HUMAN	ho60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5058	18186	31161	1.18	4.5E-01	BE963445.2	EST_HUMAN	80165725R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5686	18960	32145	1.67	4.5E-01	AW608814.1	EST_HUMAN	QV2-PT0012-140100-031-c08 P T0012 Homo sapiens cDNA
6740	18986	34120	1.38	4.5E-01	Q00956	SWISSPROT	COAT PROTEIN
7571	20943	34120	0.91	4.5E-01	M37036.1	NT	Rat nuclear proteins B23.1 and B23.2

Page 58 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7765	20841	34333	2.39	4.5E-01	A1858849.1	EST_HUMAN	w32602.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8502	21583		1.11	4.5E-01	M32861.1	NT	SW/ISNF COMPLEX 170 KDA SUBUNIT. ;
8598	21679	35217	2.87	4.5E-01	A1848596.1	EST_HUMAN	D melanogaster Shaw2 protein mRNA, complete cds
							tz5g11.x1 NCI_CGAP_Ov65 Homo sapiens cDNA clone IMAGE:2282644 3'
8756	21835	35378	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE)
8981	22060		2.36	4.5E-01	11444786	NT	(PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA
9200	22278	35817	0.88	4.5E-01	AE000218.1	NT	POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
10145	23183		0.96	4.5E-01	9630816	NT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
10713	23746	37352	25.59	4.5E-01	M86006.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10713	23746	37353	25.59	4.5E-01	M86006.1	EST_HUMAN	Bombyx mori nuclear polyhedrosis virus, complete genome
							EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
							EST02631 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
							xc14h01.x1 NCI_CGAP_U8 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT8_MOUSE
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
11225	24294	37835	2.16	4.5E-01	11430789	NT	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
11500	24586		1.3	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
12184	28162		5.58	4.5E-01	BE871481.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12895	25592		1.2	4.5E-01	BF33753.1	EST_HUMAN	602035275F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183280 5'
12970	25630		12.42	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2084	15234		1.11	4.4E-01	6680503	NT	Mus musculus Integral membrane-associated protein 1 (limap1), mRNA
							VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED
							FACTOR)
2462	15589	28715	4.18	4.4E-01	P49765	SWISSPROT	
3390	16560	29575	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	16560	29576	1.54	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	16565	29580	2.12	4.4E-01	BF056726.1	EST_HUMAN	7191602.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	17492		1.35	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5536	18733	31749	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733	31750	1.31	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	S65019.1	NT	mucln [rat, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013	32319	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
							ql62h11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6074	18286	32584	1.12	4.4E-01	A188413.1	EST_HUMAN	UNKNOWN PROTEIN ;

Page 59 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	19256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q02h11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29108 Q29108 UNKNOWN PROTEIN
6370	19339	32899	1.87	4.4E-01	AW080795.1	EST_HUMAN	xc27608.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685510 3' similar to TR:Q95164 Q95164 AFLATOXIN B1-ALDEHYDE REDUCTASE
6458	19825		1.05	4.4E-01	AA778132.1	EST_HUMAN	ae55d11.s1 Strabagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970985 3' similar to gb:M16038 TYROSINE-PROTEIN KINASE LYN (HUMAN)
7667	20629	34104	1.14	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 48 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11879.1	NT	S. tuberosum mRNA for induced stolon tip protein (partial)
8862	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	z68a03.s1 Strabagene colon (8937204) Homo sapiens cDNA clone IMAGE:509838 3'
9352	22427	35985	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 09107.v6 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	38023	0.62	4.4E-01	AW612578.1	EST_HUMAN	h05608.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954222 3' similar to SW:MSH6 HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN
10167	23204	36798	1.95	4.4E-01	AI268650.1	EST_HUMAN	q036709.x1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1610921 3'
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337	36942	4.84	4.4E-01	P36590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23620	37228	1.78	4.4E-01	S76404.1	NT	beta-HKA=H.K-ATPase beta-subunit [rate, Genomic, 8983 nt, segment 2 of 2]
10585	23620	37227	1.76	4.4E-01	S76404.1	NT	beta-HKA=H.K-ATPase beta-subunit [rate, Genomic, 8983 nt, segment 2 of 2]
10829	23882	37486	0.48	4.4E-01	P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24576	36256	1.64	4.4E-01	6691408	NT	Tarabralina retusa mitochondrion, complete genome
12435	25308	32087	4.23	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
13051	26689		1.41	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619	26659	2.42	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26660	2.42	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
1633	14765	27871	1.11	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2635	16112		1.34	4.3E-01	AW935289.1	EST_HUMAN	CM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3127	16303	26316	0.95	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4626	13619	26659	1.27	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
4526	13619	26660	1.27	4.3E-01	AF155218.1	NT	Callitrix jacchus MW/LW opsin gene, upstream flanking region
5071	16109		1.04	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5220	18342		0.94	4.3E-01	9635250	NT	Xestia cingulum granulovirus, complete genome
5480	18679	31683	0.95	4.3E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5480	18679	31694	0.95	4.3E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

Page 60 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6009	19194	32512	1.31	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-c08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.99	4.3E-01	AF179825.1	NT	Salmih soluteus olfactory receptor (SSC186) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Columix columix japonica ffrG gene
6925	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7586	20558		1.28	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158296 5'
8622	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-fla) genes, complete cds
9455	22671	36137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9928	22868	36556	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
9928	22868	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868554 5'
10433	23468	37075	0.89	4.3E-01	AW170589.1	EST_HUMAN	yn83e05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2898400 3' similar to
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	TR:000189 000189 MU-ADAPTIN-RELATED PROTEIN 2 ;
13162	25754		1.56	4.3E-01	AJ003022.1	NT	Equus caballus microsatellite LEX027
1389	16036	27618	1.17	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
2002	15143		1.02	4.2E-01	AA761953.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3697	16858	29862	4.1	4.2E-01	AE003947.1	NT	nz24e09.s1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'
3727	16888	29892	1.09	4.2E-01	AI280338.1	EST_HUMAN	Xyella fastidiosa, section 83 of 228 of the complete genome
3803	18477		0.73	4.2E-01	N81203.1	EST_HUMAN	q94501.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3884	17141	30146	0.74	4.2E-01	AW835527.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07878, Z40483
4819	17952	30937	2.57	4.2E-01	AA634093.1	EST_HUMAN	QV0-LT0015-180200-127-H01 LT0015 Homo sapiens cDNA
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	h59h01.s1 NC1 CGAP_P10 Homo sapiens cDNA clone IMAGE:597777 similar to gb:M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5832	18023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	y77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5901	19080	32404	1.63	4.2E-01	AW854162.1	EST_HUMAN	901879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108483 5'
6334	18605	32863	0.89	4.2E-01	AL163247.2	NT	RC3-C10234-060400-028-q04 C10254 Homo sapiens cDNA
7090	20184	33609	8.72	4.2E-01	AU158472.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
7151	25839	33727	3.21	4.2E-01	S82504.1	NT	AL158472 PLAGE2 Homo sapiens cDNA clone PLACE2000470 3'
7242	20323	33770	6.61	4.2E-01	AL161547.2	NT	AU158472 PLAGE2 Homo sapiens cDNA clone PLACE2000470 3'
7745	20805	34294	0.81	4.2E-01	AL163252.2	NT	Brca1-breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
8182	21264	34786	4.01	4.2E-01	AW957448.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8182	21264	34787	4.01	4.2E-01	AW957448.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C032
							EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
							EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA

Page 61 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
8511	22578	35141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22578	35142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10176	23212	37364	0.81	4.2E-01	AA705007.1	EST_HUMAN	z98801.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482649 3'
10714	23747	37364	1.44	4.2E-01	AW683666.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
11288	24364	38005	1.43	4.2E-01	AB023489.1	EST_HUMAN	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11679	24678	38388	1.87	4.2E-01	BE969485.2	EST_HUMAN	601600352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3606085 3'
1118	14283	27338	2.11	4.1E-01	AB05491.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1127	14292	27347	1.48	4.1E-01	AV703243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.48	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AB056948.1	EST_HUMAN	PM-BT103-270469-884 BT103 Homo sapiens cDNA
2775	15890	29007	1.48	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
3008	16181	29202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3008	16181	29203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3375	16547	29561	0.86	4.1E-01	AA908344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG resequenced, MAGG Homo sapiens cDNA
4389	17532	30513	0.73	4.1E-01	AW961292.1	EST_HUMAN	EST373384 MAGG resequenced, MAGG Homo sapiens cDNA
4422	17563	30513	0.99	4.1E-01	AJ249207.1	EST_HUMAN	Rhodococcus sp. AD46 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ

Page 62 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11078	24153	37790	40.17	4.1E-01	X58700.1	NT	Zea mays ZMIPMS2 gene for 19 kDa zein protein
11075	23903	37525	1.88	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK) (HBK1)
12810	26139		2.33	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1084	14229	27286	1.49	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds
1514	14667		5.48	4.0E-01	6670258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2081	16053	28318	1.08	4.0E-01	Z96933.1	NT	Ascorbus immerus masc2 gene
2081	16053	28317	1.08	4.0E-01	Z96933.1	NT	Ascorbus immerus masc2 gene
2866	13369	28402	1.11	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recognin (Ubr1), mRNA
3033	16209	29231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	29232	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (Y1C), Y1D (Y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3786	18947	29855	1.87	4.0E-01	AF088903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4938	18068		8.59	4.0E-01	Q31849	SWISSPROT	EST382691 IMAGE resequencing, MAGK Homo sapiens cDNA
6031	19214	32535	1.07	4.0E-01	AW970810.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
8588	19730	33108	0.62	4.0E-01	P27285	SWISSPROT	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
8113	21195	34714	0.51	4.0E-01	BF092834.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
8201	21283	34808	0.73	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
9208	22286	35827	1.11	4.0E-01	AA323289.1	EST_HUMAN	EST28086 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11869	24857		1.67	4.0E-01	BF030262.1	EST_HUMAN	60158283F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
12021	25005		2.38	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
12463	26978		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
13027	26116		1.38	4.0E-01	Z49301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL029w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	hab4605.x1 Soares_NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SWNTOR_BOVIN 018875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1:
13222	26907		1.26	4.0E-01	Z49301.1	NT	S. cerevisiae chromosome X reading frame ORF YJL029w
1408	14563	27638	1.84	3.9E-01	AF206818.1	NT	Garilla garilla carboxyl-ester lipase (CEL) gene, complete cds
2707	15825	28940	3.34	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2770	15885	28994	5.03	3.9E-01	X82032.1	NT	H. sapiens B-myb gene

Page 63 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2770	15885	28995	5.03	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3198	16341	29349	4.24	3.9E-01	AJ226896.1	NT	Sinorhizobium meliloti egl, syB2, cya3 genes and orf3
4180	17340	30333	1.48	3.9E-01	BF582011.1	EST_HUMAN	761d01.x1 NCL CGAP_B16 Homo sapiens cDNA clone IMAGE:3339189 3'
5106	18234	31203	1.47	3.9E-01	BET28667.1	EST_HUMAN	507553848F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833688 5'
6055	19237	32562	4.58	3.9E-01	BF208036.1	EST_HUMAN	6071862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19579	32840	0.84	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.89	3.9E-01	U78415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-1) gene, complete cds
9082	22141	35986	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	602018944F1 NCL CGAP_B167 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22509	36075	1.73	3.9E-01	AW186888.1	EST_HUMAN	xs86d04.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:4155322 5'
9745	22809	36387	1.59	3.9E-01	A1937337.1	EST_HUMAN	O94821 KIAA0713 PROTEIN
10082	23120	36722	2.88	3.9E-01	M19879.1	NT	wp7ea02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW:RFX5_HUMAN P48382 BINDING REGULATORY FACTOR, ;
10150	23188		0.88	3.9E-01	D86722.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10369	23404	37015	0.92	3.9E-01	D86722.1	NT	Porphyra purpurea mitochondrion, complete genome
10362	23597	37203	0.81	3.9E-01	BF361856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10862	23597	37204	0.81	3.9E-01	BF361856.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10836	23869		0.47	3.9E-01	AB037832.1	NT	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
12049	25030	36736	1.89	3.9E-01	AV702823.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBC11 6'
12221	26055		4.03	3.9E-01	AF304354.1	NT	AV702823 ADB Homo sapiens cDNA clone ADBDBE06 5'
12918	26603		1.75	3.9E-01	11433335	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
164	13389		7.58	3.9E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
518	13711		6.1	3.9E-01	AB020291.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1919	16062		1.36	3.9E-01	AEO03870.1	NT	Mus musculus pen-1 mRNA for pericentriolar material-1, complete cds
2637	16700	26874	1.84	3.9E-01	AF214117.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2697	16069	26931	5.2	3.9E-01	6678002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3068	16242		0.71	3.9E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 8 (Slc1a8), mRNA
3113	16289	29305	1.91	3.9E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 89SE-MP-1213)
3672	16737	29752	8.7	3.9E-01	AL161518.2	NT	Pleuronectes americanus aminopeptidase N (ampn) gene, partial cds
3628	16762		1.09	3.9E-01	A1807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
							wf38b12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'

Page 64 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		0.97	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3852	17012	30012	1.07	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	6754085	NT	Mus musculus general transcription factor III (Gt2), mRNA
5727	18920	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	18636		0.83	3.8E-01	S46825.1	NT	prion protein [mink, Genomic, 2446 nt]
8761	19917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
6899	20214	33644	4.39	3.8E-01	AI374601.1	EST_HUMAN	contains Alu repetitive element;
7079	20132	33649	1.38	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7885	20750		4.27	3.8E-01	X81597.1	NT	M.musculus gene for kallikrein-binding protein
8483	21574	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8754	21833	35373	2.04	3.8E-01	AB048851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8828	21905	35444	1.08	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22096	36636	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9761	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	Alu repetitive element contains PTR5 repetitive element;
							AV755814 BM Homo sapiens cDNA clone BMFBCE07 5'
11699	24696	38398	1.57	3.8E-01	U92071.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), callitricin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
11824	24813		2.87	3.8E-01	BE19219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	38681	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11992	24977	38682	2.5	3.8E-01	R42550.1	EST_HUMAN	yf92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12589	26082		2	3.8E-01	U94788.1	NT	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
13108	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31833	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2851	18676	28799	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	30135	10.87	3.7E-01	AF053336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3874	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	ok39c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510186 3'
4440	17580	30559	1.31	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC98 section 50 of 206 of the complete genome

Page 65 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31368	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31369	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX4) gene, complete cds
6071	19253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6639	19798	33187	0.7	3.7E-01	M10808.1	NT	Chicken (White Leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	19819		0.8	3.7E-01	L10353.1	NT	Mus sexicola haemoglobin mRNA, complete cds
7263	20375	33832	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7965	21015	34527	0.89	3.7E-01	T68802.1	EST_HUMAN	y650a07.3 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:66324 5'
8324	21603	35143	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.88	3.7E-01	AA02912.1	EST_HUMAN	ak43b11.s1 NCI_CGAP_L162 Homo sapiens cDNA clone IMAGE:1616701 3'
9402	22478		1.34	3.7E-01	AJ271388.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (BCDO gene)
10373	23408		0.5	3.7E-01	K00891.1	NT	mouse Ig germline alpha membrane exon region
10414	23449	37054	4.21	3.7E-01	A133641.1	EST_HUMAN	q146a07.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
10783	23818	37437	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23818	37438	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11265	24351	37898	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11265	24351	37900	2.02	3.7E-01	AJ297357.1	NT	Homo sapiens partial LMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37588	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12004	24989		1.42	3.7E-01	AA973540.1	EST_HUMAN	0048003.s1 NCI_CGAP_L165 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:1M77698
12066	25047		3.5	3.7E-01	6877678	NT	TRANSCRIPTIONAL REPRESSOR-PROTEIN YY1 (HUMAN);
12137	26654		1.17	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12314	26228		3.04	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	26289		1.82	3.7E-01	D88976.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12621	26548		2.84	3.7E-01	AL121164.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12802	26697	31971	6.99	3.7E-01	Y18000.1	NT	DKFZp782K075.1 782 (synonym: hmd2) Homo sapiens cDNA clone DKFZp782K075 5'
271	13489	26520	0.77	3.6E-01	AJ009009.1	NT	Homo sapiens NF2 gene
1020	14191		9.07	3.6E-01	U8924.1	NT	Braconia rapae mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mlbp gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 'N1B Homo sapiens cDNA clone IMAGE:24443 5'
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 'N1B Homo sapiens cDNA clone IMAGE:24443 5'
1986	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2847419 3'
1986	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2847419 3'

Page 66 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28253	5.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	15251		1.15	3.6E-01	AF056027.1	NT	Rattus norvegicus repeat element associated with the Rasgr1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15560		2.8	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2556	15681	28808	2.68	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181095-011-g07 ST0171 Homo sapiens cDNA
2694	15814	28929	1.69	3.6E-01	P24208	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2864	18475		8.47	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3568	18723	28738	1.98	3.6E-01	X76750.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3558	18723	28739	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4528	17666	30852	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-612 HT0545 Homo sapiens cDNA
4863	17966	30981	0.69	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW339389.1	EST_HUMAN	h02g04x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872568 3'
5209	18330	31302	0.92	3.6E-01	BE067689.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5498	18697	31713	0.64	3.6E-01	AJ008666.1	NT	Homo sapiens lipo gene intron 5
6211	19388	32735	0.96	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6607	18767	33155	1.63	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7298	20380		3.85	3.6E-01	R94090.1	EST_HUMAN	y74a06.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:275987 5'
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	w72c10x1 Soares thymus_NHFTb Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8419	21500	35032	0.75	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN, [1];
8474	21555	35087	16.45	3.6E-01	AL161583.2	NT	SCQ-SPONDIN
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
9179	22257	35798	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504856	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504856	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

Page 67 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9393	22468	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9599	22654	36225	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9599	22654	36226	1.13	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9659	22631		0.58	3.6E-01	X62825.1	NT	C. perfingens plc gene for phospholipase C upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	Q53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11187	24259	37891	2.42	3.6E-01	BE802390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958987 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915	37540	4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	26205		3.16	3.6E-01	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
12420	25267		3.63	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.88	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vthorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW190228.1	EST_HUMAN	X60611.X1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2879118 3' similar to gb:K00568 TUBULIN ALPHA-1 CHAIN (HUMAN);
13146	25745		1.38	3.6E-01	Z54173.1	NT	Pyrococcus sp. pol gene
214	13437	26487	3.71	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
695	13678	26911	1.03	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26965	1.53	3.5E-01	7709136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
743	13924	26966	1.53	3.5E-01	7709136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13981	27033	4.66	3.5E-01	BF129796.1	EST_HUMAN	601811060RT NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1670	14822	27805	1.28	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2871	16068	28908	1.34	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.e1 StrataGene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
3785	16956		0.73	3.5E-01	BF214381.1	EST_HUMAN	601845470F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076880 5'
4378	17521	30501	2.82	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5048	18176	31163	4.34	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5323	13349	26376	0.9	3.5E-01	AL161636.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
5449	18649	31627	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5449	18649	31628	1.1	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18861	32146	1.29	3.5E-01	D42045.1	NT	Human mRNA for KIAA0088 gene, complete cds
6367	19537		1	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA

Page 68 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6539	19742	33124	0.69	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6803	19958	33358	0.9	3.5E-01	O24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7201	20066		3.38	3.5E-01	X98505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (36PD)
7713	20778	34264	0.59	3.5E-01	P47281	SWISSPROT	S.scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34265	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8265	21347	34862	0.82	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p83-binding protein, 2 (TP53BP2), mRNA
8662	21742		0.77	3.5E-01	AF051581.1	NT	RC4-ET0024-260600-014-c07 ET0024 Homo sapiens cDNA
9127	22206	35749	1.17	3.5E-01	4507810	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9337	22676	36567	1.75	3.5E-01	Q02294	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
10090	23128	36731	4.78	3.5E-01	Z28823.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL L
10172	23209	36802	1.12	3.5E-01	BE174794.1	EST_HUMAN	TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
10972	24052	37685	2.62	3.5E-01	X81084.1	NT	Xlae1s gene for albumin including HIP1 enhancer
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	C.griseus rhodopsin gene for opsin protein
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11892	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11980	24965	38667	1.53	3.5E-01	U05145.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
12271	26209		1.51	3.5E-01	AF297468.1	NT	yz90h12.r1 Soares_multiple_sclerosis_2NHMSF Homo sapiens cDNA clone IMAGE:280375 5'
12344	25249		6.66	3.5E-01	XG4565.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12507	25348		2.91	3.5E-01	AE001774.1	NT	Schistosoma mansoni strain NIMRI chromatin assembly factor 1 small subunit-like protein (RBAP-48) mRNA, complete cds
12710	25472		1.5	3.5E-01	AE001891.1	NT	B.taurus atpA1 gene for F10F(1) ATP synthase alpha-subunit
13198	26026	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	Thermotoga maritima section 38 of 136 of the complete genome
13196	26026	31674	3.18	3.5E-01	H80814.1	EST_HUMAN	Thermotoga maritima section 3 of 136 of the complete genome
725	13907		1.78	3.4E-01	AJ242856.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
988	14169	27230	8.2	3.4E-01	Y08798.2	NT	ys64f11.1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:219697 5'
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	ys64f11.1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:219697 5'
1357	14512	27585	2.35	3.4E-01	Y00554.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
2474	15601	28726	2.54	3.4E-01	D90909.1	NT	Pseudomonas fluorescens colR_colS genes, orf222 and partial lnaA gene

Page 69 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3055	16241	29261	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3055	16241	29262	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16392	29403	1.09	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16593	29608	0.76	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GpE (gpeE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3990	17049		1.89	3.4E-01	BF449010.1	EST_HUMAN	7n94001.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q8UJ16
4163	17313		1.48	3.4E-01	AA884196.1	EST_HUMAN	Q8UJ15 DJ18C9.1
4767	17802	30884	1.79	3.4E-01	BE069912.1	EST_HUMAN	nt11610.st NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:11100347 3'
5066	18194		4.3	3.4E-01	AI240973.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5802	18992	32295	2.64	3.4E-01	AL161594.2	NT	q95c05.x1 NCI_CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contain Alu repetitive element
5932	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02971.1	NT	zn12d11.st Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6154	19330	32878	0.98	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204505.1	EST_HUMAN	60167181T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6364	19534	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	UI-H-BH-sel-e-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6882	20034		1.39	3.4E-01	N95226.1	EST_HUMAN	DKFZp761A249_t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
7086	20180	33604	1.07	3.4E-01	AI468082.1	EST_HUMAN	z653g12.st Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.6	3.4E-01	BF678702.1	EST_HUMAN	tm89g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:337431
8090	21172		0.48	3.4E-01	AEC00493.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.68	3.4E-01	Y14830.1	NT	602085283F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249365 5'
8684	21784		1.38	3.4E-01	AA337083.1	EST_HUMAN	Escherichia coli K-12 MG1635 section 383 of 400 of the complete genome
8760	21839	35380	0.71	3.4E-01	LO4690.1	NT	Homo sapiens TCRBV28 gene, allele A4, partial
9053	22132	35676	1.87	3.4E-01	9933024	NT	EST141765 Endometrial tumor Homo sapiens cDNA 5' end
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	Orcutulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Bovine enterovirus strain K2577, complete genome
9521	22876		0.57	3.4E-01	AB017510.1	NT	INTEGRIN BETA-8 PRECURSOR
9645	21086	34602	4.98	3.4E-01	U18492.1	NT	INTEGRIN BETA-8 PRECURSOR
							Ephedra fluviatilis mRNA for PLC-gamma5, complete cds
							Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds

Page 70 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9845	21088	34603	4.88	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	22837	36522	0.88	3.4E-01	U68768.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10695	23728		0.73	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11287	24336		3.26	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38068	1.86	3.4E-01	AF045981.1	NT	Rudius arcasi cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-globin/MUC18, complete cds
11817	24806	38502	3.23	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38785	1.59	3.4E-01	BF061948.1	EST_HUMAN	7688d12.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3480646.3'
12110	25090	38793	1.65	3.4E-01	Q27546	SWISSPROT	INOSINE-URIDINE PREFERING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)
12150	25120		2.03	3.4E-01	U69604.1	NT	Citrus variegation virus putative replicase gene, partial cds
12264	25198		1.55	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12367	25912		1.16	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cvi8p (cvi8) gene, complete cds
12489	25338		10.71	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
12517	25944		2.39	3.4E-01	BE218652.1	EST_HUMAN	hva2h08.x1 NCI CGAP J424 Homo sapiens cDNA clone IMAGE3176127.3' similar to contains PTR5.0
12579	26052		1.79	3.4E-01	9888361	NT	PTR5 repetitive element
12700	25466	32023	1.36	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12854	26160		1.96	3.4E-01	AJ288948.1	NT	Mus musculus SLI, MAP_17, CYP_a, SOL & CYP_b genes
13055	25691		2.26	3.4E-01	AF019413.1	NT	Clostridium cellulosum partial spoIVB gene and spoIVB gene, strain ATCC 35319
15	13253	26253	6.72	3.5E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (B1), and complement component C2 (C2) genes
108	13263	26263	3.19	3.5E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
461	13658	26894	1.41	3.5E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5.1 nodX gene
650	13836	26863	1.97	3.5E-01	7662485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1227	14387	27450	2.57	3.5E-01	Q12448	SWISSPROT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1335	14492	27582	3.39	3.5E-01	BF569890.1	EST_HUMAN	PROLINE-RICH PROTEIN LAS17
							602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251.3'

Page 71 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	14788	27873	1.28	3.3E-01	6753885	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1674	14828		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Res recognition component (Krc), mRNA
1777	14926		1.02	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2477	15604		6.23	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidino-5'- decarboxylase) (UMPS) mRNA
3014	16190	29215	1.81	3.3E-01	AJ251805.1	NT	Bacteriophage phi-YeO3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaeus mifamycin biosynthetic genes
3584	16749	29786	1.04	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3811	17070	30088	2.72	3.3E-01	084845	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3821	17080	30076	0.82	3.3E-01	P22802	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17228	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17262	30282	1.81	3.3E-01	AF200448.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17627		2.37	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17945		1.91	3.3E-01	AI539114.1	EST_HUMAN	1p78b12.x1 NCI_CGAP_U93 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17976	30966	1.02	3.3E-01	M24481.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4950	18089	31095	1.14	3.3E-01	D84003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2888768
5439	18539	31617	2.55	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5439	18539	31618	2.55	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5507	18096	32411	0.88	3.3E-01	BF213873.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6067	19249	32576	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3875753 3'
6067	19249	32577	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3875753 3'
6162	19338	32694	1.29	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6932	20247	33080	0.59	3.3E-01	AB034233.1	NT	Flavobacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
6932	20247	33691	0.59	3.3E-01	AB034233.1	NT	Flavobacter litoralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	AI628131.1	EST_HUMAN	1y84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7029	20165	33587	4.63	3.3E-01	AI628131.1	EST_HUMAN	1y84h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7961	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

Page 72 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21838	35379	23.1	3.3E-01	BF883954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
9314	22360	35941	0.83	3.3E-01	Q62825	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9578	22720	36289	1.16	3.3E-01	BE828461.1	EST_HUMAN	CN3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9578	22720	36290	1.16	3.3E-01	BE828461.1	EST_HUMAN	CN3-ET0041-180500-187-410 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	N69866.1	EST_HUMAN	z667h01.s1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone IMAGE:297849 3'
9752	22830	36260	2.81	3.3E-01	BF378745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10196	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10865	23887	37620	0.74	3.3E-01	AE000631.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10960	24041	37675	3.35	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	X63953.1	NT	D. mauritiana Adh gene
11279	24345		2.1	3.3E-01	BF526499.1	EST_HUMAN	h51g02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11507	24565	38242	9.35	3.3E-01	BE219361.1	EST_HUMAN	GALECTIN-3 (GALECTOSE SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-26) (CBP30)
11626	24708	38399	3.7	3.3E-01	P47953	SWISSPROT	
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	6071g02.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
12036	13253	28253	2.33	3.3E-01	X07890.1	NT	Rhizobium leguminosarum sym plasmid pRL5.1J nodX gene
12250	25190	38357	1.85	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
13044	25885		22.03	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
469	13654		2.5	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
738	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14467	27535	1.48	3.2E-01	Z50202.1	NT	P. vulgaris arcs-1 gene
1421	14575	27648	6.74	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1683	14815		1	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14964	28057	1.3	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1823	14974	28069	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST368264 MAGE resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Btlyls cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28490	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx1knotted 1 homeobox (Pbx1), mRNA
2774	15889	29000	1.23	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

Page 73 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3696	16857		0.78	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.83	3.2E-01	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4514	17653	3084.1	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4821	17758	30740	1.35	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4880	17953		6.99	3.2E-01	BF693817.1	EST_HUMAN	602081972F1 NIH_MGC_B1 Homo sapiens cDNA clone IMAGE:4246503 5'
5386	18988	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CM6-H10559-060300-2689-H10 HT10589 Homo sapiens cDNA
6078	19260	32589	1.08	3.2E-01	L27221.1	NT	Glandia intestinalis pyruvate:ferredoxin oxidoreductase and flanking genes
6433	19601	32865	0.73	3.2E-01	AF018494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
6728	19855	33277	0.65	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FH7A Homo sapiens cDNA clone FHTAABH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0381 gene, KIAA0381 protein
8040	21123	34643	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8386	21446	34989	1.5	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8461	21642	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12Wax1
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21646	35187	14.52	3.2E-01	BF311838.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126833 5'
8666	21736		1.24	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8688	21778	36310	0.89	3.2E-01	BF246771.1	EST_HUMAN	601855560F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	36311	0.89	3.2E-01	BF246771.1	EST_HUMAN	601855560F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
8871	21950	35485	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
8871	21950	35486	0.86	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9267	22344	35895	0.67	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS210004
9278	22354		2.54	3.2E-01	M85511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10198	23235	36824	4.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	h98105.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3'
10518	23553		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T08813.1	EST_HUMAN	EST04702 Fetal brain, Striatal gene (cat#836206) Homo sapiens cDNA clone HF8DZ21
12289	28083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12881	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus insulin 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25689		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
							y60h08.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2736	15853	28967	3.39	3.1E-01	R18051.1	EST_HUMAN	gb:M64241 QM PROTEIN (HUMAN);
2782	16001	28985	3.77	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2782	16001	28988	3.77	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2920	16098		1.28	3.1E-01	AW629036.1	EST_HUMAN	h44h08.x1 Soares_NFL_T_CGC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3242	16416		3.51	3.1E-01	AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KIAMRE, exon 6
4016	17173	30181	0.94	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5077	18205	31177	0.7	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5595	18790	31838	0.24	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	HYPOTHETICAL PROTEIN H1238
5718	18911	32206	0.75	3.1E-01	Z74883.1	NT	S. cerevisiae chromosome XV reading frame ORF YOL141w
5729	18922		0.83	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6595	19755	33141	1.3	3.1E-01	AW963549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6683	19822	33209	0.96	3.1E-01	A1264458.1	EST_HUMAN	q13901.x1 NCI_CGAP_Co6 Homo sapiens cDNA clone IMAGE:1874689 3'
6821	19974	33392	0.79	3.1E-01	X71887.1	NT	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6905	20220		0.89	3.1E-01	AW377354.1	EST_HUMAN	MR2-C10222-281099-005-h05 C10222 Homo sapiens cDNA
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7856	20911	34416	0.7	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8849	21928	35487	0.84	3.1E-01	R45318.1	EST_HUMAN	y64601.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:356939 3'
10106	23144	38742	0.88	3.1E-01	6679322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10272	23307	36903	1.04	3.1E-01	BF686639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10272	23307	36904	1.04	3.1E-01	BF686639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
							q161e11.x1 NCI_CGAP_K18 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
10334	23369	36979	1.68	3.1E-01	A1244001.1	EST_HUMAN	HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
							y647h08.s1 Striatal gene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar
10510	23545		0.98	3.1E-01	T55325.1	EST_HUMAN	to gb:M91036_m22 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'

Page 75 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24633	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xs82g09.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24818	38507	2.08	3.1E-01	7682291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11828	24817	38508	1.87	3.1E-01	R35735.1	EST_HUMAN	y89b05.r1 Soares infant brain 1N18 Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element
12123	25103		1.3	3.1E-01	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25298		1.22	3.1E-01	AF294308.1	NT	Arabis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304162.1	NT	Silvestrolium vitreum 40S ribosomal protein S11 mRNA, partial cds
12613	25412		3.73	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26877		3.82	3.1E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
13068	26123		1.22	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp1-pending), mRNA
74	15879	26336	1.85	3.0E-01	8755083	NT	Mus musculus protein kinase C, epsilon (Pkce), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xs83f08.x1 NCL_CGAP_Ki671 Homo sapiens cDNA clone IMAGE:2774343 3'
1337	14690	27769	5.77	3.0E-01	AJ008755.1	NT	Baleenoptera physalus gene encoding atrial natriuretic peptide
1838	14984	28084	1.2	3.0E-01	X98082.1	NT	A. limnerus putative gene encoding integrase, Mars2 (RP)
3069	18245		0.8	3.0E-01	AB008877.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	18457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 tlyPG gene for polyglutamate lyase, complete cds
3968	17128	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ008755.1	NT	Baleenoptera physalus gene encoding atrial natriuretic peptide
5258	18649	28695	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5467	18667	31646	5.1	3.0E-01	BE741629.1	EST_HUMAN	60159490F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5548	18746	31780	0.64	3.0E-01	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF228247.1	NT	Canthaleo orthopoxvirus hemagglutinin gene, complete cds
5621	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5621	18815	31894	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5658	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6970	20108	33624	2.82	3.0E-01	D16313.1	NT	Mouse cyclophilin 15 gene, complete cds
6989	18518	31511	0.76	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34167 kDa laminin-binding protein mRNA, partial cds
7085	20118	33532	1.15	3.0E-01	AF228247.1	NT	Canthaleo orthopoxvirus hemagglutinin gene, complete cds

Page 76 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33806	0.98	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20568	34028	4.3	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7670	20738	34214	1.61	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PepA (pspA) gene, partial cds
8111	21193	34713	1.34	3.0E-01	AE001755.1	NT	Thermotoga maritima section 87 of 190 of the complete genome
8598	21649		3.1	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3e9), mRNA
8658	21738	35279	0.48	3.0E-01	Z70200.1	NT	H. sapiens gene for U5 snRNP-specific 200kD protein
8671	21751	35288	1.23	3.0E-01	BE56083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881594 5'
9029	22108	35649	0.69	3.0E-01	AF141878.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbc) gene, partial cds
9072	22151		0.82	3.0E-01	7681686	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9419	22483	36059	1.09	3.0E-01	AF220507.1	NT	Anabaena POC7120 cytosine-specific DNA methyltransferase (dmnB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds, and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOTHEICAL 59.5 KD PROTEIN IN WZA-ASNA INTERGENIC REGION
9927	22967		0.48	3.0E-01	D80904.1	NT	Synechocystis sp. PCC6803 complete genome, 8/27, 830555-781448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4298336 5'
10346	23381	36992	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10346	23381	36993	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetemcomitans Tada (tada), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10606	23640	37248	0.6	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.xt Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2608035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpa gene for ER chaperone BiP, complete cds
10629	23663	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'
10629	23663	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301087 5'
12067	25048	38755	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194107 5'
12087	25048	38756	2.16	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297633.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13081	26121		4.49	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ249893.1	NT	Mus musculus mas proto-oncogene and lgt2 gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1930	15073	28178	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.9E-01	AE000736.1	NT	Aquifex acidicus section 88 of 109 of the complete genome
2322	15454	28565	1.01	2.8E-01	AF222718.1	NT	Chrysodidymus synurideus mitochondrion, complete genome
3253	16427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

Page 77 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3323	18408	29613	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3323	18496	29614	2.88	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
4003	17160	30166	1.12	2.9E-01	AI610836.1	EST_HUMAN	tp21a1.1.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb.D16050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	wf4d10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F6.7 CE16676;
4183	17333	30325	0.61	2.9E-01	AB010426.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4186	17345		0.78	2.9E-01	AW002902.1	EST_HUMAN	wf02f10.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480395 3'
4808	17745	30724	0.98	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4957	18087	31063	0.59	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.99	2.9E-01	AI670899.1	EST_HUMAN	wad8f03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1, L2 L1 repetitive element;
5320	18087	31063	0.65	2.9E-01	AB018029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18576		1.59	2.9E-01	R37485.1	EST_HUMAN	y77e12.x1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28291 3'
5511	20137	33555	0.98	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	19073	32381	5.27	2.9E-01	X56098.1	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18, 18, 28, 30 and levansucrase
5884	19073	32382	5.27	2.9E-01	X56098.1	NT	B. subtilis levansucrase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P18, 18, 28, 30 and levansucrase
5897	19085	32397	5.53	2.9E-01		NT	Mus musculus Eph receptor A3 (Epha8), mRNA
6181	19357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	z067b12.1 Soares NIHMPUL S1 Homo sapiens cDNA clone IMAGE:767711 5'
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	wc27c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1, L1 L1 repetitive element;
6455	19622	32986	2.22	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7128	18552	31466	1.4	2.9E-01	AF142329.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Uighi protein (Uighi) gene, partial cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR060C
							Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BING1), tapasin (tapasin), RagDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1 3-galactosyl tr>
7310	20392	33852	1.54	2.9E-01	AF100956.1	NT	
8104	21186	34705	1.61	2.9E-01	BE540422.1	EST_HUMAN	60105830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21186	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	60105830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'

Page 78 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.64	2.9E-01	AJ237837.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237837.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4085113 5'
8534	21615		0.53	2.9E-01	AF197456.1	NT	Buchnera aphidicola plasmid pLeu isolate M1 2-isopropylmalate synthase (leuA) gene, partial cds; 3-isopropylmalate dehydrogenase (leuB) gene, complete cds; and isopropylmalate dehydrogenase subunit (leuC) gene, partial cds
8794	21873	35412	0.82	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
9125	22204	35747	1.09	2.9E-01	AF228908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9233	22311	35863	0.81	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36126	0.96	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 6/6
10405	23440	37047	0.46	2.9E-01	AW284100.1	EST_HUMAN	U14H-B12-atg-b-02-Q-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
10405	23440	37048	0.46	2.9E-01	AW284100.1	EST_HUMAN	U14H-B12-atg-b-02-Q-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726714 3'
11133	24206	37830	1.94	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38169	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38169	1.79	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11881	24869	38566	2.71	2.9E-01	AA933373.1	EST_HUMAN	repetitive element; 1
11886	24874	38571	3.12	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/8
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
12677	25452	32017	1.85	2.9E-01	AW005871.1	EST_HUMAN	wz88f06.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:25655921 3' similar to contains element
12774	25518		1.89	2.9E-01	V00202.1	NT	MER29 repetitive element
12777	25519	32001	2.23	2.9E-01	AF092453.1	NT	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene 1
13125	25734	31944	1.24	2.9E-01	Y08937.1	NT	Homo sapiens TNF-e-inducible RNA binding protein (TIRP) gene, complete cds
13125	25734	31945	1.24	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31919	1.4	2.9E-01	AF200418.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
582	13774		2.04	2.8E-01	U87136.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-1 mRNA, complete cds
587	13778		1.96	2.8E-01	L26145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1107	14272	27331	3.34	2.8E-01	AF168050.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1306	14462	27529	2.19	2.8E-01	BE313442.1	EST_HUMAN	Gtra guira oocyte maturation factor Mes (c-mos) gene, partial cds
1306	14462	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D66550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
							Human mRNA for serine/threonine protein kinase, complete cds

Page 79 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW86020.1	EST_HUMAN	QV1-CT0364-120200-085-005 CT0364 Homo sapiens cDNA
2069	15210	28326	1.49	2.8E-01	AL047820.1	EST_HUMAN	DKFZp586i2321.J1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586i2321
2200	15335	28462	1.51	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812333 3'
2542	15567	28791	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2542	15567	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2612	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15848	28958	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyletransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	29234	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3036	16212	29235	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3468	16633	29652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (477)
4103	17257	30257	1.67	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 86 of 70) of the complete genome
4240	17388		0.8	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PAO1, section 11 of 629 of the complete genome
4315	17458		2.17	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element/contains element MER22 repetitive element
4682	17710	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF076238.1	NT	Hepatitis G virus isolate 60 (SZVAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31090	1.52	2.8E-01	BF528188.1	EST_HUMAN	602042601FT.NCI.CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180129 5'
5006	18135	31109	3.66	2.8E-01	AI272666.1	EST_HUMAN	q159c11.x1 Soares_NihMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element/contains element LTR6 repetitive element 1
5318	18473	31404	0.61	2.8E-01	X60797.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5429	25804	31602	23.61	2.8E-01	AA349897.1	EST_HUMAN	EST87072 Infant brain Homo sapiens cDNA 5' end
5723	18916	32211	2.57	2.8E-01	AB018625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW992583.1	EST_HUMAN	QV1-BN0024-160200-178-g12 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA763296.1	EST_HUMAN	ce01d06.s1 NCI.CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539.FK608-BINDING PROTEIN (HUMAN);
6059	19241		0.84	2.8E-01	AA404576.1	EST_HUMAN	z141f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element
6305	26212		0.87	2.8E-01	M36668.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6347	19517	32874	1.85	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF511216.1	EST_HUMAN	UI-H-B14-ae1-104-0-UI.s1 NCI.CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthomyx heteroduct cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	A1346126.1	EST_HUMAN	qp49t01.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8284	21366	34885	1.31	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	qp49t01.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
							MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
							Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	35328	0.6	2.8E-01	AA911629.1	EST_HUMAN	c02h05.s1 NCL CGAP_C012 Homo sapiens cDNA clone IMAGE:1419893 3' similar to gb:M87789 IG
8789	21858		7.72	2.8E-01	BF347847.1	EST_HUMAN	GAMMA-1 CHAIN C REGION (HUMAN);
9666	22628	36189	1.14	2.8E-01	U17251.1	NT	502022987F1 NCL CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4158525 5'
9912	22952		1.16	2.8E-01	L13654.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
10092	23130	36733	0.98	2.8E-01	AF132728.1	NT	Lyoperoson esculentum peroxidase (TPX1) mRNA, complete cds
10092	23130	36734	0.98	2.8E-01	AF132728.1	NT	Escherichia coli translocated histidine receptor Tir (tir) gene, complete cds
10152	23189	36786	0.46	2.8E-01	AE001310.1	NT	Escherichia coli translocated histidine receptor Tir (tir) gene, complete cds
							Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23193	36789	0.7	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10285	23300	36898	3.8	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10519	23554		1.1	2.8E-01	9628164	NT	Fujhami sarcoma virus, complete genome
10561	23565	37202	0.5	2.8E-01	BE959727.2	EST_HUMAN	501854822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
10982	24061	37695	1.88	2.8E-01	BF241062.1	EST_HUMAN	501880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10982	24061	37696	1.88	2.8E-01	BF241062.1	EST_HUMAN	501880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24090	37727	3.01	2.8E-01	BF695970.1	EST_HUMAN	501852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
							Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11119	24191	37823	1.53	2.8E-01	AF051662.1	NT	
11556	24611		3.58	2.8E-01	BF874023.1	EST_HUMAN	502137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4279853 5'
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
11851	24840	38534	1.66	2.8E-01	AJ248286.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25502	31987	7.61	2.8E-01	BE178999.1	EST_HUMAN	PM4-HT0608-030-000-001-007 HT0608 Homo sapiens cDNA
12875	25582	31998	1.29	2.8E-01	BE900116.1	EST_HUMAN	501873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
13052	26066		1.59	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

Page 81 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
489	13683	26717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13613	26835	13.64	2.7E-01	AA450061.1	EST_HUMAN	z36b10.s1 Soares fetal_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1290	14448	27512	2.04	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01	X78815.1	NT	Glabria SR2 gene
1788	14917	28012	3.18	2.7E-01	W58067.1	EST_HUMAN	zfd2h10.f1 Soares fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14968	28059	1.48	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	16057		3.1	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular morphine transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	A137272.1	EST_HUMAN	EST175678 Infant brain, Bento Soares Homo sapiens cDNA clone UHIB01R 5' end
2260	15383	28511	0.94	2.7E-01	A137272.1	EST_HUMAN	EST175678 Infant brain, Bento Soares Homo sapiens cDNA clone UHIB01R 5' end
2440	15568	28695	7.07	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITTO089PU (M88), partial
2528	16651	28775	4.38	2.7E-01	A1310858.1	EST_HUMAN	ta36t11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046838 3' similar to contains element L1 repetitive element;
3046	18225		0.98	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3361	16533	29547	0.68	2.7E-01	8393820	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.84	2.7E-01	A1928015.1	EST_HUMAN	wc92et11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17286	30281	0.88	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4133	17286	30282	0.88	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.46	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-076-e03 CT0286 Homo sapiens cDNA
5381	18583	31452	1.98	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOXA4)
5607	18602		1.31	2.7E-01	AB033171.1	NT	Asiatic myelophthelina mitochondrial cytb gene for cytochrome b, partial cds
6472	19639	32988	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6472	19639	32989	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6745	19901	33293	1.05	2.7E-01	AE001094.1	NT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6745	19901	33294	1.05	2.7E-01	AE001094.1	NT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1)
6918	20233	33667	1.74	2.7E-01	Q61554	SWISSPROT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7167	20062		0.77	2.7E-01	A1540070.1	EST_HUMAN	Archaeoglobus fulgidus section 13 of 172 of the complete genome
7511	20585	34058	0.92	2.7E-01	Q11079	SWISSPROT	FIBRILLIN 1 PRECURSOR
							z408r08.x1 NCL_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2075103 3'
							HYPOTHETICAL 20.8 KD PROTEIN B0563.3 IN CHROMOSOME X

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20795	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20795	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7865	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7885	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20968	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7917	20968	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7976	21026	34540	0.66	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.66	2.7E-01	AA013147.1	EST_HUMAN	z35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE360567 3' similar to contains Alu repetitive element
8330	21412	34638	0.56	2.7E-01	AW668503.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8380	21461	34664	0.69	2.7E-01	R39257.1	EST_HUMAN	yc91h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE23511 3'
8486	21567	35104	0.83	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22569	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9634	22596	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9637	22602		2.66	2.7E-01	P37628	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36636	0.8	2.7E-01	D86660.1	NT	Rattus norvegicus DNA for peroxidase assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10323	23358	36968	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10455	23490	37100	1.08	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10749	23762		0.51	2.7E-01	AB011679.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.98	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.98	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11061	24137	37772	2.58	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12616	26942		1.48	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfite transporter, complete cds
13034	26881		2.75	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
482	16013	26710	2.8	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

Page 83 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip
483	13888		1.94	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812345 5'
1488	14822	27705	1.09	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1845	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1945	15088	28189	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							b60-d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14889_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2169	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	M11844.1	NT	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
2611	16735		11.68	2.6E-01	BE272440.1	EST_HUMAN	EST386835 IMAGE resequences, MAGM Homo sapiens cDNA
3181	16838		1.11	2.6E-01	AW974531.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3871	16834	29845	0.84	2.6E-01	M22342.1	NT	
3733	16994	29899	1.67	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 6
4215	17364	30352	0.79	2.6E-01	AW968510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4476	17616	30597	1.71	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-930 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4617	17764	30735	0.89	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17764	30736	0.89	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4670	17905	30794	1.14	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Strad gene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838477 5'
4770	17905	30887	2.25	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3-1) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radicata metatase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	y51e08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
5155	18277		0.61	2.6E-01	AA884625.1	EST_HUMAN	am33b11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468805 3'
5457	18657		1.29	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5565	18762	31802	0.67	2.6E-01	M96060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CopAx genes, complete cds
5689	18883		0.84	2.6E-01	AB62398.1	EST_HUMAN	MER35 repetitive element;
5865	19083	32394	0.64	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shd-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g+

Page 84 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6198	26211		2.57	2.6E-01	AE001811.1	NT	Thermoboga maritima section 123 of 139 of the complete genome
6330	19501	32959	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02e12.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element ;
6330	19501	32860	1.96	2.6E-01	AI582557.1	EST_HUMAN	is02e12.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR1 repetitive element ;
6552	19714	33090	0.98	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 87
6807	19961	33364	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
6807	19961	33365	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936156 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	is048c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148981.1	EST_HUMAN	GM0-HT0246-031169-086-f04 HT0245 Homo sapiens cDNA
7587	25848		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 46
7626	20695		0.78	2.6E-01	AA106149.1	EST_HUMAN	z92a01.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627872 5'
7918	20989	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	y37a03.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12617 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	y982a07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	MR0-HT0166-181199-003-412 HT0166 Homo sapiens cDNA
8529	21610	35148	2.97	2.6E-01	BF343598.1	EST_HUMAN	602014422F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150398 5'
8605	21696	35223	1.74	2.6E-01	Q10189	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN G11C11.02 IN CHROMOSOME II
8892	21971	35506	4.06	2.6E-01	BE830336.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9667	22623	36200	0.92	2.6E-01	X17604.1	NT	S. occidentalis INV gene for Invertase (EC 3.2.1.26)
9840	22879		0.5	2.6E-01	AF057121.1	NT	Lentia canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10072	23110	36714	1.13	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10393	23428		0.63	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10727	23760		1.09	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10940	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RPTP-alpha protein
11815	24804		31.14	2.6E-01	X31755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	26070		4.14	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12535	25365	32069	3.86	2.6E-01	AF31896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXVD2) gene, complete cds, alternatively spliced

Page 85 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
13007	25663		1.78	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 139 of the complete genome
13057	25662		2.38	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
13098	15739		1.43	2.6E-01	BE272440.1	EST_HUMAN	901128016F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2880043 5'
13107	25722		2.04	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13160	25748		2.4	2.6E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	26503	1.87	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
252	13472	26503	1.7	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
255	13484		2.51	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U00964.1	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1055	14251		1.76	2.5E-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11g07.11 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.53	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15608		11.21	2.5E-01	AE000676.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2553	15688	28814	1.22	2.5E-01	6678216	NT	Mus musculus protein-L-isopartate (D-aspartate) O-methyltransferase 1 (Pomt1), mRNA
2565	15690		1.02	2.5E-01	AA251987.1	EST_HUMAN	zot1a12.1 NCL CGAP GCBT Homo sapiens cDNA clone IMAGE:684862 5'
2702	15920	28936	1	2.5E-01	X85310.1	NT	B. taurus mRNA for D-aspartate oxidase
3499	16665		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385464 MAGe resequences, MAGM Homo sapiens cDNA
3639	16803	29815	7.18	2.6E-01	AL161617.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
3650	17108	30105	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3650	17108	30105	1.25	2.6E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4438	17576		0.88	2.8E-01	Q03314	SWISSPROT	RHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6) gene, complete cds; and Nai3 gene, exons 2-9 and 11-16
4871	18004		1.13	2.6E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30993	3.99	2.5E-01	AF007768.1	NT	Chlosterneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4904	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 63 of the complete chromosome
4925	18055		3.54	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31080	0.8	2.5E-01	BE898785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922800 5'

Page 86 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
4994	18123	31101	0.61	2.5E-01	U83858.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.62	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA418208.1	EST_HUMAN	z635a05.1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:755900 5' similar to g1c:M88278
5441	18641	31620	12.21	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6080	19262	32591	0.6	2.5E-01	AJ006345.1	NT	Homo sapiens KVLQT1 gene
6081	19263		0.81	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6762	19918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7190	20055	33465	0.64	2.5E-01	8394138	NT	Rattus norvegicus rab3 (RABIN3), mRNA
7607	20581	34054	0.71	2.5E-01	U13992.1	NT	Feline calicivirus CF168 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7536	20609		1.13	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7770	20828	34319	0.62	2.5E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
7814	20969	34365	4.23	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8028	21111	34630	2.22	2.5E-01	BF109040.1	EST_HUMAN	757a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8039	21122	34642	0.61	2.5E-01	BE980712.1	EST_HUMAN	601653391R2 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3828198 3'
8421	21502	35034	1.9	2.5E-01	BF038665.1	EST_HUMAN	601458238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	ETB PROTEIN, SMALL T-ANTIGEN (ETB 19K)
8837	21818	35454	4.07	2.5E-01	H53236.1	EST_HUMAN	y48407.11 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:202501 5'
9076	22155	35699	1.05	2.5E-01	M88628.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9716	22781	36361	16.85	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36339	2.44	2.5E-01	U89851.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9772	22768	36340	2.44	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10303	23338	36943	1.31	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10560	23685	37183	0.51	2.5E-01	AW581897.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10783	23796	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	Porphyria purpurea chloroplast, complete genome
10787	23800	37422	1.61	2.5E-01	X38491.1	NT	xg40c10.x1 NCJ_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
11332	24395	38043	2.96	2.5E-01	D50914.1	NT	Mouse L1Md LINE DNA
12204	25158	38834	5.16	2.5E-01	AF200528.1	NT	Human mRNA for KIAA0124 gene, partial cds
12233	26167		6.12	2.5E-01	AL161641.2	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

Page 87 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.5E-01	AF325363.1	NT	Dalia brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA036916.1	EST_HUMAN	on70d04.a1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	002132442F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271578 6'
1332	14489	27557	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1332	14489	27558	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1415	14559	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLJ-1 gene, partial
1808	16041		26.78	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1949	15002	28193	1.43	2.4E-01	AF251708.1	NT	Zaocye dhumades fructose-1,6-bisphosphatase mRNA, complete cds
2091	15231	28353	1.64	2.4E-01	AJ742958.1	EST_HUMAN	TR:060287 060287 KIAA0512 PROTEIN. ;
2206	15340	28467	1.17	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P43324	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT1 PROTEASE)
2336	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 108 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D. discoideum (Ax3-K) pona gene
2820	15934	29045	2.22	2.4E-01	X71783.1	NT	S. pombe swi6 gene
2848	16900	29069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofl (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74209.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3858	17016	30018	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17283		0.65	2.4E-01	D29980.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31286	0.65	2.4E-01	AW078598.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31287	0.65	2.4E-01	AW078596.1	EST_HUMAN	xb18a02.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5334	18447	31415	1.89	2.4E-01	U89914.1	NT	Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfurtransferase, hypothetical 16.1 kDa transcriptional regulator and hypothetical 18.2 kDa>
5335	18448	31416	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.46	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5578	18773	31819	0.9	2.4E-01	AI925707.1	EST_HUMAN	wc33d05.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457120 3'
5602	18767	31847	0.59	2.4E-01	D50871.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18984	32266	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5772	18984	32267	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds

Page 88 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5800	18950		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	25816		0.97	2.4E-01	AJ133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene)
							7154d04.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:338503 3' similar to SW:SFR4_HUMAN
							Q06170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6018	19200	32517	2.54	2.4E-01	BF592336.1	EST_HUMAN	
8108	19286	32620	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
8215	19380	32738	2.49	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
8269	19443	32792	0.94	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cAADE11 5'
8516	19681	33051	0.87	2.4E-01	AA398672.1	EST_HUMAN	z170d02.s1 Scars_testis_NHT Homo sapiens cDNA clone IMAGE:727683 3'
							w682c11.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb:J03464
6685	19824	33212	1.59	2.4E-01	AI698989.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7498	20573	34046	7.79	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7902	20954	34461	0.68	2.4E-01	AF228644.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8271	21353	34868	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8392	21473	34996	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8544	21625	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8798	21877	35416	1.18	2.4E-01	BF242784.1	EST_HUMAN	60187676F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
8332	22408	35961	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
8332	22408	35962	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
							wd43602.x1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
8763	22701	36287	8.39	2.4E-01	AI693515.1	EST_HUMAN	MER22.b1 TAR1 repetitive element ;
9905	22945	36530	0.66	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22945	36531	0.66	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10654	23689	37297	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11008	24085	37722	2.15	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11074	24148	37788	1.96	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24508	38174	1.8	2.4E-01	BE268017.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE268017.1	EST_HUMAN	601176416F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537	38175	8.04	2.4E-01	Z21647.1	NT	P.asiatica mosaic virus genomic RNA
12159	25127	38827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
12289	25932		1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12360	26258		1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)

Page 89 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12588	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for e-adlin
12839	26151		1.37	2.4E-01	BF228975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
13072	25701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BR gene)
13102	25718		4.16	2.4E-01	AL163261.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13507	26633	1.39	2.3E-01	S75898.1	NT	aromatase [Poephila gutturalis-zebra finches, ovary, mRNA, 3188 nt]
654	13840		5.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
684	13869	26900	28.31	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 160 of the complete genome
957	14130	27188	3.57	2.3E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1634	14788	27872	1.11	2.3E-01	AJ245480.1	NT	Braesica napus sig gene for S-Hocus glycoprotein, cultivar T2
1681	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2103	15242		1.78	2.3E-01	AJ236353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2517	15643	28764	1.85	2.3E-01	BE297718.1	EST_HUMAN	601175592F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531013 5'
2717	15835	28945	0.98	2.3E-01	M11919.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB015033.1	NT	Methanobacterium formicicum gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
3028	16204	29227	1.08	2.3E-01	AA601379.1	EST_HUMAN	no16008.s1 NCI_CGAP_Phat1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element T-HR repetitive element;
3153	16328		7.08	2.3E-01	R21732.1	EST_HUMAN	y21b07.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:130357 3'
3456	16623	29644	1.32	2.3E-01	H69836.1	EST_HUMAN	y67h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3944	17103	30100	0.98	2.3E-01	S62821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, Intron 1) [Rats, Morris hepatoma cell line, Genomle, 2212 nt, segment 1 of 3]
4046	17202		5.15	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4470	17610	30586	0.86	2.3E-01	R82252.1	EST_HUMAN	y17101.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:148017 5'
4520	17658		1.91	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4573	17710	30893	1.12	2.3E-01	D90896.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4611	17748	30728	2.76	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4678	17811	30800	5.65	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 16) (PP16) mRNA
6159	18281	31246	0.87	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5223	18345		1.03	2.3E-01	M10364.1	NT	Human gamma-B-crystallin (gamma 2-1) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5260	18379	31343	0.63	2.3E-01	BF574604.1	EST_HUMAN	602132270F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5419	18620	31596	2.47	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	7k30b08.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476699 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5647	18841	32122	5.25	2.3E-01	X96687.1	NT	C.familiaris rom1 gene
5766	18968		0.99	2.3E-01	L39112.1	NT	Vittiforma coneum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6062	19244	32569	1.98	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6062	19244	32570	1.98	2.3E-01	A1708940.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6794	19949	33348	0.66	2.3E-01	AF198089.1	NT	Oryzobagus cuticulus cytochrome oxidase subunit VIa (cox1a2) mRNA, complete cds; nuclear gene for mitochondrial product
7017	20153	33573	4.63	2.3E-01	A1718148.1	EST_HUMAN	as42H12.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element.
7260	20343	33795	0.88	2.3E-01	8923823	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7440	20517	33959	0.76	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7573	20646	34123	2.54	2.3E-01	AF176388.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7576	20648	34125	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLDGB08 5'
7576	20648	34128	5.37	2.3E-01	AV719681.1	EST_HUMAN	AV719681 GLC Homo sapiens cDNA clone GLDGB08 5'
7784	20840		4.26	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
7789	20845	34338	1.58	2.3E-01	BE888071.1	EST_HUMAN	601511973F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7931	20981		2.8	2.3E-01	N80983.1	EST_HUMAN	za12e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282358 5'
7968	21018	34530	0.71	2.3E-01	11416821	NT	Homo sapiens protobacterin alpha cluster (LOC639960), mRNA
7968	21018	34531	0.71	2.3E-01	11416821	NT	Homo sapiens protobacterin alpha cluster (LOC639960), mRNA
8036	21118	34637	0.52	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
8183	21265	34788	1.73	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8690	21770	35300	0.62	2.3E-01	U57099.1	NT	Mus musculus prosaposin (psap/SGP-1) gene, complete cds
8872	22051	35594	0.58	2.3E-01	AW080541.1	EST_HUMAN	xc9e06.x1 NCL CGAP Brn35 Homo sapiens cDNA clone IMAGE:2591554 3'
9089	22168	35715	0.52	2.3E-01	AW064460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9341	22417	35970	0.64	2.3E-01	AA372184.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9341	22417	35971	0.64	2.3E-01	AA372184.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9780	22820	36398	0.5	2.3E-01	6078318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9930	22970	36559	0.53	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2966739 5'
9985	23024	36616	0.81	2.3E-01	AW064460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
10037	23075	36875	1.57	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))

Page 91 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10071	23108	38712	0.63	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281298-001-04 DT0036 Homo sapiens cDNA
10138	23176	38773	2.62	2.3E-01	BE173060.1	EST_HUMAN	MRQ-HIT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	38823	2.48	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10888	23692	37302	0.94	2.3E-01	AF201829.1	NT	Murine hepatitis virus strain 2, complete genome
10871	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601846155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
11485	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11485	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11833	24713	38404	2.43	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 64 of the complete genome
12098	25078		1.36	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
12281	25210		3.07	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-8 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25264		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCOE44 5'
12385	25873		1.23	2.3E-01	AA08819.1	EST_HUMAN	chm1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12464	26086	31657					xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12500	26143	31552	4.08	2.3E-01	AW303623.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element;
12553	25378		7.05	2.3E-01	BE882484.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908889 5'
12812	25411		1.77	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12708	25470		2.74	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	25411		1.22	2.3E-01	U49645.1	NT	Pleurodeles waltii distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
			1.84	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
13009	25865						nac39h12.x1 Lupeki_celatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
			2.36	2.3E-01	BF47581.1	EST_HUMAN	MER38 repetitive element;
92	13327	26355					oz14at10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1875280 3' similar to
1596	14749	27833	1.13	2.2E-01	AJ052190.1	EST_HUMAN	TR:Q13040 O13040 ATP-BINDING CASSETTE PROTEIN;
2155	15291	28418	2.74	2.2E-01	AF187860.1	NT	Homo sapiens PPAR delta gene, promoter region
2476	15903	28728	2.19	2.2E-01	M34640.1	NT	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2654	16777	28890	7.18	2.2E-01	BF677638.1	EST_HUMAN	60208608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249869 5'
2654	16777	28891	1.63	2.2E-01	BE618258.1	EST_HUMAN	601482629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	29136	1.63	2.2E-01	BE618258.1	EST_HUMAN	601482629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866190 5'
2946	16123	29137	4.94	2.2E-01	BE155025.1	EST_HUMAN	PM2-HT0353-261299-003-a12 HT0353 Homo sapiens cDNA
			4.94	2.2E-01	BE155025.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2987	16163		2.07	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3479	16848		2.35	2.2E-01	AL161682.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82

Page 92 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3848	17008	30009	0.82	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17380	30349	0.89	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.8	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	6.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K ⁺ channel subunit (Kcnk6) genes, complete cds
4379	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meik1) mRNA, complete cds
4379	17522	30503	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Meik1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.08	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31059	2.2	2.2E-01	AA211216.1	EST_HUMAN	zq87c05.r1 Stratagene hNT neuron (zq87233) Homo sapiens cDNA clone IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13298.1	NT	Mus musculus vinculin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog 2 (DIAPH2), transcript variant 156, mRNA
6874	19084		3.75	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538989
6122	19301	32640	0.78	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U87087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6845	19886	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukulin, complete cds
7168	20299	33742	10.63	2.2E-01	AV755238.1	EST_HUMAN	AV755238 BM Homo sapiens cDNA clone BMFAHC06 5'
7279	20362	33815	1.81	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7279	20362	33816	1.81	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphoglycerate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7442	20519	33991	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7855	20723	34199	0.62	2.2E-01	AE000035.2	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7878	20930	34436	0.88	2.2E-01	AF287987.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7905	20957	34463	0.71	2.2E-01	AB024553.1	NT	Bacillus halodurans DNA, complete and partial cds, strain C-125
8210	21292		2.45	2.2E-01	AF155143.1	NT	Mus musculus mm23-M1 gene, promoter region
8280	21362	34881	2.68	2.2E-01	Z46933.1	NT	E.coli sepA and sepB genes
8748	21827	35363	0.81	2.2E-01	AJ132918.1	NT	Pan troglodytes MeCP2 gene 3'UTR
9083	22182	35705	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds

Page 93 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
9097	22176	35720	4.58	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
9117	22198	35740	0.48	2.2E-01	U09564.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-5) gene, complete cds
9224	22302		2.88	2.2E-01	AW855038.1	EST_HUMAN	PM3-CT0263-241288-009-507 CT0263 Homo sapiens cDNA
9315	22391	35942	1.98	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9399	22473	36039	1.13	2.2E-01	BF375354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9489	22546	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	z0408.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:281561 5'
9507	22773	36345	15.08	2.2E-01	P48834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9552	22817	36187	0.76	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9576	22718	36286	4.29	2.2E-01	IM89843.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9820	22860	36441	0.65	2.2E-01	Q80980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36654	3.84	2.2E-01	AF187941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-hsP21) mRNA, complete cds; nuclear gene for chloroplast product
10159	23196	36792	1.53	2.2E-01	BF206607.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10380	23416	37024	1.11	2.2E-01	9629571	NT	Human herpesvirus 5, complete genome
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	y633d08.r1 Stragene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10540	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y633d08.r1 Stragene ovary (8937217) Homo sapiens cDNA clone IMAGE:75855 5'
10560	23615	37220	0.6	2.2E-01	AF068264.1	NT	Pseudomonas aeruginosa quinolone protein ethand dehydrogenase (exaA) gene, partial cds; cytochrome c680 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthase A (pqqA) genes, complete cds; and pyrroloquinone synthase A (pqqA) gene, partial cds
10659	23693		0.79	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37345	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	23888	37603	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exons 11 and A5
11389	24450	38111	1.85	2.2E-01	AF257772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24704	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68G glue gene cluster
11748	23934	37580	3.7	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25161		1.33	2.2E-01	BE870959.1	EST_HUMAN	601449937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3860870 5'
12319	28158		1.98	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>

Page 94 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	25286		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.86	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12519	25353		1.47	2.2E-01	AW661922.1	EST_HUMAN	h17602.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
13115	26148		3.08	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAH502 5'
893	14165	27228	1.88	2.1E-01	AA569289.1	EST_HUMAN	nm31et1.s1 NCL_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
996	14167	27228	0.72	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14395	27446	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1225	14395	27447	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1540	14692	27771	4.29	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and lgi2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1963	15105	28206	2.15	2.1E-01	AA908924.1	EST_HUMAN	ck73602.e1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gb:K02785
2224	15358	28488	3.55	2.1E-01	BF693073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN); 602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2991	16167	29183	2.52	2.1E-01	6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3533	16858	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	nc80b10.s1 NCL_CGAP_Cos9 Homo sapiens cDNA clone IMAGE:1159579 3'
3908	17087		5.81	2.1E-01	8938361	NT	Beta vulgaris mitochondrion, complete genome
4126	17279		0.87	2.1E-01	AE001793.1	NT	Thermotoga maritima section 105 of 136 of the complete genome
4165	17315	30310	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4165	17315	30311	1.57	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4495	17635		1.63	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
4757	17892	30871	0.93	2.1E-01	X93161.1	NT	P. falciparum mRNA for small GTPase rab11
5138	18281	31228	0.7	2.1E-01	D13587.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
5416	18618	31502	6.31	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4263001 5'
7027	20163	33585	1.05	2.1E-01	AJ223392.1	NT	Drosophila melanogaster 16S rRNA gene, partial
7038	20091	33508	1.8	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7564	20636	34111	0.77	2.1E-01	Q01986	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7564	20636	34112	0.77	2.1E-01	Q01986	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7575	20647		1.88	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7683	20935	34441	1.64	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KR19) gene, complete cds
7930	20980	34488	1.38	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

Page 95 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7930	20960	34489	1.38	2.1E-01	AF068887.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21346		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (EpB4.113), mRNA
8700	21780	35313	4.76	2.1E-01	U68399.1	NT	Hemophilus influenzae hmcD, putative haemodin processing protein (hmcC), putative ABC transporter (hmcB), putative haemodin structural protein (hmcA), and haemodin immunity protein (hmcI) genes, complete cds
8997	22076	35915	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
8997	22076	35916	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0614_11 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0614 5'
9189	22237		0.5	2.1E-01	AB022624.1	NT	Homo sapiens APCOL gene, exon 9
9237	22314	35858	6.7	2.1E-01	Z35786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9704	22763	36323	0.69	2.1E-01	N42536.1	EST_HUMAN	Y11010.11 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270954 5'
9704	22753	36324	0.68	2.1E-01	N42536.1	EST_HUMAN	Y11010.11 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270954 5'
9713	22778	36348	2.72	2.1E-01	X97378.1	NT	A. thaliana mRNA for AIRANBP1b protein
9817	22887	36437	1.02	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10536	23570	37178	1.31	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10568	23604	37209	1.97	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIACYLGLYCEROL KINASE)
10576	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	802131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'
11776	24768		1.34	2.1E-01	AI141875.1	EST_HUMAN	q65908.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1891761 3'
11862	24850		1.68	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11878	24867	38565	2.8	2.1E-01	BE180422.1	EST_HUMAN	RC3-H70622-040500-013-b11 H70622 Homo sapiens cDNA
12688	25459		1.82	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12894	25848		1.39	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916876 5'
13158	25753	31928	1.19	2.1E-01	AJ276805.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
205	13428	28460	1.92	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
547	13740		1.97	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
717	13999	26937	1.37	2.0E-01	M77088.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VH2
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1036	14204	27261	1.83	2.0E-01	D90905.1	NT	Synedocystis sp. PCC6803 complete genome, 7/27, 781449-620916
1149	14313	27369	2.81	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment H821C013
1263	14439	27508	1.19	2.0E-01	AJ132895.5	NT	Homo sapiens rac1 gene
1336	14493	27663	1.99	2.0E-01	AW384937.1	EST_HUMAN	FV1-H70422-291299-002-c06 H70422 Homo sapiens cDNA
1516	14699	27752	22.4	2.0E-01	4503408	NT	Homo sapiens dystrobrein, alpha (DTNA), mRNA
1552	14734	27815	2.68	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0605

Page 98 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14882	27973	0.98	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14804		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1796	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8822238	NT	Homo sapiens hypofibrin protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Nar-D-glucose cotransport regulator gene
2955	16132		0.79	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH85A11
3576	16741	29758	0.72	2.0E-01	P46607	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3659	16821		0.91	2.0E-01	AW238005.1	EST_HUMAN	xp18602.x1 NCI_CGAP_HNG Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3798	16959	29983	0.86	2.0E-01	P34841	SWISSPROT	MER21 repetitive element;
3802	16983		0.6	2.0E-01	6680797	NT	CED-11 PROTEIN
4688	17823		8.71	2.0E-01	BE826166.1	EST_HUMAN	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA
5152	18274	31243	6.41	2.0E-01	8922080	NT	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5243	18959	29983	0.6	2.0E-01	P34841	SWISSPROT	Homo sapiens hypofibrin protein ASH1 (ASH1), mRNA
5561	18758	31797	2.55	2.0E-01	X85600.1	NT	CED-11 PROTEIN
5859	19049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5963	19149	32484	0.82	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32709	5.99	2.0E-01	U15300.1	NT	F. rubripes DNA encoding for valyl-tRNA synthetase
6303	19476		0.74	2.0E-01	M75997.1	NT	Saccharomyces cerevisiae Halp (HAL 5) mRNA, complete cds
6559	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
6659	19818	33208	3.74	2.0E-01	AW360865.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141089-001-g06 CT0247 Homo sapiens cDNA
7603	20673	34147	0.83	2.0E-01	P84422	SWISSPROT	Mus musculus phosphotransferase-1 C isozyme (PfkC) gene, exons 3 through 7
8139	21221		6.16	2.0E-01	AF028028.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21476	35003	3.12	2.0E-01	X91191.1	NT	Andes Virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8921	22000		0.48	2.0E-01	BE562247.1	EST_HUMAN	M. musculus sp2 gene exon 14
9551	22816	36186	1.17	2.0E-01	U82511.1	NT	M. musculus sp2 gene exon 14
9590	22845	36215	0.82	2.0E-01	U71122.1	NT	Dichostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds
9758	22694		5.42	2.0E-01	AE001278.1	NT	Arabidopsis thaliana pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9847	22986	36579	0.82	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
9847	22986	36580	0.82	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10095	23133		2.24	2.0E-01	AF146692.1	NT	DAUGHTERLESS PROTEIN
							Homo sapiens filamin 2 (FLN2) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23406	37016	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23406	37017	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23484		0.8	2.0E-01	X78388.1	NT	D melanogaster DNA mobile element (hoppe)
10616	23650	37269	0.88	2.0E-01	X97121.1	NT	R. norvegicus mRNA for NTR2 receptor
11079	24164	37781	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11079	24164	37782	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	38997	1.33	2.0E-01		7524759	Chlorella vulgaris chloroplast, complete genome
11908	24895	38998	1.33	2.0E-01		7524759	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	AF208837.2	NT	Pinophytes promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12699	25965		1.64	2.0E-01	AF302773.1	NT	Homo sapiens p91n1-Lm isoform (p91n1) mRNA, complete cds
12812	25978	31851	1.63	2.0E-01	AW976287.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12952	25982	31958	1.63	2.0E-01	AI023592.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12977	26636		17.48	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
113	13344		4.89	1.9E-01		7549743	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arlnt1), mRNA
362	13673	26604	5.58	1.9E-01	AF004363.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13659	26889	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
673	13659	26900	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/delta protein kinase C-interacting protein mRNA, complete cds
680	13666	26897	6.31	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
681	13666	26897	6.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01		7305160	Mus musculus interleukin 2 receptor, gamma chain (IL2g), mRNA
1128	14283	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST67784 Fetal lung II Homo sapiens cDNA 5' end
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1466	14620		4.34	1.9E-01	AF184923.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2466	16584	28711	3.66	1.9E-01	U68066.1	NT	Homo sapiens hypodermal protein FLJ10581 (FLJ10581), mRNA
2999	16166	29181	3.81	1.9E-01	J00922.1	NT	Sigmodon hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01			Galus gallus ovalbumin (Y) gene, complete cds
3482	16850	29668	4.07	1.9E-01	D13187.1	NT	Mouse gene for immunoglobulin diversity region D1
3569	16734	20750	4.04	1.9E-01	R16467.1	EST_HUMAN	yf42f10.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129847 5'
3907	17066	30065	1.09	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4100	17255	30258	3.68	1.9E-01	AB006784.1	NT	Schistosoma haematobium DNA for cytoplasmic dynein heavy chain, complete cds
4193	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4281	17397		1.31	1.9E-01	AE001912.1	NT	Deinoceratops radiodurans R1 section 49 of 229 of the complete chromosome 1

Page 98 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489	30471	0.89	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-280700-007-d04 FN0010 Homo sapiens cDNA
4592	17728	30711	0.8	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18250		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.9E-01	AW130149.1	EST_HUMAN	x28a07.x1 NCL CGAP_UH1 Homo sapiens cDNA clone IMAGE:2819444 3' similar to gb:M73779 RETINOIC
5761	18953	32256	8.03	1.9E-01	AF127937.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
5862	19148	32463	1.08	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6008	19181		2.46	1.9E-01	AL133116.1	EST_HUMAN	Mus musculus Wrm protein (Wrm) gene, complete cds
6467	19624	32987	1.03	1.9E-01	AI762391.1	EST_HUMAN	AU133119 NT2RP4 Homo sapiens cDNA clone NT2RP401328 5'
6518	19683	33054	1.1	1.9E-01	AW148452.1	EST_HUMAN	W15402.x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:2394099 3'
7112	18538	31495	1.54	1.9E-01	R43212.1	EST_HUMAN	x14c08.x1 NCL CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2818030 3' similar to gb:X03559 ATP
7138	20273	33712	0.74	1.9E-01	AF034920.1	NT	SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7138	20273	33713	0.74	1.9E-01	AF034920.1	NT	y908a12.a1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13
7409	20487	33957	0.92	1.9E-01	U73846.1	NT	repetitive element;
7638	20707	34186	0.78	1.9E-01	U93698.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7661	20728	34204	1.38	1.9E-01	U80922.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7708	20773	34258	2.84	1.9E-01	AF072724.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
8174	21256	34778	1.83	1.9E-01	AL161557.2	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
8885	21984	35500	13.56	1.9E-01	AB033024.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
9146	22225	35768	1.5	1.9E-01	M14588.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
9146	22225	35769	1.5	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10079	23117	36719	0.77	1.9E-01	AA912486.1	EST_HUMAN	Marsupial cat beta-globin gene mRNA, partial cds
10447	23482	37090	0.81	1.9E-01	BE830353.1	EST_HUMAN	096g10.s1 NCL CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu
10447	23482	37091	0.81	1.9E-01	BE830353.1	EST_HUMAN	repetitive element;
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	RC5-E T0082-060700-022-A02 ET0082 Homo sapiens cDNA
10880	23965	37594	1.38	1.9E-01	AL161503.2	NT	RC5-E T0082-060700-022-A02 ET0082 Homo sapiens cDNA
10882	24071	37704	2.18	1.9E-01	AF223391.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
12025	25009	38711	2.21	1.9E-01	AJ243213.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
12047	25028	38736	1.48	1.9E-01	L07344.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
						NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
						NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

Page 99 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	28274	1.85	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds
270	18009	28519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	28625	1.9	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13546	28693	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1005	14178	27235	1.8	1.8E-01	AI912212.1	EST_HUMAN	wd7102.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14279	27335	2.14	1.8E-01	AF000580.1	NT	Dicotyledium discoidium plasmid Ddp5, complete genome
1317	14473	27540	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1633	14683	27765	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1633	14686	27766	1.49	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1815	15059		1.91	1.8E-01	AI733708.1	EST_HUMAN	qg22x10.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1781811 3' similar to TR:075936 075938 GAMMA BUTYROBETAINE HYDROXYLASE;
1865	15103	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	16673		3.34	1.8E-01	AW935728.1	EST_HUMAN	QV3-D70018-031289-036-g04 D70018 Homo sapiens cDNA
2863	16140		2.3	1.8E-01	AF184589.1	NT	Jonopodium aculea LEAFY protein (LEAFY2) gene, partial cds
2868	16144	29163	1.10	1.8E-01	AW182300.1	EST_HUMAN	xj4ta03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2650756 3'
3194	16369	29375	1.61	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3452	16619	29638	0.77	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4040621 3'
3712	16673	29877	0.87	1.8E-01	H03389.1	EST_HUMAN	y45601.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3712	16673	29878	0.87	1.8E-01	H03389.1	EST_HUMAN	y45601.s1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4453	17593		0.92	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4678	17813	30801	5.61	1.8E-01	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
4895	18025	31011	2.58	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya6, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A6 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5129	18254	31219	0.93	1.8E-01	X79784.1	NT	N. tabacum mRNA pNLA-35
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g08 ST0203 Homo sapiens cDNA
5206	18327	31297	2.55	1.8E-01	AF181268.1	NT	Mesocricetus auratus Na-laurocholate cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	AI439881.1	EST_HUMAN	u57e04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5291	18409	31376	1.2	1.8E-01	Y08310.1	NT	M.barkeri miaC and miaB genes

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18615	31589	0.61	1.8E-01	BE082826.1	EST_HUMAN	RC6-BT0641-300300-011-H03 BT0641 Homo sapiens cDNA
5929	19115	32426	1.19	1.8E-01	AL181594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6047	19230	32554	0.95	1.8E-01	N28828.1	EST_HUMAN	Yx38f08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:264063 5'
6256	19430	32776	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 8 (Trif8), mRNA
6258	19430	32777	0.89	1.8E-01	6678428	NT	Mus musculus Trif receptor-associated factor 8 (Trif8), mRNA
6641	19800	33189	1.16	1.8E-01	Q90Y14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6688	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	Y62H02.r1 Soares_multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:278163 5'
7146	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7146	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7202	20697	33477	0.67	1.8E-01	BE961353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
7604	20874	34148	0.81	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21889	35431	0.58	1.8E-01	AW066118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
9543	22808	36176	1.58	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9574	22716	36284	1.62	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9692	22741		0.6	1.8E-01	AA483751.1	EST_HUMAN	nh02a05.s1 NCI_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1
9774	22814	38392	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	S.commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S.commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9881	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9986	23026	36617	0.71	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.46	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10765	23918	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
10873	23958	37586	2.02	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10917	24000	37633	5	1.8E-01	U38906.1	NT	Bacteriophage T1 integrase, repressor protein (ro), dUTPase, holin and lysis genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10975	24064	37688	4.41	1.8E-01	AF019107.1	NT	Dictyostellium discoideum unknown (DG1041) gene, complete cds
11270	24338	37976	2.06	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24606	38284	1.41	1.8E-01	AW275728.1	EST_HUMAN	xp-40h10.x1 NCI_OGAP_HIN11 Homo sapiens cDNA clone IMAGE:2742683 3'

Page 101 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23936	37563	8.94	1.8E-01	X57033.1	NT	B. laurus mRNA for potassium channel
12061	25042	38761	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thrombosane receptor (Tbx2r), mRNA
12124	25104	38808	1.77	1.8E-01	AA095094.1	EST_HUMAN	cp2798 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12239	25183		1.79	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.28	1.8E-01	BF348623.1	EST_HUMAN	602019928F1 NCL CGAP Bm87 Homo sapiens cDNA clone IMAGE:4155318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q96882	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12842	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	yh48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12888	25643		4.98	1.8E-01	Y111114.1	NT	E. dispar mRNA for hexokinase (hok1)
13035	26134	31548	1.7	1.8E-01	8506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcobe), mRNA
591	13782	26801	6.4	1.7E-01	BE386184.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615788 5'
828	14006	27063	3.16	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
983	14156		1.78	1.7E-01	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1083	14249	27305	0.89	1.7E-01	AF031810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1083	14249	27308	0.89	1.7E-01	AF031810.1	NT	Lymnaea dispar nucleopolydnavirus, complete genome
1860	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2038	15178		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2922	16100	29113	2.13	1.7E-01	AF000718.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2983	16169	29186	1.47	1.7E-01	AA336909.1	EST_HUMAN	ES741651 Endometrial tumor Homo sapiens cDNA 5' end
3081	16237	29267	1.09	1.7E-01	AJ288736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3081	16237	29258	1.09	1.7E-01	AJ288736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3174	16349	29368	1.65	1.7E-01	AF081614.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16616	29637	0.81	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16699	29710	1.62	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17205	30215	6.06	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4681	17816		2.49	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4884	18014	30988	0.59	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4961	18090	31066	1.31	1.7E-01	A1247835.1	EST_HUMAN	qh57e09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element ;
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme lib (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	001587266F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5312	18429	31399	0.91	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (c-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470686.1	EST_HUMAN	nc13a02.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:U17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5524	18721	31738	1.88	1.7E-01	AA470686.1	EST_HUMAN	nc13a02.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:U17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5710	18903	32198	0.92	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6459	19626	32988	12.64	1.7E-01	H72118.1	EST_HUMAN	ys20g06.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:213658 3'
6517	19692	33052	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6517	19682	33053	0.72	1.7E-01	A1370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6992	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	000944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960249 3'
7019	20155		1.94	1.7E-01	AF026562.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7140	20275		0.69	1.7E-01	Z82910.1	NT	Homo sapiens HFE gene
7369	20448	33911	1.38	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7448	20525	33998	8.91	1.7E-01	BE734179.1	EST_HUMAN	601663022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843984 5'
7649	20718	34195	1.21	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
7668	25850	34208	0.64	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
8045	21128	34648	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
8150	21232	34752	0.75	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8472	21553	35083	7.35	1.7E-01	AF150669.1	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8472	21553	35084	7.35	1.7E-01	AF150669.1	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8895	21974	35511	0.5	1.7E-01	AW982873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8925	22004	35543	1.93	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
9049	22124	35666	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.51	1.7E-01	R77002.1	EST_HUMAN	y66g02.11 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:144242 5'
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22829	36407	9.03	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36524	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9899	22939	36525	0.54	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA

Page 103 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9916	22956	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9992	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human Immunodeficiency virus type 1 (B7.05) env gene (partial)
9992	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human Immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36645	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10605	23839	37247		1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10607	23841	37249	1.66	1.7E-01	AA629792.1	EST_HUMAN	nc60e07.s1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
10918	24002	37636	9.54	1.7E-01	BE330835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
11045	24122	37756	2.12	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613268 5'
11373	24434	38090	6.81	1.7E-01	7106300	NT	cd43a03.s1 NCL CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
11373	24434	38091	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24736	38427	1.71	1.7E-01	AA863375.1	EST_HUMAN	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
12011	24956		1.5	1.7E-01	P16272	SWISSPROT	cd45f09.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1460287 3'
12042	25023	38727	1.67	1.7E-01	P55899	SWISSPROT	ANP NUCLEOSIDASE
12042	25023	38728	1.67	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FCN LARGE SUBUNIT P51 PRECURSOR (FCN) (NEONATAL FC RECEPTOR)
12142	25117	38825	2	1.7E-01	11418157	NT	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12275	26087		1.45	1.7E-01	AL163278.2	NT	(IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12567	25920		1.18	1.7E-01	AJ824404.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
12907	25900	31972	7.24	1.7E-01	U01317.1	NT	Homo sapiens chromosome 21 segment HS21C078
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	cd45g05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC
897	15985	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	ACID RECEPTOR ALPHA-1 (HUMAN);
1561	14703	27783	4.26	1.6E-01	AF298117.1	NT	Human beta globin region on chromosome 11
1910	16053		1.27	1.6E-01	AJ235272.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
1871	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	y17512.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 9'
2041	15182		1.43	1.6E-01	U10334.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
2457	16063	28712	1.09	1.6E-01	X94232.1	NT	Rickettsia prowazekii strain Madrid E, complete genome; segment 3/4
2562	16987	28813	2.73	1.6E-01	AB037729.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2957	16134	29149	14.1	1.6E-01	AF185589.1	NT	Craoostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	H. sapiens mRNA for novel T-cell activation protein
							Homo sapiens mRNA for KIAA1308 protein, partial cds
							Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
							Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

Page 104 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	29889	1.23	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3723	16884	29889	1.23	1.6E-01	AJ003185.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3872	17031	30030	0.82	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 83 of the complete chromosome
4144	17296	30288	1.21	1.6E-01	AF084456.1	NT	Crithidia fasciculata trypanothione 1 (bnt1) gene, complete cds
4448	17688	30569	10.91	1.6E-01	AF170880.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.6E-01	AW968601.1	EST_HUMAN	EST390677 IMAGE resequences, MAGJ Homo sapiens cDNA
4586	17723		4.39	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5060	18188	31162	1.39	1.6E-01	AA088343.1	EST_HUMAN	zB4h09.s1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:571361 3' similar to TR:E221955
5083	18211	31183	1.8	1.6E-01	AJ006359.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
5083	18211	31184	1.8	1.6E-01	AJ006359.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5345	18459		0.93	1.6E-01	AF045283.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.6E-01	L40608.1	NT	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 29
5639	18833	31809	2.9	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31809	2.9	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31809	2.9	1.6E-01	AW197496.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5651	18845	32126	1.99	1.6E-01	AF034716.1	NT	HYPOHETICAL 127.6 KD PROTEIN ;
6152	19328	32674	0.73	1.6E-01	BE925803.1	EST_HUMAN	HYPOHETICAL 127.6 KD PROTEIN ;
6558	19720	33096	2.06	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6558	19720	33097	2.06	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6939	20252	33688	0.79	1.6E-01	AB046786.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6985	20213		0.66	1.6E-01	BF683630.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7103	18530	31485	4.15	1.6E-01	AW291215.1	EST_HUMAN	Homo sapiens mRNA for KIAA1566 protein, partial cds
7451	20528	34001	0.71	1.6E-01	Z49632.1	NT	602139855F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301004 5'
7955	21005	34516	1.63	1.6E-01	AW246359.1	EST_HUMAN	U1H-B12-agg-b-06-0-U1.s1 NCJ CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7982	21031	34544	0.84	1.6E-01	67533237	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
7986	21035		1.03	1.6E-01	AL136525.1	EST_HUMAN	2822248.fpr1me NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8053	21136	34657	1.62	1.6E-01	L49349.1	NT	Mus musculus Ca-2+ dependent activator protein for secretion (Cedps), mRNA
8215	21297		0.53	1.6E-01	BE244087.1	EST_HUMAN	AU136525 PLAGE1 Homo sapiens cDNA clone PLAGE1004466 5'
8310	21392	34916	0.77	1.6E-01	U38243.1	NT	Corilla gorilla androgen receptor gene, partial exon
							TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia BAYOR-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
							Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds

Page 105 of 550
Table 4.

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21912	35450	1.08	1.6E-01	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2987771 to 3213410
9026	22105	35948	0.77	1.6E-01	R13673.1	EST_HUMAN	Y60108.11 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28873 5'
9133	22212		0.74	1.6E-01	L36861.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35792	1.85	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJ001w
9311	22387		0.76	1.6E-01	AF111167.2	NT	Homo sapiens lun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041198-011-R01 ST0200 Homo sapiens cDNA
9864	22894	36475	1.89	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJ001w
9891	22931		1.16	1.6E-01	BE155664.1	EST_HUMAN	PM2-HT0353-270100-004-F11 HT0353 Homo sapiens cDNA
10826	23859	37482	0.5	1.6E-01	11128016	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37609	2.34	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37951	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37952	1.34	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37958	1.62	1.6E-01	BE259849.1	EST_HUMAN	601145763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24438		3.5	1.6E-01	AF108064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24894	38386	7.53	1.6E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
12277	25207	38383	3.89	1.6E-01	AV719586.1	EST_HUMAN	AV719585 GIC Homo sapiens cDNA clone GICEMF07 5'
12597	25402	32043	2	1.6E-01	L14933.1	NT	Rat convertase PCS mRNA, 5' end
12630	25423		1.38	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-R01_1 LT0074 Homo sapiens cDNA
12733	25993		11.64	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12933	25915		2.71	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00704 protein, partial cds
13029	25978		5.04	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25980	31964	1.69	1.6E-01	8506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
13080	25984		1.4	1.6E-01	BE287894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3348038 5'
13169	25782		1.29	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
258	13477	26508	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
258	13477	26509	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
600	15984		2.5	1.6E-01	AV711086.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1118	14281	27337	1.44	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1121	14286	27341	2.7	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.5E-01	AW195516.1	EST_HUMAN	xs38d11.x1 NC1_GCAP_Kid11 Homo sapiens cDNA clone IMAGE:2886083 3'

Page 106 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27626	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrodipicamide succinyltransferase, complete cds (exon 1-15)
1304	14480	27627	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrodipicamide succinyltransferase, complete cds (exon 1-15)
1511	14684	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1957	15100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H-BIB-ekb-b-09-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2980	16156		0.9	1.5E-01	AW572916.1	EST_HUMAN	W556a02.2 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831878 3' similar to gb:X55072_mai
3100	16278	29280	0.91	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16294	29308	0.62	1.5E-01	O78887	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3433	16601	29620	6.78	1.5E-01	AA935049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3454	16821	29841	0.73	1.5E-01	Z23104.1	NT	α68405.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3454	16621	29842	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
						NT	L. stagnalis mRNA for G protein-coupled receptor
3851	17011	30011	2.35	1.5E-01	U09984.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3887	17028	30025	0.83	1.5E-01	7108368	NT	Mus musculus (CR/Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3881	17040	30037	0.77	1.5E-01	M67882.1	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3970	17128	30131	2.45	1.5E-01	AW65983.1	EST_HUMAN	XYNA; Thermotomacoccus; xynA; 4182 base-pairs
3987	17144	30149	0.88	1.5E-01	AJ003165.1	NT	h10106.x1 Soaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3987	17144	30150	0.88	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4161	17312	30308	1.16	1.5E-01	AW368559.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
4210	17359	30348	0.67	1.5E-01	Z12928.1	NT	RC2-H10149-191089-012-c09 H10149 Homo sapiens cDNA
4299	17442	30428	9.85	1.5E-01	AL163284.2	NT	B. napus mitochondrion DNA for ORF158
4847	17680	30669	1.54	1.5E-01	BF687665.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
4874	18691	29002	2.33	1.5E-01	BF69381.1	EST_HUMAN	602057192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4068223 5'
5114	18242	31207	1.5	1.5E-01	AL161560.2	NT	602033269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5370	18573	31441	1.81	1.5E-01	P07966	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5399	18601	31571	1.33	1.5E-01	AF256652.1	NT	THROMBOSPONDIN 1 PRECURSOR
						NT	Canian crocodilus MHC class II beta chain (hclbeta) gene, complete cds
5443	18843		5.95	1.5E-01	P15186	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
6555	18849	32131	4.8	1.5E-01	AW650754.1	EST_HUMAN	IL3-C10219-180200-064F10 C10219 Homo sapiens cDNA
5697	18891	32182	6.86	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
5697	18891	32183	6.86	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6029	18212	32532	0.82	1.5E-01	4506810	NT	Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA

Page 107 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32847	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6128	19307	32848	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6188	19344	32890	2.19	1.5E-01	AJ276905.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32852	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6376	19545		1.98	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19841	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6631	25828	33179	3.68	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6661	19820	33207	4.73	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (CSORF3), mRNA
6672	19831	33220	1.51	1.5E-01	P48608	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6823	19976	33383	0.88	1.5E-01	AA714780.1	EST_HUMAN	nc90d10.s1 NCL_CGAP_GC50 Homo sapiens cDNA clone IMAGE:1241671 3'
6892	20005	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31600	6	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGC resequences, MAGK Homo sapiens cDNA
7188	25840		0.8	1.5E-01	AA811545.1	EST_HUMAN	cb73f02.s1 NCL_CGAP_GC51 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element
7365	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20822	34089	1.63	1.5E-01	AF73157.1	EST_HUMAN	wf52a08.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF296073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF296073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7778	20832	34322	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1-HF-BNO-akk-d-05-Q-U1.7 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7778	20832	34323	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1-HF-BNO-akk-d-05-Q-U1.7 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077408 5'
7818	20970	34477	0.79	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of baf1-1 (SOL3) gene, complete cds
8248	21330	34846	0.88	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21495	35026	1.1	1.5E-01	AA970317.1	EST_HUMAN	o085g12.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8507	21688		1.06	1.5E-01	BE894799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8594	21675		14.14	1.5E-01	C16800.1	EST_HUMAN	601510523FT NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (48572) Homo sapiens cDNA clone GEN-528H09 5'
8793	21872	35411	2.17	1.5E-01	D84476.1	NT	Pengaslanodon gigas growth hormone (GH) mRNA, complete cds
8814	21863		0.79	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9038	22117	35660	3.12	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
							Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9305	22381	35932	2.56	1.9E-01	N74226.1	EST_HUMAN	z59e03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298866 3' similar to
9394	22469	36033	1.34	1.9E-01	BF585465.1	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9401	22475		2.52	1.9E-01	AV754819.1	EST_HUMAN	GV:O000404 Human Pscircles Differential Display Homo sapiens cDNA
9605	22660		0.64	1.9E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9632	21095	34609	6.7	1.9E-01	U00485.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3C00080 5'
10022	23060	36656	0.71	1.9E-01	M77144.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10125	23163	36761	7.82	1.9E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10125	23163	36762	7.82	1.9E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.9E-01	X88852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10485	23530		0.51	1.9E-01	AB027759.1	NT	P. leniusculus mRNA for integrin beta subunit
10516	23551	37161	2.36	1.9E-01	A1814046.1	EST_HUMAN	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37162	2.36	1.9E-01	A1814046.1	EST_HUMAN	wk53112.x1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA
10588	23633	37242	1.22	1.9E-01	U40682.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10761	23794	37413	1.69	1.9E-01	AJ011984.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10761	23794	37414	1.69	1.9E-01	AJ011984.1	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10835	24017	37849	1.87	1.9E-01	BE088492.1	EST_HUMAN	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds.
10835	24017	37850	1.87	1.9E-01	BE088492.1	EST_HUMAN	Claviceps purpurea ps1 gene
11063	24139	37773	4.46	1.9E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
11063	24139	37774	4.46	1.9E-01	AL163280.2	NT	Claviceps purpurea ps1 gene
11331	24394	38042	1.38	1.9E-01	AW841915.1	EST_HUMAN	GM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11925	24911		1.34	1.9E-01	AI193704.1	EST_HUMAN	GM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
12232	25693		38.98	1.9E-01	BF700582.1	EST_HUMAN	GM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
12629	25422		1.64	1.9E-01	AF030358.2	NT	Homo sapiens chromosome 21 segment HS21C080
12633	25426		1.23	1.9E-01	AJ238332.1	NT	Homo sapiens chromosome 21 segment HS21C080
12696	25976		6.64	1.9E-01	R83077.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12749	25498		1.52	1.9E-01	AP001514.1	NT	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
12778	25620	32002	1.41	1.9E-01	AV741272.1	EST_HUMAN	qe72e01.x1 Soares fetal_lung_Nhl-19W Homo sapiens cDNA clone IMAGE:1744536 3' similar to
12807	26000		2.59	1.9E-01	AV741272.1	EST_HUMAN	gb:MI17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12832	25896	31857	7.68	1.9E-01	AL130074.2	NT	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285649 5'

Page 108 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13183	25769	31932	6.61	1.6E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	26138		2.28	1.6E-01	8631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13826		1.23	1.4E-01	AF009863.1	NT	Homo sapiens T cell receptor beta locus, TCRBV21S2A2 region
633	14108		3.24	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1288	14444		2.89	1.4E-01	T91884.1	EST_HUMAN	cd54c01.s1 Soares fetal liver spleen TNLPS Homo sapiens cDNA clone IMAGE:112092 3'
1787	14936		1.46	1.4E-01	6679680	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
1854	15097		1.27	1.4E-01	AW135741.1	EST_HUMAN	UI-H-B11-ecf-a-09-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720616.1	EST_HUMAN	ny72807.s1 NCL_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1283821 3'
2544	15869	28793	1.02	1.4E-01	P30706	SWISSPROT	GLYGEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2853	15987	29077	3.34	1.4E-01	AI633498.1	EST_HUMAN	wm74601.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2241665 3'
4289	17434	30421	9.45	1.4E-01	AI689094.1	EST_HUMAN	ts66c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	AI689094.1	EST_HUMAN	ts66c02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4352	17465	30475	4.28	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4531	17669		0.7	1.4E-01	AA776287.1	EST_HUMAN	z60b01.s1 Soares fetal liver spleen TNLPS S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gbX01057_mai1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element
4798	17933	30920	0.79	1.4E-01	5459881	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (Drosophila)-homolog phosphodiesterase E2)
5322	18436	31408	0.62	1.4E-01	AJ005180.1	NT	(PDE4A), mRNA
5421	18622	31598	5.21	1.4E-01	T90877.1	EST_HUMAN	lyc15c11.s1 Stratiogene lung (8637210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31621	4.33	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18644	31622	4.33	1.4E-01	AB004558.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6427	19595	32651	3.17	1.4E-01	BE326891.1	EST_HUMAN	h07c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135336 3'
6611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6611	19771	33162	4.46	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6701	19859	33249	3.7	1.4E-01	AW082798.1	EST_HUMAN	xb71d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2681761 3'
6716	19873		1.61	1.4E-01	BE266536.1	EST_HUMAN	601193523.F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3537581 5'
6739	19895	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-409 UM0036 Homo sapiens cDNA
7278	20359		0.71	1.4E-01	AL118588.1	EST_HUMAN	DKFZ761A0910_r11761 (synonym: ham2) Homo sapiens cDNA clone DKFZ761A0910 5'
7545	20617		1.78	1.4E-01	AW015373.1	EST_HUMAN	UI-H-B10-ecf-c-09-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7618	20688		0.73	1.4E-01	AI762827.1	EST_HUMAN	w04f12.x1 NCL_CGAP_G111 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN P49862 CASPASE-4 PRECURSOR ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20691	34167	0.63	1.4E-01	TS3770.1	EST_HUMAN	ya90f11.r2 Stratagene placenta (#337225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains
7689	20855	34345	0.95	1.4E-01	U85845.1	NT	Alu repetitive element
7732	20882	34490	1.02	1.4E-01	A1305192.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
8162	21244		0.54	1.4E-01	BF310268.1	EST_HUMAN	q190b12.x1 Soares_NIHMP_U_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8670	21750		1.32	1.4E-01	AV539047.1	EST_HUMAN	601894760.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
							AV569047 GLC Homo sapiens cDNA clone GLCFSH06 3'
8884	22063		0.6	1.4E-01	A1436093.1	EST_HUMAN	tr92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
9114	22193	35738	4.04	1.4E-01	AA307073.1	EST_HUMAN	TR:002710 002710 GAG POLYPROTEIN ;
9194	22272	35810	0.76	1.4E-01	AW023636.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22398	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	y110h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9368	22463	36027	8.52	1.4E-01	BF310959.1	EST_HUMAN	y110h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
							601895465.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9475	22632	36096	1.72	1.4E-01	W93411.1	EST_HUMAN	z194a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	element KER repetitive element ;
9547	22612	36181	0.54	1.4E-01	X73293.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9558	22623	36194	1.65	1.4E-01	Y10198.1	NT	M.vannielii genes rpoH, rpoB and rpoA
9558	22623	36195	1.65	1.4E-01	Y10198.1	NT	Homo sapiens PHEX gene
							Homo sapiens PHEX gene
9849	21092	34607	1.81	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	zinc finger protein (DNZ1) genes, complete cds
							C.perfringens ORF for putative membrane transport protein
10192	23229	36821	0.89	1.4E-01	AF023813.1	NT	Macromitrium levetum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10263	23328	36831	0.81	1.4E-01	AW021908.1	EST_HUMAN	partial cds
10293	23328	36932	0.81	1.4E-01	AW021908.1	EST_HUMAN	d129h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10463	23498	37109	0.76	1.4E-01	BF376285.1	EST_HUMAN	d129h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10463	23498	37110	0.76	1.4E-01	BF376285.1	EST_HUMAN	MP3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10680	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	MP3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10825	23958	37481	0.7	1.4E-01	Z99117.1	NT	y474d03.r1 Soares fetal liver spleen rNFLS Homo sapiens cDNA clone IMAGE:111366 5'
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
11081	24156	37793	2.67	1.4E-01	R53400.1	EST_HUMAN	ca59a03.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1320364 3'
11282	24348	37885	1.69	1.4E-01	AW104982.1	EST_HUMAN	y70c05.r1 Soares breast 2NbHb1st Homo sapiens cDNA clone IMAGE:154088 5'
11354	24416	38071	1.58	1.4E-01	T86102.1	EST_HUMAN	xd73e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							y47g10.r1 Soares fetal liver spleen rNFLS Homo sapiens cDNA clone IMAGE:120930 5'

Page 111 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11364	24416	38072	1.58	1.4E-01	T88102.1	EST_HUMAN	ye47g10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120930 5'
11366	24418	38075	2.36	1.4E-01	P08948	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24827	38308	1.85	1.4E-01	X88092.1	NT	C. parvum ORF for putative membrane transport protein
11613	20817		1.57	1.4E-01	AW015373.1	EST_HUMAN	UHR-B10-eat-c-09-Q-UJ.st NCI CGAP Subt Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24805		1.51	1.4E-01	X52102.1	NT	Mus musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tahp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H6AR (H6ar) gene, complete cds
12560	25382	32038	4.68	1.4E-01	X74773.1	NT	P. salina plasmid gene secY
12574	25390		3.28	1.4E-01	11968117	NT	Rattus norvegicus deamin (Doe), mRNA
12605	25405		1.71	1.4E-01	BE98433.2	EST_HUMAN	8C1658490R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886671 3'
12827	28178		2.83	1.4E-01	BE513802.1	EST_HUMAN	8C1318638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834329 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12742	25493		4.02	1.4E-01	D64004.1	NT	Synochocystis sp. PCC6803 complete genome, 23/27, 2888767-3002865
12834	28193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25812		1.45	1.4E-01	X68192.1	NT	V. plantifolia mRNA for methyltransferase
13084	25977		3.36	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25765		1.68	1.4E-01	AW377988.1	EST_HUMAN	MRO-H10208-221298-204-cds H10208 Homo sapiens cDNA
332	13548	26576	2.27	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13946	26577	2.27	1.3E-01	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13736	26769	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13838	26868	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
887	14043	27108	1.55	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27157	1.28	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1032	14218	27274	2.14	1.3E-01	AL117078.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115285.1	NT	Borrelia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27462	1.67	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CIMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	6880957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Babylis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.09	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidiphila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucO genes and ORF151
2364	15495		1.38	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2653	15776	28889	2.78	1.3E-01	ME6918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3440	16608	29626	1.21	1.3E-01	AF195779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3816	16976	29979	0.85	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3816	16976	29980	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3822	16982	29885	1.55	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl transacylase 4 [AKR 1C4], exon 2
3905	17064	30063	0.66	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4098	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	13839	26856	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NL/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NL/Girlington/93/UK
4162	13839	26887	0.88	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NL/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NL/Girlington/93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-e03 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17445	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	xx2310.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30778	2.54	1.3E-01	BE272339.1	EST_HUMAN	601126086F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890083 5'
4748	17883	30865	0.73	1.3E-01	BF579654.1	EST_HUMAN	602154308F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4295544 5'
5314	18431	31401	0.78	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 984001-1168000 nt. position (9/7)
5440	18640	31619	1.01	1.3E-01	AW466988.1	EST_HUMAN	hs07008.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1 L1 repetitive element
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0063-100400-189-a06 UM0093 Homo sapiens cDNA
5618	18812		0.92	1.3E-01	AF107783.1	NT	Emeticella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

Page 113 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5702	18895		0.67	1.3E-01	AF056880.1	NT	Hepatitis C virus 68_C1.10 genome polyprotein gene, partial cds
5842	18032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32821	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32622	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6698	19856	33246	2.25	1.3E-01	X88891.1	NT	C. jacchus Intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	2893 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782926.1	EST_HUMAN	601486957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886079 5'
6974	20202	33629	0.7	1.3E-01	BE782926.1	EST_HUMAN	601486957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886079 5'
7195	20289		0.74	1.3E-01	BF529660.1	EST_HUMAN	602044345F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181866 5'
7412	20490		1.97	1.3E-01	H48864.1	EST_HUMAN	y33d02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
8146	21228		0.79	1.3E-01	BE272339.1	EST_HUMAN	601126006F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980063 5'
8160	21242	34762	1.58	1.3E-01	11423284	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
8182	21274	34787	1.32	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
8469	21650	35080	0.66	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL054c
8580	21661		4.96	1.3E-01	8823919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8726	21805	35342	1.26	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4289074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	y33g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL28_RAT P29316 60S RIBOSOMAL PROTEIN;
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	y33g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL28_RAT P29316 60S RIBOSOMAL PROTEIN;
9420	22494	36060	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9420	22494	36061	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9672	22634	36204	4.19	1.3E-01	AF023126.1	NT	Oryzias latipes cuniculus H+K-ATPase alpha 2c subunit mRNA, complete cds
9973	23012		0.73	1.3E-01	N86348.1	EST_HUMAN	J7937F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
10267	23292		1.07	1.3E-01	8363940	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10336	23370	36980	0.85	1.3E-01	AW861599.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdl4), mRNA
10603	25604	37244	1.08	1.3E-01	AL163246.2	NT	MR2-CT0222-201099-001-a01 CT0222 Homo sapiens cDNA
10743	23766	37389	0.65	1.3E-01	AU121231.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10797	23830	37464	0.46	1.3E-01	AW247836.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10868	23963		2.31	1.3E-01	BF330998.1	EST_HUMAN	2820837.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820837 3'
11458	24616		1.34	1.3E-01	BF092708.1	EST_HUMAN	MR4-BT0358-130700-010-108 BT0358 Homo sapiens cDNA
							MR4-TN0112-120900-102-a08 TN0112 Homo sapiens cDNA

Page 114 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11529	24585	-	3.2	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11616	24667	383364	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11618	24667	383355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.98	1.3E-01	BE279449.1	EST_HUMAN	601198052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24985	-	1.41	1.3E-01	AF012836.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	38708	1.72	1.3E-01	BE619384.1	EST_HUMAN	601473369F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683556.1	EST_HUMAN	602139780F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300863 5'
12399	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368	-	6.39	1.3E-01	AJ242790.1	NT	Gallus gallus scyt gene for lymphoblastin, exons 1-3
12984	25627	-	1.31	1.3E-01	AB026829.1	NT	Ephedra fluviatilis mRNA for sALK-6, complete cds
12995	25647	-	1.87	1.3E-01	AW001114.1	EST_HUMAN	wc24409.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 O60287 KIAA0539 PROTEIN. ;
394	13691	25668	13.87	1.2E-01	AA21744.1	EST_HUMAN	tt93b02.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb.U05760_mal
437	13237	-	1.42	1.2E-01	U88912.1	NT	ANEXIN V (HUMAN);
561	13753	-	3.82	1.2E-01	AF039442.1	NT	Dicystotellum discoideum ORF DG1016 gene, partial cds
1408	14592	27636	2.32	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1408	14592	27637	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14598	-	3.35	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1419	14572	-	0.94	1.2E-01	AL445066.1	NT	AV735249 cDNA Homo sapiens cDNA clone cDNAJB11 5'
1538	14689	-	0.94	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome, segment 4/5
1680	14812	27897	1.1	1.2E-01	Q14634	SWISSPROT	al48a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1682	14834	27919	2.88	1.2E-01	AJ285402.1	EST_HUMAN	Q16671 ANTHMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1808	14857	-	25.75	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1970	15113	-	1.66	1.2E-01	AW449368.1	EST_HUMAN	qt69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2253	15396	28514	1.66	1.2E-01	BF248490.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
2450	15378	-	0.99	1.2E-01	Z21405.1	EST_HUMAN	UHF-B13-akt-e-10-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2656	15779	28893	1.84	1.2E-01	AW996556.1	EST_HUMAN	601821567F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2903	16083	29098	1.16	1.2E-01	U18018.1	NT	HSAXAEBZT TEST1, Human adult Testis tissue Homo sapiens cDNA
2967	16143	29102	1.9	1.2E-01	AJ720470.1	EST_HUMAN	QV3-BN0046-220300-129410 BN0046 Homo sapiens cDNA
							Human ETA enhancer binding protein (ETA-F) mRNA, partial cds
							as80c09.x1 Barstead cdon HPLR187 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.U05005
							60S RIBOSOMAL PROTEIN L30 (HUMAN);

Page 115 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3001	16177	29188	3.44	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
3068	16244	29265	0.91	1.2E-01	X56882.1	NT	W heat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	16476	29498	2.62	1.2E-01	AW370658.1	EST_HUMAN	QV1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA
3330	16503		0.74	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
3568	16733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	16774	29789	1.12	1.2E-01	X56882.1	NT	W heat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	16733		1.22	1.2E-01	Z99118.1	NT	W heat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3865	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4298	17441	30428	2.1	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MRT7)
4431	17571	30552	0.59	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. suavis mitochondria orf1
5364	18557	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	my63c04.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282050 3'
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5425	18626	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	2208402.r1 Scores: parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321869 6'
5484	18683	31700	1.65	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18816	31885	1.14	1.2E-01	Z48234.1	NT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE620945.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6428	19596	32982	2.26	1.2E-01	AW845275.1	EST_HUMAN	IL0-C70031-221099-113-e04 CT0031 Homo sapiens cDNA
6493	19599	33022	1.52	1.2E-01	M2925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6561	19723	33101	0.58	1.2E-01	AA747535.1	EST_HUMAN	nx85601.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1268024 3'
6785	19940	33339	1.18	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCI CGAP_Binn7 Homo sapiens cDNA clone IMAGE:4168388 5'
7154	20288	33731	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80104.r1 Scores: fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183759 5'
7164	20288	33732	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80104.r1 Scores: fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for Interleukin enhancer binding factor 3 (alternative transcripts drbp7a, drbp7b gamma, drbp7c alpha and ILF3)
8076	21158		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-290300-002-009 BN0137 Homo sapiens cDNA
8149	21231	34751	2.45	1.2E-01	AB131753.1	EST_HUMAN	wc89g03.x1 NCI CGAP_Gc3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8197	21279	34801	0.84	1.2E-01	Q02369	SWISSPROT	Q89735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II;
8504	21585	35119	0.66	1.2E-01	A1832691.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
							aa71b10.x1 Barated colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8590	21671		10.76	1.2E-01	AY063652.1	EST_HUMAN	xc49d07.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sln (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	35266	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35267	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8887	21988		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8920	21989		0.77	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9771	22787	36338	1.3	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
10709	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
1125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24393		3.03	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38294	2.78	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAL1 (DNAL1) gene, exon 17
11593	24648	38329	1.72	1.2E-01	R40249.1	EST_HUMAN	yf80c02.s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:28980 3'
11798	24788		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12522	25355		4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12614	26126	31544	2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12732	25486		1.65	1.2E-01	AF188992.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12734	13753		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863	25574		1.4	1.2E-01	X63981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12968	25529	31981	4.89	1.2E-01	A1299902.1	EST_HUMAN	q120g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12992	25644		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12997	26050		6.44	1.2E-01	O90433	SWISSPROT	CYCLIN T
13031	26679	31060	1.47	1.2E-01	AE004428.1	NT	Vibrio cholerae chromosome II, section 85 of 93 of the complete chromosome
13221	25795		1.23	1.2E-01	AF080141.1	NT	Chryseobacterium meningosepticum G0B-1 carboxypeptidase gene, complete cds
578	13770	26792	1.56	1.1E-01	A1561003.1	EST_HUMAN	tn18c08.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2167983 3'
630	13815	26838	1.33	1.1E-01	AA569006.1	EST_HUMAN	nm00811.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06885_ma1 HEME OXYGENASE 1 (HUMAN);

Page 117 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1079	14246	27302	1.61	1.1E-01	BF697308.1	EST_HUMAN	602128847F1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.65	1.1E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1188	16031	27405	3.67	1.1E-01	AW972198.1	EST_HUMAN	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1278	14435	27503	1.88	1.1E-01	D64004.1	NT	Synechococcus sp. PCC6803 complete genome, 23/27, 2888767-3002865
1849	14701	27780	2.78	1.1E-01	AU140363.1	EST_HUMAN	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2255	15388		1.73	1.1E-01	AJ008701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2388	15519		2.02	1.1E-01	8765215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2603	15959		1.08	1.1E-01	6978678	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2833	16768		1.27	1.1E-01	AW821809.1	EST_HUMAN	RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA
2817	16085	29107	0.89	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [Homo sapiens, Genomic, 700 nt, segment 4 of 6]
3098	16274	29288	0.81	1.1E-01	F03285.1	EST_HUMAN	HSCYRF022 normalized Infant brain cDNA Homo sapiens cDNA clone c-1702 3'
3422	16591		1.56	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caena1g), mRNA
3608	16676	28685	2.09	1.1E-01	BE363186.1	EST_HUMAN	607308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29718	1.47	1.1E-01	X82135.1	NT	C reinhardtii nuclear gene on linkage group XIX
3580	16745	29763	0.71	1.1E-01	R96946.1	EST_HUMAN	y482g08.s1 Scores fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3873	18838	29846	0.7	1.1E-01	Y07695.1	NT	Alu repetitive element;
3791	16952		0.96	1.1E-01	P97364	SWISSPROT	A.immeraus gene for transposase
3800	16981	29985	1.28	1.1E-01	X52708.1	NT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (GAP-50)
4226	17374	30359	1.2	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-260100-025-g07 ST0280 Homo sapiens cDNA
							MR3-ST0280-260100-025-g07 ST0280 Homo sapiens cDNA
4233	17380		0.83	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
4367	17510		11.46	1.1E-01	AF157068.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4401	17644	30528	0.76	1.1E-01	AW802058.1	EST_HUMAN	IL5-UM0070-020500-068-008 UM0070 Homo sapiens cDNA
4762	17897	30877	0.92	1.1E-01	S44957.1	NT	Tape-1=Integral membrane protein TAPA-1 [Homo sapiens, Genomic, 1973 nt, segment 1 of 7]
4853	18083	31059	1.23	1.1E-01	Y07885.1	NT	A.immeraus gene for transposase
5134	17380		0.75	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete
5787	18979		2.69	1.1E-01	AA747216.1	EST_HUMAN	ntx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;

Page 118 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	18047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	19082	32393	0.87	1.1E-01	AL110985.1	NT	Bethydia cinerea strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32425	0.96	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4186818 6'
5927	19113	32428	0.98	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4186818 5'
5958	19144	32459	1.79	1.1E-01	X88851.1	NT	S. pombe ste8 gene encoding protein kinase
5982	19177	32498	5.15	1.1E-01	IM86533.1	NT	Providencia rettgeri penicillin G amidase gene
6150	19326	32671	1.86	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32693	1.37	1.1E-01	BE769152.1	EST_HUMAN	PM3-F70024-130600-004-f12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280989-011-a01 CT0254 Homo sapiens cDNA
6554	19716	33092	0.61	1.1E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6582	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035748 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg76d08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6742	19888	33269	3.68	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19956		2.73	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6934	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7193	20058	33488	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33489	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	26217		1.01	1.1E-01	BF382798.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853 5'
7456	25845	34007	0.98	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (877)
7708	20771	34255	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7708	20771	34256	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20888	34391	2.16	1.1E-01	P41087	SWISSPROT	TRAB PROTEIN
7872	20926		0.64	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433	3.06	1.1E-01	AA788784.1	EST_HUMAN	ar31506.s1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb:J03483
8155	21237	34758	1.98	1.1E-01	U87492.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.55	1.1E-01	AA463674.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35013	1.55	1.1E-01	AA463674.1	EST_HUMAN	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8449	21530	35039	1.28	1.1E-01	X91233.1	NT	nt04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8489	21570		0.94	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
8546	21627	35165	2.31	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-090200-001-f09 ST0270 Homo sapiens cDNA
							DKFZp547P194.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547P194.5'
							Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC
9018	22097	35637	5.67	1.1E-01	U02482.1	NT	and papD genes, complete cds

Page 119 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2398816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35663	2.25	1.1E-01	AA192153.1	EST_HUMAN	z083b12.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9243	22320	35684	2.25	1.1E-01	AA192153.1	EST_HUMAN	z083b12.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9335	22411	35864	0.71	1.1E-01	Y12727.1	NT	P. furiosus partial dph5 gene and argF gene
9366	22441	36001	2.78	1.1E-01	T72675.1	EST_HUMAN	y019h03.a1 Soares fetal liver spleen tNfLS Homo sapiens cDNA clone IMAGE:108725 3' similar to
9392	22467		0.83	1.1E-01	BE863260.1	EST_HUMAN	gbM81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9622	22677		0.89	1.1E-01	BE142305.1	EST_HUMAN	607436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3822048 5'
9698	22745		2.33	1.1E-01	BF086149.1	EST_HUMAN	CM3-H10142-271086-026-g11 HT0142 Homo sapiens cDNA
10114	23162		0.77	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-e08 GN0027 Homo sapiens cDNA
10470	23449		1.23	1.1E-01	R80590.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10544	23579	37186	1.29	1.1E-01	U60529.1	NT	y06e09.e1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147084 3'
10914	23987	37631	1.38	1.1E-01	AF245277.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
11044	16274	29288	1.78	1.1E-01	F03265.1	EST_HUMAN	Dicystotellum discoidium kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
11162	24233		2.47	1.1E-01	AF169032.1	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
11300	24386	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	Carassius auratus actin/beta A precursor, mRNA, complete cds
11483	24542	38212	2.6	1.1E-01	Z11810.1	NT	yA35f1.2.1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z.mobilis lgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11610	24568	38245	1.69	1.1E-01	BE802974.1	EST_HUMAN	Z.mobilis lgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11588	24639	38319	3.21	1.1E-01	P17437	SWISSPROT	601876924F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959088 5'
11971	24966		1.33	1.1E-01	AL161511.2	NT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
12378	25289		3.78	1.1E-01	BE767023.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12649	25910		3.18	1.1E-01	BE974556.1	EST_HUMAN	RC2-NT0112-120600-014-403 NT0112 Homo sapiens cDNA
13136	25738	31947	1.98	1.1E-01	BF239763.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
1228	14388		1.51	1.0E-01	O62855	SWISSPROT	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1301	14457	27523	2.18	1.0E-01	AI985499.1	EST_HUMAN	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1423	14577	27650	2.3	1.0E-01	AL151504.2	NT	w08d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2486577 3' similar to contains MER7.13 MER7 repetitive element;
2558	15683	28808	1.01	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3813	16973	29976	1.11	1.0E-01	BF239818.1	EST_HUMAN	U1-H-813-alc-4-07-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
4064	17220	30228	2.6	1.0E-01	BF365703.1	EST_HUMAN	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	17665	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.76	1.0E-01	A1792349.1	EST_HUMAN	ar32cd0.4, y6 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST384414 IMAGE resequences, MAGB Homo sapiens cDNA
5261	18360	31346	0.61	1.0E-01	BE389100.1	EST_HUMAN	601296969F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5436	18636		9.49	1.0E-01	W88490.1	EST_HUMAN	z652h0.4, s1 Soares fetal_liver_spleen_NF1L5_S1 Homo sapiens cDNA clone IMAGE:416695 3'
5534	18731		0.67	1.0E-01	X54015.1	NT	Xcampestis genes for sensor and regulator protein
6001	19186		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32993	0.9	1.0E-01	AA481879.1	EST_HUMAN	z641g10.51 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766258 3' similar to contains L1.13 L1 repetitive element
6479	19846	33008	0.72	1.0E-01	AA406036.1	EST_HUMAN	z667c12.51 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7164	20297		1.87	1.0E-01	R23921.1	EST_HUMAN	y634h06.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element
7914	20965		2.39	1.0E-01	Y12488.1	NT	M.musculus whn gene
8118	21200	34721	0.89	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.51 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN)
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.96	1.0E-01	AW189797.1	EST_HUMAN	x09501.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element
9387	22462	36026	1.12	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synatron mRNA, complete cds
9695	22744	36314	0.87	1.0E-01	R444933.1	EST_HUMAN	y633h04.51 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9707	22756		1.9	1.0E-01	M76726.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9750	22888		3.15	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9764	22761	36331	0.65	1.0E-01	W01955.1	EST_HUMAN	z66c10.51 Soares fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:327282 3'
10028	23064	36661	1.88	1.0E-01	BF240164.1	EST_HUMAN	601905661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW957425.1	EST_HUMAN	EST369616 IMAGE resequences, MAGC Homo sapiens cDNA
10351	23366	36965	0.62	1.0E-01	T51952.1	EST_HUMAN	y628a08.51 Stralagene fetal spleen (4837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10537	23572	37179	1.27	1.0E-01	BE782750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3639096 5'
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	AU169127 THYROT1 Homo sapiens cDNA clone THYROT100895 3'

Page 121 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
11286	24352	37891	2.17	1.0E-01	BF242946.1	EST_HUMAN	60187703F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4106089 5'
11286	24352	37982	2.17	1.0E-01	BF242946.1	EST_HUMAN	60187703F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4106089 5'
11685	24694	38374	3.64	1.0E-01	BE780543.1	EST_HUMAN	601682558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3896734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O157:H7 genomic DNA, prophage (Sakai-VT1) Inserted region, substrain:RIMD 0509952
12684	25633		1.73	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12609	26408		1.73	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12839	26119		3.11	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12873	25633		1.8	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	26085		25.82	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25728		6.58	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 69 of the complete genome
2839	15953	28060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-Ril) mRNA, complete cds
2847	15961	28070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15961	28071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16513	28528	1.31	9.9E-02	AF096810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
7110	18536	31492	5.66	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blestidin S deaminase, complete cds
8098	21181	34899	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NOI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
8098	21181	34700	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c08.x1 NOI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9457	22573	36139	1.35	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Plip), mRNA
12132	25112	38816	3.67	9.9E-02	D86880.1	NT	Human mRNA for KIAA0227 gene, partial cds
577	13769		2.18	9.8E-02	X56338.1	NT	O saliva RAmY3C gene for alpha-amylase
3214	16388	29398	3.66	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dihydrogenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17482	30463	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17482	30464	9.93	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.16	9.8E-02	M61043.1	NT	Human laminin B1 chain gene, exon 26
11747	23933	37559	1.73	9.8E-02	BF037421.1	EST_HUMAN	601460783F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
12332	26240		1.29	9.8E-02	8893751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14538	27811	1.92	9.7E-02	AB005808.1	NT	Alse arboriscentis mRNA for NADP-malic enzyme, complete cds

Page 122 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15466	28601	2.56	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-s04 HT0516 Homo sapiens cDNA
4091	17246		4.05	9.7E-02	Q99796	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
							Caudobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661	31639	0.59	9.7E-02	AF099189.1	NT	Caudobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661	31640	0.59	9.7E-02	AF099189.1	NT	complete cds
8138	18316	32857	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST366546 MAGe resequences; MAGe Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2997771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8171	21253	34775	1.54	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
							wz78509.s1 NCJ_CGAP_Qx38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
9050	22129	35673	1.49	9.7E-02	A1953984.1	EST_HUMAN	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
11472	24531		1.72	9.7E-02	U58337.1	NT	Mus musculus ligatin (Lgtn) mRNA, partial cds
2073	15213	28330	1.33	9.8E-02	A1080721.1	EST_HUMAN	oz47411.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2073	15213	28331	1.33	9.8E-02	A1080721.1	EST_HUMAN	oz47411.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4464	17604	30582	6.67	9.8E-02	Z32686.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
5117	18244	31209	0.95	9.8E-02	AW966230.1	EST_HUMAN	EST378303 MAGe resequences; MAGe Homo sapiens cDNA
6231	19408		2.75	9.8E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8017	21068		0.79	9.8E-02	6878753	NT	Mus musculus lymphocyte antigen 78 (LY78), mRNA
8571	21652		0.85	9.8E-02	AU137084.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone PLACE1005740 5'
9744	22808	36386	1.48	9.8E-02	AV687898.1	EST_HUMAN	AV687898 GKG Homo sapiens cDNA clone GKGAAH02 5'
10076	23114		1.34	9.8E-02	BE894896.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10245	23280	36876	1.04	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877	1.04	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877	1.04	9.8E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36870	0.82	9.8E-02	BF677270.1	EST_HUMAN	602086789F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10354	23388	36898	1.56	9.8E-02	AB013985.1	NT	Antirrhinum majus transposon T am3 pseudogene for transposase (in S-5 copy)
10354	23389	36999	1.56	9.8E-02	AB013985.1	NT	Antirrhinum majus transposon T am3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.8E-02	P08174	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR (CD56)
10961	24060	37694	6.27	9.8E-02	Z79702.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
12019	25003	38704	2.8	9.8E-02	AA625755.1	EST_HUMAN	zid91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
13015	25668		1.7	9.8E-02	HI14599.1	EST_HUMAN	ym19h03.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:48653 3'

Page 123 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	26743	31949	1.41	9.6E-02	AJ295624.1	NT	Gallus gallus ALPHA 10 nAChR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.18	9.5E-02	AW092395.1	EST_HUMAN	GM2-BN0023-50200-087-12 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7453	20532	34006	4.64	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34262	7.77	9.5E-02	AL161638.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8084	21146	34666	2.85	9.6E-02	BF035681.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34667	2.85	9.5E-02	BF035681.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.6E-02	BF035681.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF035681.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	26084		1.82	9.5E-02	7657416	NT	Mus musculus odd Oz12-n homolog 3 (Drosophila) (Odz3), mRNA
13097	25715		2.81	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281817 5'
3885	17142	30147	4.64	9.4E-02	Z30350.1	NT	M. capitulum DNA for CONTIG MC073
6447	19614	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7789	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and tp35 gene, partial cds
8799	21878		2.5	9.4E-02	Z46863.1	NT	Acinetobacter sp. oyeD, cobQ, cobR, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and tp35 gene, partial cds
12214	26011		7.72	9.4E-02	U31816.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13196	25760	31936	4.84	9.4E-02	U27699.1	NT	Human pepHBT-1 beta1ne-GABA transporter mRNA, complete cds
3054	16230		2.37	9.3E-02	4808260	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912625	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3329	16502	29521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133088F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4268	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601285082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4268	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601285082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4857	17980		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5778	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 174
8442	21523	35052	0.56	9.3E-02	AW566007.1	EST_HUMAN	EST68 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9324	22400		0.5	9.3E-02	AL113176.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9911	22951	36537	2.3	9.3E-02	BE962631.2	EST_HUMAN	601655988F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23429	37035	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23429	37036	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10526	23561		3.96	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B1-afix-h05-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723563 3'
12485	25933		2.08	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit
12905	25964		22.03	9.3E-02	AW469850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
13139	26010						Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1 3-galactosyl tr>
238	13460	26486	4.72	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	RS4156.1	EST_HUMAN	Y99807.r1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:41618 5'
3247	18421	29437	3.7	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMI-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3379	16551	29564	1.01	9.2E-02	AA634364.1	EST_HUMAN	trf79e01.s1 NCI_CGAP_C33 Homo sapiens cDNA clone IMAGE:926136 3'
3676	16839		1.14	9.2E-02	0755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptare), mRNA
4353	17496		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE289722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880176 5'
4760	17895	30876	3.44	9.2E-02	X96402.1	NT	G.gallus Mier-OK gene
8198	21280	34802	1.82	9.2E-02	T49920.1	EST_HUMAN	y98909.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:69808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X95256.1	NT	H.vulgaris Xylose isomerase gene
13120	28201		1.2	9.2E-02	11466872	NT	Podospira anserina mitochondrion, complete genome
436	13236	26237	2.23	9.1E-02	X77665.1	NT	O. curvulus k12 keratin gene
3760	16921		0.97	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161289-001-402 BT0349 Homo sapiens cDNA
4607	17744	30723	1.78	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 64
5848	19038	32346	1.23	9.1E-02	AF129766.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7459	26218		0.81	9.1E-02	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7546	20619	34094	12.21	9.1E-02	AW180058.1	EST_HUMAN	ca74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7852	20607	34411	0.95	9.1E-02	AP000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7887	20839	34445	1.02	9.1E-02	U98073.1	NT	Mus musculus thymoprotein zeta mRNA, complete cds
9124	22203	35746	0.98	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10642	23676		1.46	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3'end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	Tg18-Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 6276 nt]

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y1187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-8, and PRL1 genes
11441	24502	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor mRNA, complete cds
12151	25121		7.04	9.1E-02	9633484	NT	Bacteriophage Mu, complete genome
12383	26124		1.42	9.1E-02	AA178801.1	EST_HUMAN	2p38h12.s1 Streptagene muscle 837209 Homo sapiens cDNA clone IMAGE:611763 3' similar to
12473	26326		1.32	9.1E-02	AF052895.1	NT	SW:TRT3_HUMAN p46378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12896	25954		13.49	9.1E-02	AJ291390.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
13230	25799		1.27	9.1E-02	AF226888.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
							Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
							FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
763	13944	26980	6.89	9.0E-02	P15328	SW/ISSPROT	h98g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176842 3' similar to contains Alu repetitive element
1684	14816	27699	7.33	9.0E-02	BE220482.1	EST_HUMAN	IL6-UM0067-240300-050-106 UM0067 Homo sapiens cDNA
2484	15882	28710	1.18	9.0E-02	AW801364.1	EST_HUMAN	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
2864	16978	29088	4.89	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
2864	16978	29088	4.89	9.0E-02	AF138522.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
3417	16886	29603	1.11	9.0E-02	AF278135.1	NT	corticosteroid-binding globulin [Salimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30541	0.8	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30542	0.8	9.0E-02	S68757.1	NT	Plasmodium falciparum P-type ATPase 3 gene
4790	17825	30913	2.03	9.0E-02	X65740.2	NT	z68a12.1 Scerea_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287694 5' similar to
6118	19298	32634	7.2	9.0E-02	W56037.1	EST_HUMAN	PIR:S62171 S62171 small G protein - human ;
6860	20012		0.93	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element
							Escherichia coli strain E2349/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), EscD (escD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
12819	25546		1.82	9.0E-02	AF022238.1	NT	902129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27708	1.25	8.9E-02	BF701593.1	EST_HUMAN	802129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27707	1.25	8.9E-02	BF701593.1	EST_HUMAN	PMO-HT0338-251198-003-d01 HT0339 Homo sapiens cDNA
2460	15587	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	Atrichum angustatum Atranfib2 protein (Atranfib2) gene, partial cds
4316	17469		1.89	8.9E-02	AF286056.1	NT	U1H-B13-alo-f-08-0UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	U1H-B13-alo-f-08-0UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088294 3'
5972	19158	32475	2.7	8.9E-02	AW452122.1	EST_HUMAN	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
5987	19172	32494	3.34	8.9E-02	11433478	NT	

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20423	33886	1.6	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20793		1.77	8.9E-02	Z78021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA20F8
8240	21322	34839	1.19	8.9E-02	P28476	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (NNOS)
8323	21405	34932	0.76	8.9E-02	BF701685.1	EST_HUMAN	(CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34933	0.76	8.9E-02	BF701685.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8787	21876	35415	5.85	8.9E-02	AA309319.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
9819	22859	36439	0.84	8.9E-02	AL285627.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9819	22859	36440	0.84	8.9E-02	AL285627.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
9834	22973	36506	0.63	8.9E-02	AA339366.1	EST_HUMAN	MER10 repetitive element;
12213	25962		1.8	8.9E-02	P19524	SWISSPROT	qu55c05.x1 NCL_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1
12366	25262		3.82	8.9E-02	BF698918.1	EST_HUMAN	MER10 repetitive element;
12637	25393		2.75	8.9E-02	U29895.1	NT	EST144454 Fetal brain I Homo sapiens cDNA 5' end
12684	25393		2	8.9E-02	U29895.1	NT	MYOSIN-2 ISOFORM
12827	26199		1.16	8.9E-02	U40493.1	NT	60212862F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12880	26133		1.54	8.9E-02	AE001514.1	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
1404	14558	27832	0.96	8.8E-02	Q27474	SWISSPROT	Human 4-hydroxyphenylpyruvate dioxygenase gene, complete cds
4012	17169	30177	1.07	8.8E-02	AA299128.1	EST_HUMAN	Ceratitis capitata mariner transposon transposase gene, complete cds
4145	17297		6.23	8.8E-02	O00268	SWISSPROT	Helicobacter pylori, strain J99 section 76 of 132 of the complete genome
4418	17539		0.76	8.8E-02	D17520.1	NT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
7716	20780		0.71	8.8E-02	D17520.1	NT	EST11695 Uterus Homo sapiens cDNA 5' end
9188	22268	35807	2.07	8.8E-02	AA151872.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII135) (TAFII-130)
11380	24441	38099	2.79	8.8E-02	BE264455.1	EST_HUMAN	(TAFI130)
11380	24441	38100	2.79	8.8E-02	BE264455.1	EST_HUMAN	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
11541	24597	38273	5.25	8.8E-02	AL040129.1	EST_HUMAN	Sheep mRNA for angiotensinogen, complete cds
12443	25314	32080	1.19	8.8E-02	Z71561.1	NT	zfp9605.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
3785	16946	29853	4.17	8.7E-02	U82695.2	NT	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 6'
							601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
							DKFZp434D1313_r1 434 (synonym: hies3), Homo sapiens cDNA clone DKFZp434D1313 5'
							S.cerevisiae chromosome XIV, reading frame ORF YNL286w
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Page 127 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16946	28954	4.17	8.7E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and placenta membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4820	17982	30050	1.4	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
6211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189408 (section 101 of 148) of the complete genome
9429	18628	31805	5.49	8.7E-02	AA286875.1	EST_HUMAN	z555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
9429	18629	31806	5.49	8.7E-02	AA286875.1	EST_HUMAN	z555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
9884	20212	33842	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
9884	20212	33843	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7188	20033	33463	0.67	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein 1 mRNA, partial cds
8048	21129		0.56	8.7E-02	AA284532.1	EST_HUMAN	z520e03.s1 Scarses ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21793	35328	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
8713	21793	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 529 of the complete genome
10951	24033		2.01	8.7E-02	L04759.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' and
11581	24844	38326	1.48	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA: ile and tRNA: Ale genes
12431	25306		2.2	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12848	25432		2.85	8.7E-02	6878057	NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X85282.1	NT	G. gallus mRNA for vigin
1281	14437	27508	7.73	8.6E-02	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2317	15449	28591	2.2	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688643 5'
3257	16431	29448	2.35	8.6E-02	L05468.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3734	16895		3.69	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
3880	17039		0.6	8.6E-02	U28187.1	NT	Mus musculus long incubation prion protein (Prnp) and prion-like protein (Prnd) genes, complete cds
4609	17746	30725	0.66	8.6E-02	U88179.1	NT	Oryctolagus cuniculus galealin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0591 protein, partial cds
6219	18384	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19670	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19670	33038	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7755	20814	34308	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8115	21197	34716	1.09	8.6E-02	5730086	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730086	NT	Homo sapiens Smf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34880	0.58	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.6E-02	U60168.1	NT	Dicystosellum discoideum proteasome subunit C2 homolog Pric (prc) gene, complete cds
9838	22977	36568	1.24	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
9975	23014		1.4	8.6E-02	AW662153.1	EST_HUMAN	h20c08.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972846 3'
10356	23391	37001	1.07	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
11188	24257	37802	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11527	24583	38259	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11527	24583	38260	3.02	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.67	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11876	24863	38559	2.29	8.6E-02	AF283680.1	NT	Bacillus stearothermophilus BarFI methylase (Flm) and BarFI restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.59	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 194 of the complete genome
5282	18410		0.68	8.5E-02	N76915.1	EST_HUMAN	y46108.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245823 5'
5786	18978	32283	0.73	8.5E-02	AA985491.1	EST_HUMAN	oc83507.s1 NCL CGAP_Kd6 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gb:K01144 HLA
5828	18016		1.99	8.5E-02	P08089	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
6135	19314	32653	6.61	8.5E-02	AF233885.1	NT	M PROTEIN, SEROTYPE 6 PRECURSOR
8805	21884	35424	1.98	8.5E-02	6754779	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
10041	23079	36680	3.27	8.5E-02	BE833054.1	EST_HUMAN	Mus musculus myosin XV (Myo15), mRNA
10041	23079	36681	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-O70037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X76731.1	NT	RC4-O70037-200700-014-e05 OT0037 Homo sapiens cDNA
10702	23735	37340	0.82	8.5E-02	11418108	NT	V armodytes gene for armodycin C
11424	24485		8.03	8.5E-02	AF155510.1	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11446	24507	38173	3.82	8.5E-02	AB001562.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
12873	23886		2.76	8.5E-02	AJ00586.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
13070	25700		2.44	8.5E-02	AA362894.1	EST_HUMAN	Anthrithum majus mRNA for MYB-related transcription factor
2732	18070	28981	4.05	8.4E-02	W69330.1	EST_HUMAN	EST12736 Ovary II Homo sapiens cDNA 5' end
5427	18027	31603	9.84	8.4E-02	BE267153.1	EST_HUMAN	z44e11.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
6828	19881	33388	1.46	8.4E-02	AK024468.1	NT	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
8218	21300	34821	6.95	8.4E-02	BE095074.1	EST_HUMAN	Homo sapiens mRNA for FLJ00050 protein, partial cds
8043	22122	35664	1.15	8.4E-02	AF218890.1	NT	CM3-B70790-280400-162-d05 BT0780 Homo sapiens cDNA
						NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2

Page 129 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23606	37211	1.84	8.4E-02	AF735184.1	EST_HUMAN	aa88g10.x1 Barreletted codon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
10531	23655		0.48	8.4E-02	AV730882.1	EST_HUMAN	O88312 GOB-4;
12351	26254	32114	1.67	8.4E-02	AV730882.1	EST_HUMAN	AV730882 HTF Homo sapiens cDNA clone HTFBM304 5'
3682	16845	29853	7.77	8.3E-02	P76324	SWISSPROT	Y83H12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149898 5'
3709	16870	29873	0.75	8.3E-02	AF436797.1	EST_HUMAN	HYPOTHETICAL LIPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29874	0.75	8.3E-02	AF436797.1	EST_HUMAN	ht82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	8.3E-02	AF436797.1	NT	ht82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19558	32817	0.74	8.3E-02	AF436797.1	EST_HUMAN	C. thummi A2b region open reading frame, complete cds
6496	19662	33025	2.87	8.3E-02	AF052883.1	NT	wo78f11.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2481881 3'
8189	21251	34771	3.08	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8202	21284		1.06	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8495	21576		1.31	8.3E-02	AA987873.1	EST_HUMAN	og88g08.s1 NCJ CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1458422 3' similar to contains L1.11 L1 L1
9738	22803	36577	1.09	8.3E-02	AW583503.1	EST_HUMAN	og81f10.s1 NCJ CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1692779 3'
9751	22889		2.02	8.3E-02	AL161985.2	NT	Subunit of sodium potassium ATPase like
10549	23584		0.72	8.3E-02	AF020409.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
12448	26128		1.81	8.3E-02	BE98458.1	EST_HUMAN	Dictyostellum discoideum DocA (docA) mRNA, complete cds
1410	14554		9.13	8.2E-02	Y08170.2	NT	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928988 5'
1525	14878	27759	2.03	8.2E-02	AF167077.2	NT	Galus gallus mRNA for OBCAM protein gamma isoform
3141	16317		1.97	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3804	17083		1.35	8.2E-02	AL161498.2	NT	Homo sapiens chromosome 21 segment HS21C006
4114	17268	30268	0.99	8.2E-02	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4389	17542	30523	6.58	8.2E-02	P48860	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30524	6.58	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4399	17542	30525	6.58	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5192	18314	31282	3.43	8.2E-02	U76009.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5450	18550	31629	1.43	8.2E-02	BE987030.1	EST_HUMAN	Mus musculus zinc transporter (ZnT-3) gene, complete cds
7165	20298	33741	3.16	8.2E-02	AF308555.1	NT	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7910	20662		0.58	8.2E-02	AF743341.1	EST_HUMAN	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8905	21984		0.69	8.2E-02	U29397.1	NT	AV743341 CB Homo sapiens cDNA clone CBLANF07 5'
8971	22050	35593	3.24	8.2E-02	AW876126.1	EST_HUMAN	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
9799	22839	36416	4.88	8.2E-02	X04197.1	NT	RC2-P10004-031289-011-d05 P10004 Homo sapiens cDNA
							Beet necrotic yellow vein virus RNA-2

Page 130 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	23004	36599	2.27	8.2E-02	BE254318.1	EST_HUMAN	60116055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12454	25318	32094	3.93	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12686	25458	32021	1.43	8.2E-02	AW862195.1	EST_HUMAN	QV4-CT0361-021289-049-b01 CT0361 Homo sapiens cDNA
12909	25875		2.58	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
5873	19063	32371	1.03	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
5809	19874	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163278.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7756	20815		0.99	8.1E-02	A1692981.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21616	35151	0.56	8.1E-02	11428974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8535	21616	35152	0.56	8.1E-02	11426974	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
10116	23154		1.93	8.1E-02	AY005150.1	NT	xv45b11.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816061 3'
10685	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	UI-H-B13-ako-g-01-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10658	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-ako-g-01-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UI-H-B13-ako-g-01-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	38477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	16003	26246	7.61	8.0E-02	AW954663.1	EST_HUMAN	EST366723 MAGE resequences, MAGEC Homo sapiens cDNA
959	14132	27191	0.65	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1733	16046	27974	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1733	16046	27975	11.83	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1952	15095	28198	4.4	8.0E-02	BE087219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2541	15666		3.21	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4076619 5'
2581	14280	27336	1.55	8.0E-02	M23449.1	NT	Dichosellum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2685	16141	29159	1.05	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 515
3919	17078	30075	0.93	8.0E-02	AW968118.1	EST_HUMAN	EST376191 MAGE resequences, MAGEC Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4935	18065		6.87	8.0E-02	X72794.1	NT	Mus musculus gene for gelatinase B
5038	18166	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydrolipoamide succinyltransferase (DHFR) gene, s
6012	19198	32513	3.59	8.0E-02	AF275948.1	NT	complete cds, and small nuclear RNAs (uRNAs)
							Homo sapiens ABCA1 (ABCA1) gene, complete cds

Page 131 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19186	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34926	2.41	8.0E-02	AL114983.1	NT	Bdylis chineae strain T4 cDNA library under conditions of nitrogen deprivation
9589	22644	36213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9589	22644	36214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10381	23368		0.49	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.64	8.0E-02	AF217798.1	NT	Homo sapiens SGG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.69	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12496	25337	32061	3.54	8.0E-02	AJ005376.1	NT	Drosophila arena hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	15376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2899510 5'
3043	16219	29240	12.63	7.9E-02	AI582026.1	EST_HUMAN	ar08c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6681044	NT	6CS RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4932	18082		1.16	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
6836	18969		1.14	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
10234	23269	36859	5.6	7.9E-02	A1081644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds
10234	23269	36860	5.6	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
13008	25664		1.27	7.9E-02	A1761636.1	EST_HUMAN	CE08611 ;
1237	14396	27457	1.49	7.8E-02	A1763275.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
1237	14396	27458	1.49	7.8E-02	A1763275.1	EST_HUMAN	CE08611 ;
4915	18045	31035	0.6	7.8E-02	BE836331.1	EST_HUMAN	wg08h01.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
5196	17003		2.97	7.8E-02	BE260048.1	EST_HUMAN	ou56d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.k3 L1
							repetitive element ;
							ou56d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.k3 L1
							repetitive element ;
							PV3-FN0058-140700-005-f08 FN0058 Homo sapiens cDNA
							600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
7223	20087	33504	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and blycyan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505	1.1	7.8E-02	U82605.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22064	35004	0.93	7.8E-02	BE897947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22160	35702	0.69	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
9253	22330	35977	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35978	0.8	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9561	22703	36269	0.9	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
10006	23044	36637	0.56	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3989281 to 4214814
10901	23085	37616	2.19	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12910	25602	31973	1.35	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVP), gene, exons 15 through 18
1431	16038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16840		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34690	5.38	7.7E-02	AA402849.1	EST_HUMAN	zu53d11.r1 Scores over tumor NBH07 Homo sapiens cDNA clone IMAGE:741717 5' similar to TR.G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
10040	23078	36879	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36981	0.84	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 80S RIBOSOMAL PROTEIN L38 (HUMAN);
10336	23371	36982	0.84	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 80S RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24331	37972	3.98	7.7E-02	11422757	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3474	18641	29660	3.1	7.6E-02	BE514432.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3494	18661	29673	0.98	7.6E-02	AA298447.1	EST_HUMAN	EST112214 Carabellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3649	19812	29825	0.96	7.6E-02	AJ400877.1	NT	Homo sapiens ASQL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6222	19397	32746	0.99	7.6E-02	AJ061276.1	EST_HUMAN	en25g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1899730 3'
6486	19563	33015	1.14	7.6E-02	BE376328.1	EST_HUMAN	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
10101	23139		0.99	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	RC1-HT0545-020800-017-d08 HT0545 Homo sapiens cDNA
10557	23592		1.04	7.6E-02	BE959638.2	EST_HUMAN	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
10815	23948	37469	0.97	7.6E-02	X92656.1	NT	L. esculentum mRNA for triose phosphate translocator

Page 133 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10815	23848	37470	0.97	7.6E-02	X82856.1	NT	Laculatum mRNA for those phosphate translocator
11974	24959	38661	1.93	7.6E-02	AW98645.1	EST_HUMAN	QV3-BN0048-160400-161-a04 BN0046 Homo sapiens cDNA
807	13987	27039	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
807	13987	27040	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1971	15114	28214	0.99	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4630	17766	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
5974	19159	32477	1.45	7.5E-02	AI848714.1	EST_HUMAN	wg24h08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.5E-02	AI864387.1	EST_HUMAN	wl32d02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428461 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
8705	21765	35318	1.39	7.5E-02	AI116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000284 5'
10238	23273		0.49	7.5E-02	BF221730.1	EST_HUMAN	7c61c05.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3578604 3' similar to contains element MER27 repetitive element;
10711	23744	37350	0.73	7.5E-02	BF206909.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
10816	23849	37471	0.82	7.6E-02	X79460.1	NT	C.fiml DSM 20113 16S rDNA
490	13684	28718	1.41	7.4E-02	AW838647.1	EST_HUMAN	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	Equine herpesvirus 4 strain NS90567, complete genome
2848	15771		0.96	7.4E-02	6755009	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3883	16846	29854	1.21	7.4E-02	AI807885.1	EST_HUMAN	wf43h01.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4826	17659	30846	1.19	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4914	18044	31034	2.65	7.4E-02	6678442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5056	18184	31159	4.42	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
6624	19784		1.69	7.4E-02	RI17477.1	EST_HUMAN	yt14g06.r1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:32339 5'
6717	19875	33266	0.68	7.4E-02	AF030422.1	NT	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
7636	20705	34184	0.84	7.4E-02	AA605132.1	EST_HUMAN	no71d02.x1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
8085	21167	34683	1.11	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885264 5'
8698	21779	35312	1.26	7.4E-02	U56089.1	NT	Human periodic tyrosinase protein 2 (PWPP2) gene, exons 15 to 21, and complete cds
9367	22442	36002	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9367	22442	36003	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9639	21082	34593	0.58	7.4E-02	AI672939.1	EST_HUMAN	wc74d02.x1 Scores_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
9839	21082	34594	0.58	7.4E-02	AI672939.1	EST_HUMAN	wc74d02.x1 Scores_Dickgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10019	23057	36953	1	7.4E-02	U62263.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10146	23184	36780	0.49	7.4E-02	BF512678.1	EST_HUMAN	U1H-BW1-amg-g-06-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3060808 3'
11266	24335	37975	1.46	7.4E-02	AA059167.1	EST_HUMAN	z64e01.r1 Soarea retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
11914	24901	38804	1.42	7.4E-02	AI125063.1	EST_HUMAN	eo11d07.s1 Barstead aorta HPLRB3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86482
12409	26288		1.22	7.4E-02	11525893	NT	GLIA MATURATION FACTOR BETA (HUMAN);
12692	26101		3.74	7.4E-02	AW370431.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12870	25580	31995	2.61	7.4E-02	BF035099.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12882	25585	31968	1.44	7.4E-02	AJ223459.2	NT	601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5'
481	13676	26708	1.15	7.3E-02	BE964981.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
481	13676	26708	1.15	7.3E-02	BE964981.2	EST_HUMAN	601688736R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
481	13676	26708	1.15	7.3E-02	BE964981.2	EST_HUMAN	601688736R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
702	13885	26917	2.65	7.3E-02	AE001788.1	NT	Thermoboga maritima section 101 of 136 of the complete genome
1510	16040	27748	3.26	7.3E-02	AW600281.1	EST_HUMAN	CMQ-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1893	16050		15.79	7.3E-02	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5112	18240		1.02	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6682	19744	33126	1.46	7.3E-02	AA779977.1	EST_HUMAN	424a02.s1 Soarea_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7981	21030		0.98	7.3E-02	BF316087.1	EST_HUMAN	PROLINE-RICH PROTEIN MP-3
8361	21442		1.36	7.3E-02	7662107	NT	601866047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
8598	21677	36214	0.5	7.3E-02	Y10887.2	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8411	22455		1.17	7.3E-02	AB011090.1	NT	Mus musculus cdh5 gene, exon 1, partial
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	Homo sapiens mRNA for KIAA0518 protein, partial cds
122	13352	26382	0.6	7.2E-02	AE000882.1	NT	424a02.s1 Soarea_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
122	13352	26383	0.6	7.2E-02	AE000882.1	NT	gb:L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
1503	14638	27739	2.6	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1038934 (section 88 of 148) of the complete genome
1505	14658	27740	2.8	7.2E-02	AL163301.2	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1038934 (section 88 of 148) of the complete genome
2614	15738		3.34	7.2E-02	U14794.1	NT	Homo sapiens chromosome 21 segment HS21C101
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
							Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (prt) gene, internal fragment, partial cds
							U1H-BW0-ajl-e-05-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732049 3'

Page 135 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4466	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4281850 5'
5402	18604	31576	2.73	7.2E-02	U67831.1	NT	Methanococcus jannaschii section 73 of 160 of the complete genome
5403	18608	31577	8.76	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	18418		1.11	7.2E-02	BF217598.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086224 5'
7318	20400	33863	1.32	7.2E-02	BF216086.1	EST_HUMAN	601883568F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7336	20418	33878					Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		0.7	7.2E-02	AF221126.1	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21463	34987	1.53	7.2E-02	6634897	NT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.6	7.2E-02	P06143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
9284	22841		0.67	7.2E-02	Y17217.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	38430	2.19	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9861	23000	36898					Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23158	36754	4.88	7.2E-02	L14561.1	NT	
10206	23242	36833	0.96	7.2E-02	BF126389.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026438 5'
10395	23430	37037	2.34	7.2E-02	AW873187.1	EST_HUMAN	h24f11.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q8Z340 Q8Z340
			0.8	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							cd62c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10560	23595	37201					Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10692	23726	37331	2.15	7.2E-02	U82595.2	NT	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		5.57	7.2E-02	BE559214.1	EST_HUMAN	601068194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10837	23870	37492	3.47	7.2E-02	BE559214.1	EST_HUMAN	228105.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:481841 3'
11153	24224	37853	0.55	7.2E-02	AF040874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
12360	25253	32104	4.14	7.2E-02	AA773598.1	EST_HUMAN	af81a04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12411	25280		3.63	7.2E-02	AI230786.1	EST_HUMAN	AI230786 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
12474	25327		2.05	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1069839 3'
12488	25937		4.23	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
13048	25687		7.37	7.2E-02	AW600982.1	EST_HUMAN	CN44-NN1008-200300-110-c11 NN1008 Homo sapiens cDNA
			1.63	7.2E-02	AA401779.1	EST_HUMAN	257c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726484 5'
1953	15098	28197	2.05	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds

Page 136 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2366	15497	28623	6.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
8091	21173	34687	1.08	7.1E-02	AI125284.1	EST_HUMAN	q392a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
10868	23898	37521	0.53	7.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12193	25190		6.46	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
541	13734	26768	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1528	14682		1.28	7.0E-02	X96877.1	NT	Martella Mitc-1 gene
1801	14950	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	z66f04.s1 Striatagene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3'
3095	16271	29268	2.02	7.0E-02	AW138152.1	EST_HUMAN	UHHB11-acy-c-07-U1.s1 NCL_OGAP_Sub8 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30167	0.66	7.0E-02	AA815438.1	EST_HUMAN	al65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376678 3' similar to gb:K03002 60S
4155	17307	30301	1.19	7.0E-02	BE070284.1	EST_HUMAN	QV4-BT0407-280100-080-a10 BT0407 Homo sapiens cDNA
4258	17403		1.14	7.0E-02	AW792862.1	EST_HUMAN	CM0-UM0001-060300-270-a12 UM0001 Homo sapiens cDNA
4330	17473	30456	1.19	7.0E-02	AF077821.1	NT	Caris familiaris inducible nitric oxide synthase mRNA, complete cds
5045	18173	31150	7.97	7.0E-02	BF381987.1	EST_HUMAN	601816281F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4050071 5'
5493	18692		0.92	7.0E-02	Y09143.2	NT	Lumbricus rubellus mRNA for cyclophilin B
7560	20632	34107	0.9	7.0E-02	AV689285.1	EST_HUMAN	AV689285 GKC Homo sapiens cDNA clone GKCCAE08 5'
7782	20838	34331	0.68	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial ezrin, XL spliced variant (ecz gene)
9289	22375	35928	1.24	7.0E-02	9828113	NT	African swine fever virus, complete genome
9797	22837	35415	1.31	7.0E-02	K02901.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
10158	23195	36791	0.88	7.0E-02	U27266.1	NT	Human myosin binding protein H (MyBP-H) gene, complete cds
11854	24733	38424	2.6	7.0E-02	AA724295.1	EST_HUMAN	ah88a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
13022	25673	31958	1.2	7.0E-02	11421638	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
527	13720	26744	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
527	13720	26745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1364	14518		1.58	6.9E-02	4507968	NT	Homo sapiens chromosome 21 segment HS21C010
3883	17052	30051	1.34	6.9E-02	Q08364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3883	17052	30052	1.34	6.9E-02	Q08364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5302	18419	31369	4.11	6.9E-02	Z76163.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24f7
7783	20849		0.87	6.9E-02	AF164967.1	NT	M.hydrophila 115 kDa protein (p115) gene, complete cds
8242	21324		1.14	6.9E-02	U12022.1	NT	Canine distemper virus strain A75/17, complete genome
8750	21829	35368	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							901340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

Page 137 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8750	21829	35367	1.01	6.9E-02	BE567435.1	EST_HUMAN	601340681F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8320	22398	35848	0.67	6.9E-02	U22987.1	NT	Barbade duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene [ovarian cancer critical region of deletion] [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.46	6.9E-02	S81752.1	NT	DPH2L=candidate tumor suppressor gene [ovarian cancer critical region of deletion] [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12346	25251		10.94	6.9E-02	X74315.1	NT	X.laevia XPD2 mRNA for fork head protein
12524	25357		1.56	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
12770	25513		3.37	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15075	28177	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15075	28178	1.18	6.8E-02	AA496759.1	EST_HUMAN	ae30102.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1986	15099	28198	3.85	6.8E-02	AF156873.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4576	17810		0.64	6.8E-02	BE141076.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
6768	19814		0.65	6.8E-02	P20792	SWISSPROT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
7040	20063		0.99	6.8E-02	BE061890.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
7432	20509	33981	8.22	6.8E-02	AL163268.2	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
7881	20915	34420	0.6	6.8E-02	U16956.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
8483	21564	35099	6.03	6.8E-02	AJ248287.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
8483	21564	35100	6.03	6.8E-02	AJ248287.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
12141	26155		1.47	6.8E-02	T03214.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
12276	25206		1.64	6.8E-02	AA758014.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
12906	25599		1.34	6.8E-02	AW875839.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
12972	25632		2.3	6.8E-02	9910685	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
13203	26091	31660	1.24	6.8E-02	6078885	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1658	14711		2.71	6.7E-02	AF115639.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1942	15085	28186	2.17	6.7E-02	AJ220285.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
3811	16971	29973	4.48	6.7E-02	P17278	SWISSPROT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4068	17221	30229	0.74	6.7E-02	U53783.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
4068	17221	30230	0.74	6.7E-02	U53783.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
7969	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
8034	21117	34635	0.74	6.7E-02	X62695.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);

Page 138 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8034	21117	34638	0.74	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35260	0.73	6.7E-02	AW082698.1	EST_HUMAN	xb61c11.1 x1 Soares_NFL_Y_GBC_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
8800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-HB11-acr-g-01-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
8800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-HB11-acr-g-01-0-JL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1379	14534	27608	0.98	6.6E-02	A1735509.1	EST_HUMAN	af12a09.x1 Bartshead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.;
2252	15385	28513	3.73	6.6E-02	AJ289241.1	NT	mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3552	16717	29731	12.38	6.6E-02	R64306.1	EST_HUMAN	y118b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:193579 3'
3567	16732	29748	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3567	16732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5083	18221	31191	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5093	18221	31192	12.07	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	19255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728082 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
5130	19255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	z174a07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728082 5' similar to gb:L04270 TUMOR NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33284	3.92	6.6E-02	X06411.1	NT	P. vulgaris mRNA for chalcone synthase
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6749	19905	33298	0.62	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6937	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
6937	19905	33298	0.68	6.6E-02	P25159	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFIN
8133	21215	34736	1.51	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8669	21749	35287	0.77	6.6E-02	AF006055.1	NT	Dicotyledon discoidium darlin (darA) gene, complete cds
8979	22058		0.53	6.6E-02	O60673	SWISSPROT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9121	22200	35741	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
9121	22200	35742	1.28	6.6E-02	9629198	NT	Human respiratory syncytial virus, complete genome
10157	23194	36790	0.64	6.6E-02	A1458752.1	EST_HUMAN	ff97g06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
10292	23327	36930	1.5	6.6E-02	Y07848.1	NT	Homo sapiens EWS, gap22, trp22 and bam22 genes
10327	23362		0.65	6.6E-02	11430559	NT	Homo sapiens vinculin (VCL), mRNA
10710	23743	37349	0.48	6.6E-02	BF694659.1	EST_HUMAN	602080608F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
11205	24274	37911	4.95	6.6E-02	BF374248.1	EST_HUMAN	MR1-SN0064-010600-008-a12 SN0064 Homo sapiens cDNA
12761	25505		4.64	6.6E-02	9937991	NT	Mus musculus DIPB gene (Dipb), mRNA
13124	25733		1.26	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

Page 139 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
695	13785	28805	1.57	6.5E-02	BF027638.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3854178 5'
1011	14183	27245	1.3	6.5E-02	7708068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1422	14576	27649	3.38	6.5E-02	U47924.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14922	28016	2.04	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 98 of 108 of the complete genome
6676	18870	32156	2.07	6.5E-02	AA443991.1	EST_HUMAN	z449h12.s1 Soares ovary tumor NRHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M28038
6673	18832	33221	0.73	6.5E-02	BF685340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-5 BETA CHAIN (HUMAN);
7113	18539	31496	1.02	6.6E-02	U22861.1	NT	602118887F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4276029 5'
10147	23186	36781	0.57	6.5E-02	BE983200.2	EST_HUMAN	Acetabacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
10147	23185	36782	0.57	6.5E-02	BE983200.2	EST_HUMAN	60166817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3856637 3'
10683	23717	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601859817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3856637 3'
10875	23960	37589	4.45	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12163	25128		3.78	6.6E-02	M21496.1	NT	z32g05.at Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12633	25363		3.67	6.5E-02	AF102693.1	NT	Rabbit microsomal epoxide hydrolase
589	13780	28789	1.49	6.4E-02	X84549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
1770	14918	28013	0.99	6.4E-02	AE001777.1	NT	A. carterae precursor of peridinin-chlorophyll-protein (PCP) gene
1770	14918	28014	0.99	6.4E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
							Thermotoga maritima section 89 of 136 of the complete genome
5566	18763	31803	1.11	6.4E-02	AI181956.1	EST_HUMAN	se07b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR.b3
6239	18413	32761	2.64	6.4E-02	AF052733.1	NT	LTR8 repetitive element ;
6239	18413	32762	2.64	6.4E-02	AF052733.1	NT	Heliodora glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6332	19896	33069	1.23	6.4E-02	AI672698.1	EST_HUMAN	Heliodora glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	we72g12.x1 Soares_Dilegraffe_colon_NHGD Homo sapiens cDNA clone IMAGE:2346790 3'
8531	21812		2.47	6.4E-02	6753323	NT	601880428R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3850503 3'
8869	21844	35478	4.17	6.4E-02	AA083305.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9327	22403	35955	0.98	6.4E-02	AF150195.1	EST_HUMAN	K1418.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9786	22828		0.61	6.4E-02	BE834083.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9818	22958	36545	1.67	6.4E-02	AB011126.1	NT	RC1-OT0083-T50600-014-g06 OT0083 Homo sapiens cDNA
10488	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0564 protein, partial cds
10488	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24993	38697	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-LA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds

Page 140 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12008	24893	38688	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	26048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
12479	25331	32056	2.61	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF108905.1	NT	Mus musculus major histocompatibility locus class III region Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3692	18854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6264	19438	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7391	20469		1.84	6.3E-02	X87889.1	NT	H. sapiens gene encoding La autoantigen
8491	22548	36111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dornine gene, exons 1-3
10218	29264	36843	3.52	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NSSA region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10954	19438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
2549	15674	28707	1.04	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4365	17508	30499	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17840		5.06	6.2E-02	Q62161	SWISSPROT	52 KD RO PROTEIN (SJOOREN SYNDROME TYPE A ANTIGEN (SS-A)) (RQSS-A)) (RQ62)
6935	20250	33685	0.78	6.2E-02	D49530.1	NT	Spirulina platensis DNA for acetylase cyclase, complete cds.
7805	20861	34354	0.88	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21067		0.58	6.2E-02	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	26225		0.82	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	420a06.s1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9881	22730	36300	1.19	6.2E-02	AF217490.1	NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2), mRNA
11415	24476	38140	1.42	6.2E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Methanohalobium anisoplae mRNA for Chymotrypsin (chyl) gene
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12617	25415		1.24	6.2E-02	BE793085.1	EST_HUMAN	501583773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937842 5'
12703	25467	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	TR:Q9Y4S6 Q9Y4S6 HYPOTHEICAL 30.3 KD PROTEIN. [1];
266	13485	28516	3.63	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
4099	17254		2.85	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds

Page 141 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8458	21839	35068	3.65	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21940	36474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
8861	21940	36475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
10867	24048	37681	3.9	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-138-C06 HT0618 Homo sapiens cDNA
12134	25114	38818	1.66	6.1E-02	AB025333.1	NT	Epitretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26083		30.03	6.1E-02	X70966.1	NT	S. japonicum mRNA for serine-enzyme
12836	25957		1.58	6.1E-02	AI886611.1	EST_HUMAN	tz59107.x1 NCI_OGAP_Oy35 Homo sapiens cDNA clone IMAGE:2292801 3'
12963	25645		6.43	6.1E-02	AI163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1281	14447	27613	1.58	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2740	15057	28969	1.17	6.0E-02	AW968848.1	EST_HUMAN	EST380824 IMAGE resequences, MAGJ Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26362	1.53	6.0E-02	AA188730.1	EST_HUMAN	2p78c04.t1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:628310 5'
3002	13335	26363	1.53	6.0E-02	AA188730.1	EST_HUMAN	2p78c04.t1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:628310 5'
3301	18475	29496	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3301	18475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE964443.2	EST_HUMAN	60165160R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876080 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0263-011199-013-b04 BT0263 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356873 3' similar to contains L1.11 L1 L1 repetitive element;
7127	18553	31467	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA
7127	18553	31468	2.86	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF60) mRNA
7338	20418	33980	2.37	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4049228 5'
7857	20912	34417	1.78	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1764189 3'
8617	21897		0.46	6.0E-02	11468495	NT	Reclinomys americana mitochondrion, complete genome
9472	22529	36092	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_OGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.29	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_OGAP_G08 Homo sapiens cDNA clone IMAGE:2237362 3'
9606	22661	36233	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9606	22661	36234	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309787.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 80 kDa-like

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA123386.1	EST_HUMAN	zn87c08.11 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gp2XG9181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12921	25606		5.12	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
239	13461	28489	5.86	5.9E-02	AW934719.1	EST_HUMAN	OR0298 KIAA0551 PROTEIN ;
3048	16224	29246	2.77	5.9E-02	AF190269.1	NT	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
4804	17997		0.77	5.8E-02	AF168111.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
8817	21896	35435	2	5.9E-02	BF242748.1	EST_HUMAN	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
9650	21093		0.97	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus irquois related homeobox 5 (Drosophila) (hx5), mRNA
11026	24104		7.39	5.9E-02	BF572539.1	EST_HUMAN	60187609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
11835	24824		1.35	5.9E-02	BF572539.1	EST_HUMAN	Mus musculus folliatin-like (Fstb), mRNA
11850	24839		1.37	5.9E-02	AJ240733.1	EST_HUMAN	Mus musculus telomere junction
958	14129		6	5.8E-02	D80110.1	NT	Galus gallus HKC9 telomere junction
1693	14845	27929	0.97	5.8E-02	Q81768	SWISSPROT	Thiohaecilius ferrooxidans merC, merA genes and URF-1
3753	16914	29917	1.98	5.8E-02	AE001775.1	NT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
4474	17614	30593	6.79	5.8E-02	AW051927.1	EST_HUMAN	Thermotoga maritima section 87 of 136 of the complete genome
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4669	17804	30792	4.84	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:MH13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4669	17804	30793	4.84	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:MH13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4898	17831		2.1	5.8E-02	AF096284.1	NT	Galus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7855	20910	34414	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7855	20910	34415	2.76	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8866	21945	35479	0.81	5.8E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12365	25261		1.65	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12881	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	no75et1.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'
3123	16239	29312	1.14	5.7E-02	AI081644.1	EST_HUMAN	ou3ip05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3139	16315	29328	1.09	5.7E-02	AF19117.1	NT	OE08611 ;
3902	17061	30060	2.3	5.7E-02	AW968791.1	EST_HUMAN	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
4807	17941		0.95	5.7E-02	M85099.1	NT	EST378695 IMAGE resequences, MAGI Homo sapiens cDNA
							Boa taurus lyszyme gene (cow 3), complete cds

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.67	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20659	34175	0.98	5.7E-02	BE87191.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7630	20659	34176	0.68	5.7E-02	BE87191.1	EST_HUMAN	601447937F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851985 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ288090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10055	23053	36895	0.82	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11464	24523	38163	3.14	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
11464	24523	38164	3.14	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
11630	24710		1.68	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
12586	25969		18.03	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12768	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12863	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13012	26165		5.21	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	y64d10.s1 Scores breast 2Nbl-Bst Homo sapiens cDNA clone IMAGE:163523 3' similar to contains L1 repetitive element;
1556	14709	27789	1.1	5.6E-02	AF094455.1	NT	Hydrocotyle reticulifolia ribosomal protein L16 (p16) gene, intron; chloroplast gene for chloroplast product
2382	15463		1.65	5.6E-02	BE904308.1	EST_HUMAN	601464578F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3896810 5'
4763	17898	30878	1.37	5.6E-02	AB013100.1	NT	Lycopodium esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30938	1.31	5.6E-02	AA290599.1	EST_HUMAN	z45a01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700418 3'
6788	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	y02e10.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIA00905 PROTEIN ;
7031	20167	33589	1.02	5.6E-02	AA866182.1	EST_HUMAN	cd47f12.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7301	20353	33842	3.3	5.6E-02	BE008001.1	EST_HUMAN	QY0-BN0147-230400-214-g07 BN0147 Homo sapiens cDNA
8010	21060	34372	1.32	5.6E-02	A183583.1	EST_HUMAN	q664g11.x1 Scores_balis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35823	2.62	5.6E-02	BE542683.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
9002	22081	35824	2.52	5.6E-02	BE542683.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
10017	23055	36851	1.18	5.6E-02	AA482864.1	EST_HUMAN	nf49d07.s1 NCL CGAP_AVI1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C.;

Page 144 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11863	24851		2.42	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	18538	28948	7.33	5.5E-02	X97809.1	NT	H. sapiens gene encoding La autoantigen
3286	16460	29481	3.33	5.5E-02	675550.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.5E-02	L41561.1	NT	Galid herpesvirus mRNA fragment
5776	18668	32272	3.49	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18668	32272	4.32	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.5E-02	675590.2	NT	Mus musculus Irfelin 1 (Tuf1), mRNA
8311	21393	34917	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21393	34918	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8855	22895	38476	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
8855	22895	38477	0.76	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
8951	22990	38583	1.24	5.5E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
							Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glyceral dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glyceral dehydratase (dhaB)>
11271	24339	37977	6.31	5.5E-02	U09771.1	NT	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3084	16260		0.85	5.4E-02	AJ277468.1	NT	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3509	18476		8.19	5.4E-02	BE073468.1	EST_HUMAN	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
4020	17177	30186	0.61	5.4E-02	U85806.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
8316	21398		1.18	5.4E-02	Z69116.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9271	22347	35897	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37653	1.86	5.4E-02	U20780.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-160700-021-D06 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC8-FN0112-160700-021-D06 FN0112 Homo sapiens cDNA
12463	26850		3.72	5.4E-02	U44604.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1535	14888	27768	20.57	6.3E-02	T84769.1	EST_HUMAN	ye37112.1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb:K01506
2566	15691	28816	3.22	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
3008	16184	29207	0.97	5.3E-02	M58417.1	NT	Pseudomonas putida tfgS gene
3008	16184	29208	0.97	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29406	4.83	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5200	18321	31290	7.98	5.3E-02	M80463.1	NT	Pseudomonas putida tfgS gene
							Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

Page 145 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31612	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
5434	18634	31613	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6228	19403	32753	1.14	5.3E-02	M85288.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
7024	20160	33580	4.02	5.3E-02	9895413	NT	Lymphocystis disease virus 1, complete genome
7241	20225	33769	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 193 of the complete genome
7617	20590		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
8061	21073	34585	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF8-SP011 INTERGENIC REGION
8000	21881		0.68	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cyclatin C (cst3) gene, complete cds
9325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospira anserina mitochondrial epsilon-actin DNA
10482	23497		0.61	5.3E-02	Y07907.1	NT	D.reio mRNA for zp-23 POU gene, splice variant (neurula, 8-16 hpf and postmitogenesis, 20-28 hpf)
10638	23573	37180	0.79	5.3E-02	X68432.1	NT	B.reio pou3f mRNA for transcription factor
13173	25761	31631	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2388	15489		64.04	5.2E-02	5031908	NT	Homo sapiens mspn A, alpha (PABA peptide hydrolase) (MEPTA) mRNA
3183	16358	28363	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	16358	28384	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17208	30216	0.8	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Cid1) mRNA, complete cds
4393	17636	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nrl-1 mRNA, complete cds
5287	18408	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32645	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.94	5.2E-02	AI830955.1	EST_HUMAN	vj80e04.x1 NC1 CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7424	20801	33972	1.23	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8389	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9831	22871	36560	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9931	22971	36561	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25483		1.8	5.2E-02	Q03030	SWISSPROT	OVALOATE DECARBOXYLASE ALPHA CHAIN
2437	15565		0.98	5.1E-02	AL134071.1	EST_HUMAN	DKFZp647D073 r1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp647D073 5'
5161	18283	31248	0.89	5.1E-02	BE967423.2	EST_HUMAN	80165505R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3888361 3'
5281	18372		0.66	5.1E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
5348	18482		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	18868	33370	0.79	5.1E-02	AF280369.1	NT	HIV-1 patient 95 from Italy protease (pol) gene, complete cds

Page 148 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6997	18516	31508	1.73	5.1E-02	BF378625.1	EST_HUMAN	QV0-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8447	21528	35058	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8542	21623	35160	1.42	5.1E-02	A131966.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
9086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36646	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10384	23419	37028	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487	26721	2.8	5.0E-02	AF098004.1	NT	Quercus melo polygalacturonase precursor (MPG3) mRNA, complete cds
495	13690	26721	2.8	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2879	14182	27244	10.88	5.0E-02	U72742.1	NT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
3418	16587		1.36	5.0E-02	7305610	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3684	16847		1.01	5.0E-02	U32782.1	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3775	16936	29842	5.9	5.0E-02	U12769.2	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
4941	18071		1.05	5.0E-02	P40232	SWISSPROT	Antheraea pernyi period clock protein homolog mRNA, complete cds
6258	19432	32779	0.64	5.0E-02	AF098264.1	NT	CASEIN KINASE II BETA CHAIN (CK II)
6438	18605		1.28	5.0E-02	AJ242825.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
7128	18554	31459	0.58	5.0E-02	P35616	SWISSPROT	Mus musculus Dmp-1 gene, exons 1-6
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
7913	20904		0.67	5.0E-02	AW062464.1	EST_HUMAN	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10403	23438	37045	1.37	5.0E-02	AF305238.1	NT	MRO-CT0064-100899-002-g10 CT0064 Homo sapiens cDNA
10855	23888		0.55	5.0E-02	BF213260.1	EST_HUMAN	Mus musculus Fes-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
11782	24772	38468	2.28	5.0E-02	U67600.1	NT	601844753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4070101 5'
12229	26004		4.7	5.0E-02	D04047	SWISSPROT	Methanococcus jannaschii section 142 of 150 of the complete genome
231	13452		11.82	4.9E-02	M14230.1	NT	NO-ON-TRANSIENT A PROTEIN
380	13588	26623	4.18	4.9E-02	AF275948.1	NT	Chicken 28 kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	26624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2937	16114	29126	0.71	4.9E-02	U32636.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3360	15532	29646	1.85	4.9E-02	P54258	SWISSPROT	Zea mays phytoene synthase (Y1) gene, complete cds
							ATROPHIN-1 (IDENTATORUBRAL-PALLIDOLYSIN A TROPHY PROTEIN)

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3660	16823		0.85	4.9E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3681	16944	28851	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	16944	28852	0.78	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4984	18093	31069	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4984	18093	31070	2.84	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5488	18885	31702	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5488	18885	31703	1.82	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7292	20374	33831	1.79	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21884		1.07	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.9E-02	BE931532.1	EST_HUMAN	MRO-H70408-170800-003-408 HT0408 Homo sapiens cDNA
8954	22033	35575	0.97	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.64	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR ES
10802	23835	37459	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.9E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24686	38376	3.46	4.9E-02	AF008303.1	NT	Homo sapiens propro placental TGF-beta gene, complete cds
12957	25624		3.23	4.9E-02	M19384.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26592	1.19	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26592	2.61	4.9E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13686	26726	11.53	4.9E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	15478	28910	2.08	4.9E-02	W51983.1	EST_HUMAN	zz46b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325511 3' similar to gb:M30598 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3280	16454	29476	1.79	4.9E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4793	17928		1.08	4.9E-02	Z54280.1	NT	S. scrofa gene for skeletal muscle tyrosine receptor
5237	18359	31328	0.98	4.9E-02	U91914.1	NT	Streptococcus constellatus D-alanine-D-alanine ligase gene, partial cds
8332	21414	34940	1.41	4.9E-02	AW389497.1	EST_HUMAN	MR2-S10129-221098-012-B02 ST0129 Homo sapiens cDNA
9329	22405	35957	1.01	4.9E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	35958	1.01	4.9E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24288	37928	1.84	4.9E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
11219	24288	37929	1.84	4.9E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.46	4.9E-02		9632893	Streptococcus thermophilus bacteriophage Sfi19, complete genome
5122	18248	31214	0.74	4.7E-02	6981261	NT	Rattus norvegicus Nestin (Nes), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6969	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	y297f09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:291017 5' similar to contains Alu repetitive element;
7025	20161	33561	0.69	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33562	0.69	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Ret statin-related protein (s1) gene, complete CDS
8445	21526	35053	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9154	22232	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9176	22254		2.97	4.7E-02	AB026678.1	NT	Gallus gallus Wpki-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-38-DNA-binding protein
9936	22875		0.7	4.7E-02	AB73042.1	EST_HUMAN	we76c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLO Homo sapiens cDNA clone GLCBK002 3'
281	13499	26531	0.69	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13939	26984	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14476		1.49	4.6E-02	A1014255.1	EST_HUMAN	em50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90553
1390	14644	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	P90553 LIMA :contains element LTR1 repetitive element ;
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HT0339 Homo sapiens cDNA
2869	13499	26531	1.78	4.6E-02	BE153583.1	EST_HUMAN	xn2403.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694653 3' similar to SW:GRF1_HUMAN
3073	16249	29270	0.64	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3419	16249	29270	0.59	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3585	16249	29270	0.84	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17385		0.92	4.6E-02	AF220385.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5852	19042	32348	1.57	4.6E-02	AF076982.1	NT	Mus musculus nucleolar RNA helicase l/Gu (ddx21) gene, complete cds
6359	19529	32887	3.67	4.6E-02	X61624.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrh2) gene, complete cds
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	C.reinhardtii ebp2 (ebpB) mRNA
6359	19529	32888	3.67	4.6E-02	X61624.1	NT	C.reinhardtii ebp2 (ebpB) mRNA
6938	20251	33687	1.41	4.6E-02	A1149574.1	EST_HUMAN	pm00003.x1 Soares_placenta_8to9weeks_2NbhHP8to9W Homo sapiens cDNA clone IMAGE:1713871 3'
8007	21057	34569	0.63	4.6E-02	6978720	NT	similar to contains L1.3 L1 repetitive element ;
8856	21935	35472	3.81	4.6E-02	BE154006.1	EST_HUMAN	Rattus norvegicus Cathepsin H (Ctsh). mRNA
11689	24687	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
							027h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

Page 149 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13079	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
460	13655	26893	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1847	14983	28095	4.93	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
3817	16977	28981	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6350	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6636	18795	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene, carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
7018	20154	33574	0.59	4.5E-02	L26487.1	NT	Methanosarcina frisia carbon monoxide dehydrogenase large subunit (cdhIA) gene, carbon monoxide dehydrogenase small subunit (cdhIB) gene, complete cds
8587	21688	35207	2.24	4.5E-02	AF036684.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10165	23162	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST128167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
10305	23340	36946	0.47	4.5E-02	X86508.1	NT	A. europaeum mRNA for legumycin-like protein
10421	23458	37061	0.79	4.5E-02	AB000470.1	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12442	25313	32089	2.61	4.5E-02	11418013	NT	Homo sapiens ret finger protein-like 3 (RFP13), mRNA
12891	26051	31684	3.79	4.5E-02	AA191097.1	EST_HUMAN	204311.1 r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632463 5'
227	13449	27273	4.35	4.4E-02	BE972733.1	EST_HUMAN	601862164F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3933988 8'
1050	14216	27273	0.77	4.4E-02	L19295.1	NT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2163	15289	28609	6.82	4.4E-02	P31568	SWISSPROT	HYPOPHYSICAL PROTEIN (ORF 2280)
2559	15884	28609	1.81	4.4E-02	AW875475.1	EST_HUMAN	QV2-PT0012-010300-070-g02 P.T0012 Homo sapiens cDNA
3730	16891	28695	1.88	4.4E-02	AF159160.1	NT	Mycobacterium xenithus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30868	1.33	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4750	17885	30867	1.33	4.4E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7287	20350	33802	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
7287	20350	33803	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35672	2.34	4.4E-02	AA736969.1	EST_HUMAN	ntw13rd3.s1 NCJ_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11328	24389	38034	2.64	4.4E-02	AF060669.1	NT	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	aa33f04.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'
12159	25126		4.55	4.4E-02	AB040928.1	NT	Homo sapiens mRNA for KIAA1463 protein, partial cds
12347	26102		1.65	4.4E-02	BF241245.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
802	13962	27034	7.26	4.3E-02	AF003249.1	NT	Marotte saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15787	28671	1.55	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA/OH08 5'
3516	16682	29683	9.18	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6625	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6625	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
8871	20023	33493	0.8	4.3E-02	AA652286.1	EST_HUMAN	ns99c12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188888
8711	21791	35327	0.69	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35621	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
9001	22080	35622	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.2	4.3E-02	AL136077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/5
845	14023	27081	1.74	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM/2000020 5'
889	14085		2.4	4.2E-02	AU123327.1	EST_HUMAN	w344g01.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
919	14094	27159	1.51	4.2E-02	AW003945.1	EST_HUMAN	L1 RETROPOSOM, ORF2 MRNA ;contains L1.13 L1 L1 repetitive element ;
1758	14907		1.37	4.2E-02	AL445068.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1818	14668	28060	0.99	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3754	19919	28918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4663	17698	30982	0.99	4.2E-02	BF342895.1	EST_HUMAN	60207105F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4162672 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32224	0.74	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE268285.1	EST_HUMAN	601124596F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2889319 5'
7695	20760	34244	4.35	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34287	0.81	4.2E-02	AV790347.1	EST_HUMAN	AV790347 HTF Homo sapiens cDNA clone HTFAV-H04 5'
9010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q18650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11295	24361	38002	1.52	4.2E-02	AA976118.1	EST_HUMAN	ont3b11.s1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1598461 3' similar to gb:M65290
11587	24640	38320	2.83	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24640	38321	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-008-010 BN0174 Homo sapiens cDNA
11785	24795	38483	1.52	4.2E-02	AF178458.1	NT	PM3-BN0174-250500-008-010 BN0174 Homo sapiens cDNA
12729	26108		6.64	4.2E-02	AI683494.1	EST_HUMAN	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
13076	25705		1.17	4.2E-02	D14711.1	NT	wt49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2810850 3'
523	13718	28743	1.85	4.1E-02	AF200529.1	NT	Staphylococcus aureus HSP10 and HSP80 genes
2741	15858	28970	1.08	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4006	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	Chlamydia muridarum, section 60 of 89 of the complete genome
4006	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177607F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4595	17732		8.4	4.1E-02	AW893484.1	EST_HUMAN	601177607F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
5228	18351		0.61	4.1E-02	X85880.1	NT	QV1-NN0012-180400-164-06 NN0012 Homo sapiens cDNA
5756	18951	32253	1.08	4.1E-02	BE251894.1	EST_HUMAN	L1 monocytogenes type 3 partial lap gene (strain 443)
5759	18951	32254	1.08	4.1E-02	BE251894.1	EST_HUMAN	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343958 5'
7022	20158		0.98	4.1E-02	X75881.1	NT	601107635F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343958 5'
7248	20331	33778	1.38	4.1E-02	AE002132.1	NT	A. italiana mRNA for plasma membrane intrinsic protein 1a
7682	20747	34228	1.79	4.1E-02	7682347	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Mus musculus proviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
7942	20992	34502	2.81	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8402	21483	35011	0.74	4.1E-02	P97857	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8845	21924	35462	0.79	4.1E-02	P34887	SWISSPROT	MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
9355	22430	35988	0.87	4.1E-02	AA372388.1	EST_HUMAN	CUTICLE COLLAGEN 34
13112	28110	31868	9.61	4.1E-02	AJ271809.1	NT	EST8281 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3316	18489	29507	3.85	4.0E-02	AB040904.1	NT	Brassica napus glh gene for psalid glutamine synthetase, exons 1-12
3900	17059	30058	1.08	4.0E-02	L11910.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
							Human retinoblastoma susceptibility gene exons 1-27, complete cds
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5495	18994	31710	5.31	4.0E-02	AF280107.1	NT	

Page 152 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75286 O75289 R29124_1;
							Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7867	20921	34428	5.99	4.0E-02	L23838.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7926	20979		0.71	4.0E-02	AL161535.2	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20953	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20953	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens erythrocyte tropomodulin (E-TMOD) gene, exon 7
7980	21029	34543	0.61	4.0E-02	AF288153.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	60215388-4F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
9844	22884		0.63	4.0E-02	BF679378.1	EST_HUMAN	Methanobacterium thermoautotrophicum strain Marburg, Thid:fumarate reductase subunit A
9869	22809	36495	2.46	4.0E-02	AJ000941.1	NT	Human mRNA for KIAA0082 gene, partial cds
10180	23227		1.08	4.0E-02	D43849.1	NT	Kluyveromyces fragilis gene for Ccr++ ATPase
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
12333	26909	31859	16.34	4.0E-02	AJ001088.1	NT	UHF-BW 7-ans-H-08-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1144	14309	27368	2.79	3.9E-02	BF516149.1	EST_HUMAN	FAS ANTIGEN LIGAND
1375	14630	27603	2.15	3.9E-02	P41047	SWISSPROT	M.musculus DNA for desmin-binding fragment DesD7
2016	15156	28261	3.22	3.9E-02	AJ403386.1	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
2769	15884		1.97	3.9E-02	4506862	NT	
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-009 S10258 Homo sapiens cDNA
6279	18398	31366	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5279	18398	31367	0.9	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5849	19039	32346	1	3.9E-02	BE698841.1	EST_HUMAN	60164987-4F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933842 5'
5977	19182	32482	0.65	3.9E-02	BF676203.1	EST_HUMAN	602138132-1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601140729-1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8023	21106	34623	1.44	3.9E-02	BF236613.1	EST_HUMAN	60190684-8F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8250	21332	34849	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11095	21071	34582	1.56	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
12184	28039		3.54	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

Page 153 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12898	25595		2.35	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV18S1, TCRBV11S1A1T, HYB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY3, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
13036	25979		64.89	3.9E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5559	18754	31792	0.8	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
8212	19387	32736	1.04	3.8E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7471	20546	34018	1.72	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
8884	21943		1.51	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10789	23822	37446	0.64	3.8E-02	7662563	NT	Homo sapiens PRO0514 protein (PRO0514), mRNA
10888	23972	37603	1.71	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1016	14167	27248	4.05	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2310	15442	28577	6.19	3.7E-02	A1984806.1	EST_HUMAN	wr65e08.k1 NCL CGAP_K1611 Homo sapiens cDNA clone IMAGE:2484502.3
2845	15768	28883	0.97	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3115	16291	28306	1.13	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3117	16293	29307	4.33	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584.5'
3543	16708		0.91	3.7E-02	6680541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
7226	26216		0.95	3.7E-02	AP000063.1	NT	Aeropyrum permix genomic DNA, section 6/7
7869	20923	34430	0.81	3.7E-02	AE003979.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
10219	23255		1.01	3.7E-02	AA762516.1	EST_HUMAN	ai65c09.s1 Soares_papillaryoid_tumor_NbHPA Homo sapiens cDNA clone 1360912.3'
12227	25175	38837	7.41	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973.5'
12961	25945	31764	3.71	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
13069	25699		1.23	3.7E-02	11467432	NT	Odontella sinensis chloroplast, complete genome
3744	16905	28909	0.82	3.6E-02	X73221.1	NT	H. vulgaris Ss1 gene for sucrose synthase
3752	16913	29916	0.9	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL096810.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	C.glutamicum gap, pdk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5617	18811	31880	0.66	3.6E-02	AF181722.1	NT	Homo sapiens RUSAS (RU2) mRNA, complete cds
5846	19939	33408	4.48	3.6E-02	AW945616.1	EST_HUMAN	CM2-EN0013.110500-192-b10 EN0013 Homo sapiens cDNA
5846	19939	33407	4.48	3.6E-02	AW945616.1	EST_HUMAN	CM2-EN0013.110500-192-b10 EN0013 Homo sapiens cDNA
7234	20318	33761	1.78	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein O2 precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	nm20a05.s1 NCL CGAP GCBO Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb.J00314_rna2
7811	20866	34360	0.94	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9591	22646	36216	2.16	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-508 HT0158 Homo sapiens cDNA
9591	22646	36217	2.16	3.6E-02	U20608.1	NT	Dicystotellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	36431	0.84	3.6E-02	BF347586.1	EST_HUMAN	Dicystotellum discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
11456	24516	38183	1.46	3.6E-02	BF131609.1	EST_HUMAN	602020453F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
11456	24516	38184	1.46	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14053	27158	0.99	3.6E-02	U09506.1	NT	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
1033	14202	27280	2.43	3.6E-02	AF263417.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
1595	14748	27831	1.4	3.6E-02	BF678085.1	EST_HUMAN	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1596	14748	27832	1.4	3.6E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.6E-02	AE001773.1	NT	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4435	17575	30556	1.11	3.5E-02	P53780	SWISSPROT	Thermotoga maritima section 85 of 136 of the complete genome
6351	19521	32878	1.76	3.6E-02	J01238.1	NT	CYSTATIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE)(CYSTEINE LYASE)
8165	21247		0.91	3.5E-02	H29951.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
8824	21903	35443	2.93	3.5E-02	BE958070.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
10224	23280	36848	0.94	3.5E-02	X76642.1	NT	Maize actin 1 gene (MAc1), complete cds
10270	23305	36902	0.81	3.5E-02	BE561042.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
11785	24775	38471	1.79	3.5E-02	AW861641.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
11788	24775	38472	1.79	3.5E-02	AW861641.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
12876	25583		1.31	3.5E-02	AF009803.1	NT	Maize actin 1 gene (MAc1), complete cds
12956	25891		2.71	3.5E-02	BE276948.1	EST_HUMAN	Maize actin 1 gene (MAc1), complete cds
592	13783	26802	47.29	3.4E-02	AK024424.1	NT	Maize actin 1 gene (MAc1), complete cds
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	Maize actin 1 gene (MAc1), complete cds
593	13783	26802	3.28	3.4E-02	AK024424.1	NT	Maize actin 1 gene (MAc1), complete cds

Page 155 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
593	13783	26803	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1076	14242	27298	2.57	3.4E-02	AW274020.1	EST_HUMAN	xx28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814263 3' similar to SW_C211_HUMAN P63801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1233	14322		5.43	3.4E-02	11346459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	yc20e06.r1 Striatogene lung (#837210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3517	16683	28694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3875	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4030	17188	30196	3.72	3.4E-02	AW784952.1	EST_HUMAN	RC6-UM0018-21020-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59789.1	NT	Mus musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6863	18612	31504	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8456	21637		3.15	3.4E-02	AI866628.1	EST_HUMAN	wf8ad04.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22026	35567	1.18	3.4E-02	AA664866.1	EST_HUMAN	nu70108.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element ;
9118	22197						zq04f11.s1 Striatogene muscle 837208 Homo sapiens cDNA clone IMAGE:628748 3' similar to TR:G1017425 G1017425
9880	23019		5.28	3.4E-02	AA194306.1	EST_HUMAN	(PISGKPLPKVTLSDRGVPLKATMRFNTEITAENLTINLKESVTADAGRYEITAAANSSGTTKAFINIVLDRPG
383	13561		0.66	3.4E-02	AI082719.1	EST_HUMAN	PPT GPVVSIDITEESVTLKWEPPKYDGSQVNTNYILLKRETSVAW TEVSA TVARTMMKYNKL ... ;
1163	14355	27413	6.8	3.3E-02	AA398733.1	EST_HUMAN	xx69h08.x1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1658	14821	27904	12.43	3.3E-02	AB035867.1	NT	z175e08.s1 Soares_Jeslie_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1778	14927		1.23	3.3E-02	AF110763.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2149	15285		1.37	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3445	16613	29631	2.02	3.3E-02	IR09112.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
4293	14821	27904	0.86	3.3E-02	H02389.1	EST_HUMAN	yc25e09.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4589	17728	30709	3.74	3.3E-02	AF110763.1	NT	y85h02.r1 Soares_placenta N52HP Homo sapiens cDNA clone IMAGE:150771 5'
6600	19722	33089	2.24	3.3E-02	6755882	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
8560	19722	33100	25.73	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp98 (Tra1), mRNA
7677	20742	34223	25.73	3.3E-02	BF245995.1	EST_HUMAN	601855910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9523	22598	36157	0.63	3.3E-02	AF124162.1	NT	601855910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8523	22598	36158	0.74	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia polyketide synthase sulphurase (cys5) gene, partial cds
			0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:3682423 3'
			0.74	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:3682423 3'

Page 156 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9824	22679	36248	0.57	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
9624	22679	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11383	24444	38104	3.28	3.3E-02	BF691107.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
12428	25303		3.1	3.3E-02	T06545.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12557	25379		1.6	3.3E-02	AF289665.1	NT	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12591	25398		1.85	3.3E-02	M81890.1	NT	ye49f11.1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:121101 5'
134	13380	26394	1.79	3.2E-02	AJ002005.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
1150	14314	27370	6.32	3.2E-02	AF096275.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1150	14314	27371	6.32	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1812	14981	28054	1.08	3.2E-02	AF128894.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2187	15322		1.09	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2902	13360	28394	0.87	3.2E-02	AJ002005.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
3204	16378	29389	13.21	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
4334	17477		16.42	3.2E-02	X94768.1	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'
4890	18020	31006	3.85	3.2E-02	AF114182.1	NT	Homo sapiens chromosome 21 segment HS21C003
5310	18427	31397	0.93	3.2E-02	AW650159.1	EST_HUMAN	H. sapiens RP3 gene (XLRP gene 3)
5652	18846	32127	1.49	3.2E-02	X88709.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5652	18846	32128	1.49	3.2E-02	X88709.1	NT	IL3-CT0210-271099-022-CD4 CT0219 Homo sapiens cDNA
5653	18812	33200	2.4	3.2E-02	M32437.1	NT	S. glisocorneum whiG-Stv gene
6656	19815		30.91	3.2E-02	T89367.1	EST_HUMAN	S. glisocorneum whiG-Stv gene
6743	19896	33280	3.7	3.2E-02	AF173845.1	NT	Rat polyomavirus left junction in cell line W98.14
7639	20989	34498	0.92	3.2E-02	11424049	NT	ye433h12.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
8496	21577	35113	8.04	3.2E-02	6880565	NT	Alu repetitive element; contains LTR1 repetitive element;
9141	22220		0.87	3.2E-02	AF109718.1	NT	Saguinus oedipus tissue kallikrein gene, complete cds
9426	22500	36065	1.2	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
9426	22500	36066	1.2	3.2E-02	A1278971.1	EST_HUMAN	Mus musculus kinesin family member 3c (Kif3c), mRNA
10262	23297		4.51	3.2E-02	AA719795.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
10566	23601	37207	1.11	3.2E-02	U96792.1	NT	gm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1892063 3'
							gm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							gm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							gb:L08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
							Mus musculus chemokine receptor CCR5 mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14446		1.92	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27559	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	6871684	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18580	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5476	18676		2.6	3.1E-02	AA278478.1	EST_HUMAN	zs81a06.r1 NCI CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:703858 5'
5764	18659	32259	0.77	3.1E-02	BF68742.1	EST_HUMAN	602060783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.98	3.1E-02	AV686088.1	EST_HUMAN	AV686088 GKX Homo sapiens cDNA clone GKCAVH09 5'
9142	22221	35764	0.48	3.1E-02	BE66092.2	EST_HUMAN	601658879R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9339	22415	35968	0.46	3.1E-02	AI672302.1	EST_HUMAN	wm57609.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2440049 3'
10237	23272	36864	2.67	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14805		2.41	3.0E-02	AF187425.1	NT	Ptychokeles minutus cytochrome oxidase I gene, partial cds; mitochondrial product
2652	15775	29888	1.08	3.0E-02	AA402242.1	EST_HUMAN	z65903.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
3743	16804	29808	2.82	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16938		0.93	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e09 ST0286 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pituitary gland II Homo sapiens cDNA 5' and
5164	18286	31250	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5164	18286	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5907	18706		3.21	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.67	3.0E-02	N99616.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element
6384	19553	32911	0.67	3.0E-02	N99616.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294908 5' similar to contains element TAR1 repetitive element
6929	20244	33677	2.87	3.0E-02	AJ242806.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.92	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M86624.1	NT	Human dystrophin gene
8317	21389		0.48	3.0E-02	BF679706.1	EST_HUMAN	602164364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286654 5'
8821	21900	35439	0.65	3.0E-02	BE512970.1	EST_HUMAN	601171626F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3545047 5'
8842	21921	35459	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-29600-108-c04 HT0704 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8983	22072		1.93	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10677	23711	37319	2.03	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10770	23803	37425	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24556	38243	2.26	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11989	24974	38578	7.11	3.0E-02	AA483216.1	EST_HUMAN	ne87604.s1 NCI CGAP_Kic1 Homo sapiens cDNA clone IMAGE:911263
12536	26168	31556	1.95	3.0E-02	R32019.1	EST_HUMAN	Y163d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3
12943	25621		11.62	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187405 NN0038 Homo sapiens cDNA
12989	26161		4.97	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Galglucosyltransferase beta-1,4-galactosyltransferase mRNA, complete cds
3650	16813	29826	0.8	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17195	30208	0.81	2.9E-02	H72805.1	EST_HUMAN	y07e10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6421	19590	32955	6.58	2.9E-02	BF032233.1	EST_HUMAN	601452061F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7398	20476	33943	9.85	2.9E-02	BE271437.1	EST_HUMAN	801140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7594	20656	34133	0.65	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
8187	21259	34793	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9187	21269	34794	0.82	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalla chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9859	22859	36482	2.14	2.9E-02	AW675979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9859	22859	36483	2.14	2.9E-02	AW675979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10078	23116		0.65	2.9E-02	AW67597.1	EST_HUMAN	EST398708 MAGC resequences, MAGN Homo sapiens cDNA
10553	23588	37198	1.25	2.9E-02	AP000084.1	NT	Aeropyrum pernix genomic DNA, section 777
11303	16813	29826	1.44	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002962 5'
579	13771		0.76	2.8E-02	AW970163.1	EST_HUMAN	EST382234 MAGC resequences, MAGK Homo sapiens cDNA
3453	16620	29639	1.2	2.8E-02	AF066083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3453	16620	29640	1.2	2.8E-02	AF066083.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
4430	17570		0.76	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5605	18800	31866	11	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
6948	20261	33698	1.08	2.8E-02	T78960.1	EST_HUMAN	y021b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108655 5'
8523	21604	35142	1.67	2.8E-02	AJ005820.1	NT	Cratogeomys plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA280762.1	EST_HUMAN	z696c06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5'
9409	22493	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

Page 159 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9513	22578	38144	0.78	2.8E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
9674	22836	38207	0.47	2.8E-02	J05109.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
9674	22836	38208	0.47	2.8E-02	J05109.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
1518	14871	27763	0.98	2.7E-02	U66059.1	NT	Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3518	16884	26695	1.98	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4319	17482	30447	1.93	2.7E-02	N47258.1	EST_HUMAN	y98h12.1 Soares_mulle_sclerosis_2N5H1MSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17482	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	y98h12.1 Soares_mulle_sclerosis_2N5H1MSP Homo sapiens cDNA clone IMAGE:280487 5'
5362	18565	31432	0.8	2.7E-02	BF246672.1	EST_HUMAN	601864811FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5587	18765	31793	1.43	2.7E-02	R12245.1	EST_HUMAN	y33d09.1 Soares fetal liver spleen 1N5LS Homo sapiens cDNA clone IMAGE:128657 5' similar to SP_JC2284 JC2284 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6022	18205	32525	0.68	2.7E-02	X61670.1	NT	T. aestivum pTTH20 mRNA for wheat type V thionin
6734	19880		1.02	2.7E-02	X97580.1	NT	A. bisporus pgkA gene
7213	20078	33491	1.92	2.7E-02	AA983571.1	EST_HUMAN	cg5h03.31 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
8549	21630		1.38	2.7E-02	A1377036.1	EST_HUMAN	tc28g08.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to contains Alu repetitive element;
8816	21895	36434	0.55	2.7E-02	S43442.1	NT	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
585	13778	26786	2.62	2.6E-02	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1398	14953		0.99	2.6E-02	AW850515.1	EST_HUMAN	IL3-CT0219-280100-062-C09 CT0219 Homo sapiens cDNA
2439	15567	28694	2.6	2.6E-02	AA490021.1	EST_HUMAN	ab02b02.v1 Stratagene fetal retina 087202 Homo sapiens cDNA clone IMAGE:839695 3'
2441	15669	28696	4.45	2.6E-02		NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15669	28697	4.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2082	16158		2.07	2.6E-02	AF109906.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and enRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5025	18154	31131	3.89	2.6E-02	L12032.1	NT	Chicken dorsalin-1 mRNA, complete cds
5176	18298	31281	1.22	2.6E-02	AE002014.1	NT	Deinococcus radiodurans RT section 151 of 228 of the complete chromosome 1
5203	18324	31283	2.54	2.6E-02	AW241154.1	EST_HUMAN	xab2b04.x1 NCI_OGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6011	19185		2.94	2.6E-02	AL161563.2	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
6349	19519		6.85	2.6E-02	AI206030.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6555	19717	33093	2	2.6E-02	BE621748.1	EST_HUMAN	cg27f11.x1 NCI_OGAP_Kid8 Homo sapiens cDNA clone IMAGE:1762317 3'
6966	20194	33619	0.83	2.6E-02	Z96004.1	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
						NT	Vaccinia virus ORF-L, strain Wyeth

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6966	20194	33620	0.83	2.6E-02	Z96064.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33520	5.63	2.6E-02	6081271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20526	33999	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8703	21793	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	ak2204.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408719 3'
9560	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22955	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces darlingensis NRRL Y-12638(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22955	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces darlingensis NRRL Y-12638(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10814	23648	37257	5.37	2.6E-02	AL183303.2	NT	encoding mitochondrial protein, complete cds
11670	24747		1.59	2.6E-02	AA279351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
11861	24849	38547	1.35	2.6E-02	AW500547.1	EST_HUMAN	z84602.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
12460	26150	31553	1.43	2.6E-02	BF343827.1	EST_HUMAN	U1-HF-BNO-ak-e-10-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077456 5'
12583	25392		1.32	2.6E-02	11422936	NT	602015301.F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4160944 5'
12947	25658		1.39	2.6E-02	R43678.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
545	13738	26762	1.75	2.5E-02	A1793130.1	EST_HUMAN	ye8607.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element:
545	13738	26762	1.75	2.5E-02	A1793130.1	EST_HUMAN	ye8607.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22845 3' similar to contains DBR repetitive element:
832	14010	27066	9.54	2.5E-02	BE974314.1	EST_HUMAN	on2606.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1657827 5'
892	14058	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	on2606.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1657827 5'
2821	15035		2.53	2.5E-02	U12571.1	NT	on2606.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1657827 5'
3021	16197	29219	2.95	2.5E-02	X99697.1	NT	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
3021	16197	29220	2.95	2.5E-02	X99697.1	NT	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
4156	18488	30302	0.92	2.5E-02	BE701165.1	EST_HUMAN	Rattus norvegicus rabphilin-3A mRNA, complete cds
4156	18488	30303	0.92	2.5E-02	BE701165.1	EST_HUMAN	Rattus norvegicus rabphilin-3A mRNA, complete cds
4322	17486	30450	4.66	2.5E-02	AW592114.1	EST_HUMAN	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
5830	19021	32327	0.72	2.5E-02	A1732776.1	EST_HUMAN	H.carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
6322	19494		4.88	2.5E-02	BE670128.1	EST_HUMAN	PM2-NN0128-080700-001-012 NN0128 Homo sapiens cDNA
6338	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	PM2-NN0128-080700-001-012 NN0128 Homo sapiens cDNA
6466	19633	32894	0.8	2.5E-02	L28029.1	NT	PM2-NN0128-080700-001-012 NN0128 Homo sapiens cDNA
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	h38h08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	h38h08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
8008	21058	34570	0.84	2.5E-02	AF129458.1	NT	z836c10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354 3'
							z836c10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354 3'
							7630a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element:
							7630a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1 repetitive element:
							601575933F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
							601575933F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
							Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
							Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
							602070562F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
							602070562F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4213406 5'
							Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds
							Chlamydomonas reinhardtii class II DNA photolyase (PHR2) gene, complete cds

Page 161 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8187	21249	34788	0.5	2.5E-02	BE262469.1	EST_HUMAN	801108291F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	35645	0.92	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9184	22242	35785	0.57	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NOI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2616370 3'
10271	23308		0.63	2.5E-02	X71303.1	NT	D radium 28S ribosomal RNA, D2 domain
10810	23943	37466	0.65	2.5E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1689982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IIBeta) genes, complete cds;
							butyrophilin-like (NG9), butyrophilin-lb
11120	24182		2.93	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12065	25046		1.87	2.5E-02	AB007646.1	NT	Homo sapiens similar to ALEX3 protein (H_sapiens) (LOC63634), mRNA
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12716	25476		1.29	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12750	25497	32032	1.83	2.5E-02	U60169.1	EST_HUMAN	Dicystidium discoidium putative protein kinase MkcA (mkcA) gene, complete cds
1628	14780	27665	1.58	2.5E-02	BE973327.1	EST_HUMAN	607652368R2 NIH_MGC_32 Homo sapiens cDNA clone IMAGE:3935513 3'
178	13401	28431	1.44	2.4E-02	A137582.1	EST_HUMAN	bc72c07.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:2070168 3'
2102	16054	28363	1.89	2.4E-02	H65984.1	EST_HUMAN	y75711.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211149 5'
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30509	1.69	2.4E-02	J05110.1	NT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6344	19514	32871	0.86	2.4E-02	W85660.1	EST_HUMAN	T thermophilus calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	HSAAAAGKXX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7988	20464	33929	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21156		0.75	2.4E-02	AW813007.1	EST_HUMAN	Rat gene for uncoupling protein (UCP)
8129	21211		0.57	2.4E-02	M16780.1	NT	RC3-ST0186-230300-018-H06 ST0186 Homo sapiens cDNA
8636	21716		0.57	2.4E-02	H76376.1	EST_HUMAN	Human retrotransposon 3' long terminal repeat
8728	21808	35344	11.69	2.4E-02	N69442.1	EST_HUMAN	yu12c05.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:233578 3' similar to contains Alu repetitive element; contains A3R repetitive element
9187	22265	35806	0.78	2.4E-02	AE001125.1	NT	za35g11.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:294558 3' similar to dbjK02909 RATSR7K Rat (RNA) contains A3R.b1 A3R repetitive element
							Borrelia burgdorferi (section 11 of 70) of the complete genome
							zu91c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 [SLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR XTR repetitive element
9211	22289	35831	0.81	2.4E-02	AA825660.1	EST_HUMAN	

Page 162 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9893	22933	36516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
9893	22933	36517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
10011	23049	36643	2.75	2.4E-02	AV692954.1	EST_HUMAN	AY592954 GK Homo sapiens cDNA clone GKGDS003 5'
10198	23223	36817	2.82	2.4E-02	AA493894.1	EST_HUMAN	nh07512.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTR5 repetitive element
10839	23872		0.5	2.4E-02	BE387111.1	EST_HUMAN	601274962F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11874	24962	38557	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
11874	24962	38558	2.45	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
12210	25163		3.98	2.4E-02	9627909	NT	Bacteriophage bIL67, complete genome
12362	25260	32116	4.45	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12478	25330	32096	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.26	2.4E-02	N42980.1	EST_HUMAN	y08a06.r1 Scarsa melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610 5'
12883	25900	31858	1.25	2.4E-02	AA179693.1	EST_HUMAN	zp13107.1 Stratagene fetal ratina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1921	15064		5.25	2.3E-02	W03340.1	EST_HUMAN	z884908.r1 Scarsa_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1936	15079		16.26	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2065	15205	28321	0.99	2.3E-02	AW797356.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2426	15554	28681	2.68	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	29940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAACADH P, Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16987		0.67	2.3E-02	L23429.1	NT	Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3'end
4267	17412	30398	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4267	17412	30399	1.17	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30660	1.08	2.3E-02	AW898107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4571	17709	30689	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30690	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4572	18469	30691	1.2	2.3E-02	AW593693.1	EST_HUMAN	xc25408.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'

Page 163 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18468	30892	1.2	2.3E-02	AW593693.1	EST_HUMAN	xa25d08.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18267	31237	0.9	2.3E-02	AW644307.1	EST_HUMAN	RC2-CN0051-290100-011-407 CN0051 Homo sapiens cDNA
5265	18384	31349	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5265	18384	31350	0.62	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18690	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pccB) homolog gene, partial cds
6365	19535	32894	0.62	2.3E-02	BF106464.1	EST_HUMAN	601822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6755	19911	33308	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31458	0.69	2.3E-02	BE141475.1	EST_HUMAN	MR0-HT0080-011099-002-008 HT0080 Homo sapiens cDNA
7619	20889	34164	0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8080	21143	34651	4.52	2.3E-02	U63610.1	NT	Human plectin (PLECT1) gene, exons 3-32, and complete cds
8687	21747	35285	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8687	21747	35286	1.12	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.75	2.3E-02	AI685390.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AI685390.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35987	0.84	2.3E-02	P41996	SWISSPROT	HYPOTHETICAL 55.8 KD PROTEIN B0260.5 IN CHROMOSOME III PRECURSOR
10063	23101	38704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1, 4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	601179958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12801	25535	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 6'
12801	25535	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12918	25604	31974	2.47	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-tucosidase precursor gene, complete cds
12976	26185		1.88	2.3E-02	U11077.1	NT	Dictyostelium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
766	13837	26882	3.59	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1766	14935		1.79	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

Page 164 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28329	2.17	2.2E-02	ZB2001.1	NT	S.pneumoniae pcpA gene and open reading frames
3521	16687		2.03	2.2E-02	AA577785.1	EST_HUMAN	nm2404.s1 NCL_CGAP_Gas1 Homo sapiens cDNA IMAGE:1084782 3'
3736	16887		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3956	17114	30110	0.99	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-803 BT0340 Homo sapiens cDNA
4029	17185	30195	0.99	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5177	18299	31262	1.37	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7398	20474	33941	3.43	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8566	21647	35188	1.41	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21647	35189	1.41	2.2E-02	AL181515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22098	36630	0.82	2.2E-02	X78468.1	NT	P.vulgata alpha tub 2 mRNA
9856	22898	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPass 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9856	22898	36479	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPass 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9888	22928	36511	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.25	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12625	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
432	13627		4.48	2.1E-02	AV761602.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
462	13657		6.62	2.1E-02	AF029726.1	NT	Dicystostellum discoidale histidine kinase C (dhkC) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1418	14571	27644	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27645	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14972	28065	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28066	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14972	28067	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28264	0.97	2.1E-02	AF190899.1	NT	Tegula eurentica major acrosomal protein precursor (TMAP) mRNA, complete cds
2092	15232	28354	1.16	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2092	15232	28355	1.16	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N28286.1	EST_HUMAN	yx3h07.r1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:264541 5'
3674	18837	29847	1.01	2.1E-02	AA461277.1	EST_HUMAN	zx63b09.r1 Soares fetal_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:786121 5'
4249	17395	30384	0.68	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

Page 165 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4427	17667	30549	0.89	2.1E-02	BF343653.1	EST_HUMAN	602016306F1 NC1 CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4161181 5'
4667	17705	30686	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30698	1.64	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17984	30953	5.95	2.1E-02	Y08601.1	NT	A italiana mitochondrial genome, part A
4852	17985	30973	0.76	2.1E-02	AA665737.1	EST_HUMAN	ag35g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	A1823432.1	EST_HUMAN	wh54a05.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5315	18432	31402	0.91	2.1E-02	BF028405.1	EST_HUMAN	60167141F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3934410 5'
5756	18948	32250	0.9	2.1E-02	AW379529.1	EST_HUMAN	CM4-H10244-111198-04D-H05 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF088199.1	EST_HUMAN	QV3-GN0058-120900-32B-a12 GN0058 Homo sapiens cDNA
8716	21796	35333	0.66	2.1E-02	9760238	NT	Mus musculus sorting nexin 1 (SNX1), mRNA
9703	22752	36322	0.54	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 6-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L26324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10266	23301	36899	0.75	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae Integrase, excisionase, repressor, protein, relaxase, UmuC MucB homolog, and
10856	23889	37508	0.49	2.1E-02	AP001519.1	NT	UmuD MucA homolog genes, complete cds; and unknown genes
11787	24777	38474	1.48	2.1E-02	6754255	NT	em88e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628732 3' similar to contains
12063	25044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	Alu repetitive element; contains element MER11 repetitive element;
12602	18493		11.16	2.1E-02	Y19213.1	NT	Bacillus halodurans genomic DNA, section 13/14
12647	25615	31862	1.22	2.1E-02	L34170.1	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp49), mRNA
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	RC4-CN0050-130200-012-H04_1 CN0050 Homo sapiens cDNA
19	13257	26257	1.28	2.0E-02	BF002932.1	EST_HUMAN	Homo sapiens putative psbHbA pseudogene for hair keratin, exons 2 to 7
20	13258	26258	14.95	2.0E-02	AW895655.1	EST_HUMAN	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
269	13488	26518	5.03	2.0E-02	6753635	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
306	13622	26556	2.05	2.0E-02	AA456338.1	EST_HUMAN	MER1 repetitive element;
821	14000	27064	3.63	2.0E-02	6753635	NT	QV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA
1111	14276	27333	0.98	2.0E-02	AL098805.1	NT	Mus musculus DnB homolog 1 (E. coli) (Dnbb1), mRNA
1228	14386	27448	0.91	2.0E-02	8922391	NT	ear15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:313307 5'
							Mus musculus DnB homolog 1 (E. coli) (Dnbb1), mRNA
							Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA

Page 166 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1226	14388	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15065	28168	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28169	1.84	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2859	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002832.1	EST_HUMAN	7951c08.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13 MER1 repetitive element:
3213	16387		1.13	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6B), mRNA
3298	16473		1.99	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4113	17267	30267	1.57	2.0E-02	M18096.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5218	18341		0.74	2.0E-02	A1271985.1	EST_HUMAN	qj83e03.x1 NCI_CGAP_K13 Homo sapiens cDNA clone IMAGE:1866076 3'
6018	19201	32520	0.59	2.0E-02	L35321.2	NT	Dicystellum discoideum class VII unconventional myosin (myoI) gene, complete cds
7723	20767	34275	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
7723	20767	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (4/7)
10081	23119		2.39	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10570	23605	37210	1.84	2.0E-02	A1640342.1	EST_HUMAN	wa17502.x1 NCI_CGAP_K11 Homo sapiens cDNA clone IMAGE:2288315 3'
10879	23964	37692	1.65	2.0E-02	Z73968.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11978	24983	38664	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11978	24983	38665	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18495	31535	1.8	2.0E-02	AA456538.1	EST_HUMAN	eat5510.r1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:813307 5'
12644	15973		2.26	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13186	25771		5.63	2.0E-02	T80037.1	EST_HUMAN	y004c09.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24676 5'
711	13893	26928	2.42	1.9E-02	AA572764.1	EST_HUMAN	nff19a07.e1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element:
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2097	15237	28359	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2870	16146	29164	9.15	1.9E-02	AA713856.1	EST_HUMAN	inv04f05.e1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
3018	16194	29217	1.92	1.9E-02	AV648680.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLCBLH07 3'
3332	16505		0.72	1.9E-02	AB033611.1	NT	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3689	18860		1.12	1.9E-02	N52230.1	EST_HUMAN	yz28502.e1 Soares_multiple_sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:284331 3'
3793	18954		8.1	1.9E-02	BE735088.1	EST_HUMAN	601572682F1NH_MGC_57 Homo sapiens cDNA clone IMAGE:3639564 5'
3808	16988	29971	0.83	1.9E-02	AI9301183.1	EST_HUMAN	qno4c07.x1 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element;

Page 167 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30305	1.3	1.9E-02	AF141940.1	NT	Myoplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4663	17708	30785	2.79	1.9E-02	A1452999.1	EST_HUMAN	46604.x1 Scores NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	16531	31609	0.96	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47672.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5808	18097	AB019507.1	0.83	1.9E-02	AB019507.1	NT	Drosophila kaneloi gene for glyceral-3-phosphate dehydrogenase, complete cds
7260	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7260	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21848	33781	1.33	1.9E-02	U19241.1	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9532	22597	36169	1.21	1.9E-02	BF316129.1	EST_HUMAN	601895130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128462 5'
9914	22954	36540	0.87	1.9E-02	L10114.1	NT	Nicotiana tabacum Type II phytochrome (phyB) gene, complete cds
10251	23288	36882	1.24	1.9E-02	BF685832.1	EST_HUMAN	601862385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10458	23493	37104	0.67	1.9E-02	D64001.1	NT	Synechocystis sp. PCC8803 complete genome, 20/27, 2539000-2644784
11021	24100	37738	1.91	1.9E-02	AF008638.1	NT	Vibrio cholerae V86 phage putative replication protein gene, complete cds
12372	25924	31866	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament glialin mRNA, complete cds
13008	25980		1.46	1.9E-02	L11058.1	NT	Candida albicans lambda Cas/B fragment
356	13567	26595	1.67	1.8E-02	AW771104.1	EST_HUMAN	hn52c06.x1 NC1_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
703	13896	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1188	14348	27408	1.43	1.8E-02	X17664.1	NT	H. francisci mRNA for myelin basic protein (MBP)
1467	14621	27704	1.38	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
2743	18960	28872	1.74	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PAO1, section 105 of 528 of the complete genome
3262	18456		0.94	1.8E-02	AI806829.1	EST_HUMAN	1e52609.x1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090298 3'
3993	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3993	17160	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA861448.1	EST_HUMAN	ak24h04.s1 Scores Testis_NHT Homo sapiens cDNA clone IMAGE:1408935 3'
4550	17888	30659	1.52	1.8E-02	AA68363.1	EST_HUMAN	QV4-DT0021-301299-071-b11 DT0021 Homo sapiens cDNA
5089	18197	31171	2.02	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJB45024.2
6949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5 REGION
7624	20694	34170	2.3	1.8E-02	BF125680.1	EST_HUMAN	601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
7650	20694	34170	0.61	1.8E-02	BF125680.1	EST_HUMAN	601783268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.86	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8663	21743	35283	0.46	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-H09 NN1073 Homo sapiens cDNA
8710	21790	35326	0.76	1.8E-02	8678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
8683	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
8693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA867543.1	EST_HUMAN	slc2a6.s1 Soares_testis NIH_T Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC
10288	23303	36900	1.7	1.8E-02	BE178274.1	EST_HUMAN	FINGER PROTEIN 91 (HUMAN);
10431	23468	37072	1.29	1.8E-02	X98933.1	NT	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5'
11721	23907	37530	1.76	1.8E-02	AB002337.2	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11721	23907	37531	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11812	24898	38002	1.55	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11826	24912	38613	2.45	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1495000 nt. position (87)
13096	25894		1.78	1.8E-02	AF202180.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
929	14104	27167	1.34	1.7E-02	BE394869.1	EST_HUMAN	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;
1920	15063		2.85	1.7E-02	AL163204.2	NT	h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;
2181	15316		13.18	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21G004
2705	15823		1.36	1.7E-02	7857495	NT	Oryctolagus cuniculus mRNA for miteugumin29, complete cds
3062	16238	29259	0.89	1.7E-02	AI147615.1	EST_HUMAN	Homo sapiens putative Rab5 GTP exchange factor homologue (RABEX5), mRNA
3602	16768		4.64	1.7E-02	AW827368.1	EST_HUMAN	h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1696982 3'
3716	16877		0.83	1.7E-02	PO4929	SWISSPROT	h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
4284	17428		1.23	1.7E-02	AA696918.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4317	17490		2.02	1.7E-02	R02506.1	EST_HUMAN	ec19f04.s1 Stratiote ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4576	17713	30697	0.74	1.7E-02	AI305279.1	EST_HUMAN	ye86f08.r1 Soares_fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:124647 5'
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	qm08g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1891270 3' similar to gb.X52359 ZINC FINGER PROTEIN 30 (HUMAN);
							h34403.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element;

Page 169 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4836	17989	30957	1.91	1.7E-02	V00641.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4834	18064		5.98	1.7E-02	A1015076.1	EST_HUMAN	ov51902.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.99	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6709	19887	33256	1.23	1.7E-02	A1038280.1	EST_HUMAN	oy85f03.x1 Soares_fetal_liver_spleen_INFIL_S_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7195	20060	33471	1.26	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400776	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34081	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7821	20872		1.71	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-30
8936	21079	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9000	22940	39528	1.28	1.7E-02	AL040554.1	EST_HUMAN	DKFZp4340314_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4340314 5'
12093	25073	39780	1.66	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE66), mRNA
12991	26111	31687	2.35	1.7E-02	AW903492.1	EST_HUMAN	OM4-NN1030-040400-130-108 NN1030 Homo sapiens cDNA
13168	26757	31928	1.46	1.7E-02	AA846926.1	EST_HUMAN	oe08d04.s1 NC1_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSRT1 repetitive element;
524	13717		4.05	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1989	14841	27926	1.37	1.6E-02	Y18896.1	NT	Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
2323	16455	29586	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	16455	29587	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2631	18754	28869	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ11 gene
2708	18826	29841	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NC1_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2758	18875		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	18778	29783	6.33	1.6E-02	AW850692.1	EST_HUMAN	IL3-CT0219-160200-069-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17556	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-407 PT0012 Homo sapiens cDNA
5367	18570	31498	0.59	1.6E-02	A1281395.1	EST_HUMAN	qla2b09.x1 NC1_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1987417 3'
5741	18934	32234	1.42	1.6E-02	6671715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6780	19938	33331	2.18	1.6E-02	AB015281.1	NT	Candida albicans CseG3R3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

Page 170 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34446	0.98	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21394	34919	0.74	1.6E-02	AJ277682.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10246	23281		2.97	1.6E-02	AF078764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23667	37276	1.61	1.6E-02	AA572818.1	EST_HUMAN	nr18g03.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10633	23667	37277	1.61	1.6E-02	AA572818.1	EST_HUMAN	nr18g03.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
11149	25868	37648	2.9	1.6E-02	Z94828.1	NT	G.gallus microsatellite DNA (LEID260 (=T611E11))
11488	24547	38219	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	38488	2.16	1.6E-02	AJ373558.1	EST_HUMAN	q28a10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12348	15455	28586	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	15455	28587	3.49	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2209	15343	28469	3.58	1.5E-02	N39621.1	EST_HUMAN	y27b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243926 3'
2244	15377	28505	1.6	1.5E-02	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3128	16304	29317	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	29318	1.04	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16978	29982	1.14	1.5E-02	BF092942.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.5E-02	AF260228.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19592	32957	2.07	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20547		1.69	1.5E-02	11487282	NT	Cyanophora paradoxa cyanelle, complete genome
7561	20633	34108	1.57	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34660	1.38	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8066	21147	34668	3.06	1.5E-02	11417739	NT	Homo sapiens vely-RNA synthetase 2 (VARS2), mRNA
9030	22106	35650	1.42	1.5E-02	BF345584.1	EST_HUMAN	602018135F1 NCJ_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9668	22630		0.89	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22766	36337	1.59	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36849	1.3	1.5E-02	R32687.1	EST_HUMAN	yf54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.5E-02	R32687.1	EST_HUMAN	yf54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10860	23893	37514	0.46	1.5E-02	T92186.1	EST_HUMAN	yef1710.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.5E-02	D26547.1	NT	Rba gene for thioredoxin h, complete cds

Page 171 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0048-140100-011-c11 CN0049 Homo sapiens cDNA
430	13626		1.54	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC61226), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1326	14483		2.49	1.4E-02	U67778.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	16458	29478	1.83	1.4E-02	AF160989.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3485	16953	29658	1.23	1.4E-02	AW074212.1	EST_HUMAN	XB08408.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3573	16738	29793	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	16738	29754	6.9	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3608	16772	29787	0.75	1.4E-02	4503828	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3746	16907	29911	12.14	1.4E-02	6869918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4812	17749	30729	9.97	1.4E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4812	17749	30730	9.97	1.4E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4988	18127	31102	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4988	18127	31103	6.22	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	28210		0.74	1.4E-02	X91338.1	NT	H. sapiens LaSS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
8333	21416		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/162
9089	22178	35722	1.44	1.4E-02	M81702.1	NT	Candida biddini methanol oxidase (AOD1) gene, complete cds
9366	22431	35989	1.41	1.4E-02	AJ272265.1	NT	Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22955	36227	1.66	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'
10760	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21 C018
12268	25164	38358	8.95	1.4E-02	X60456.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12640	25430		1.84	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12859	25925		1.45	1.4E-02	11426868	NT	Homo sapiens sperm associated antigen 7 (SPA7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1913	15058		1.19	1.3E-02	BE739263.1	EST_HUMAN	601558462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2612	15638	28759	0.98	1.3E-02	AE002445.1	NT	Neisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	16459	29478	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129479F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129479F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D28547.1	NT	Rice gene for thirtedoxin h, complete cds
5360	18563	31478	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5360	18563	31479	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6293	19466	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
6327	19499	32856	1.05	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7101	18528	31482	1.3	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	ov06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8676	21768	35264	1.67	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23446	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.96	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW268563.1	EST_HUMAN	xv34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12645	26127		1.7	1.3E-02	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12753	25499		2.56	1.3E-02	9833069	NT	Human herpesvirus 6B, complete genome
12965	25895		30.16	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP7, DOB, DQB2 and RING8, 9, 13 and 14 genes
365	13675	26606	4.38	1.2E-02	AA050293.1	EST_HUMAN	z655g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;
465	13660	26696	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR53 REGION
767	13938	26983	2.67	1.2E-02	AI183522.1	EST_HUMAN	q68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1 L1 repetitive element;
2248	15379	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

Page 173 of 550
Table 4
: Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2514	15640	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	x37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15040	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	x37c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16345		7.3	1.2E-02	AA075418.1	EST_HUMAN	zm88e03.r1 Strabegene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:646020 5'
3368	16531	28545	2.05	1.2E-02	R62805.1	EST_HUMAN	y11503.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:136903 3'
3362	16534	28548	0.69	1.2E-02	AI668694.1	EST_HUMAN	zb66a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
5036	18163						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5194	18278	31139	2.02	1.2E-02	U91328.1	NT	Cynops pyrrhogaster Cplbq1 mRNA, partial cds
5186	18317	31286	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19081	32368	1.78	1.2E-02	D76589.1	NT	Rana rugosa mRNA for cathectin, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr8 (WBSOR8) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	y334h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7465	20540	34014	8.54	1.2E-02	AV732053.1	EST_HUMAN	AV732053 HTF Homo sapiens cDNA clone HTFBUC09 5'
7729	20791	34280	0.66	1.2E-02	BF216650.1	EST_HUMAN	601882949F1 NIH_MGC_S7 Homo sapiens cDNA clone IMAGE:4095253 5'
8186	21299	34792					GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA-2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-
8321	21403	34929	2.3	1.2E-02	Q11206	SWISSPROT	GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT 4B)
8321	21403	34930	0.66	1.2E-02	R68831.1	EST_HUMAN	y43106.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34993	1.22	1.2E-02	AF193812.1	NT	Homo sapiens placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34994	1.22	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
9091	22170		1	1.2E-02	T76987.1	EST_HUMAN	Homo sapiens fringe protein mRNA, partial cds
9639	22879	36481	2.54	1.2E-02	AB031013.1	NT	y472c08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:113774 3'
9872	22912	36497	1.24	1.2E-02	AJ246003.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	Homo sapiens Spast gene for spastin protein
12974	26534		6.24	1.2E-02	C18119.1	EST_HUMAN	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-557308 5'
1743	14892	27986	1.49	1.1E-02	X75491.1	NT	zm66e11.s1 Strabegene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14892	27987	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2096	16236	28357	5.35	1.1E-02	BF345283.1	EST_HUMAN	H. sapiens LIPA gene, exon 4
							602018037F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153808 5'

Page 174 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2842	16119		5.31	1.1E-02	N99523.1	EST_HUMAN	zn40c05.r1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	29792	3.59	1.1E-02	AI653508.1	EST_HUMAN	iq95b10.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2216339 3' similar to SW_XPF_HUMAN
4222	17370		0.68	1.1E-02	AW813788.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4951	18081	31057	1.27	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp588E0924 s1 585 (synonym: hute1) Homo sapiens cDNA clone DKFZp588E0924
6277	19451	32800	0.89	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaB (ybaA), YnaB (ybaB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ybaA), YnaB (ybaB), YnaC (ybaC), YnaD (ybaD), YnaE (ybaE), YnaF (ybaF), YnaG (ybaG), YnaH (ybaH), YnaI (ybaI), YnaJ (ybaJ), xylan beta-1,4-xylosyl-
7773	20830	34321	2.19	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-018-h07 HT0256 Homo sapiens cDNA
7989	21039	34561	1.25	1.1E-02	9631294	NT	Melanoplus sanguihipes entomopoxvirus, complete genome
8451	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21620	35458	0.59	1.1E-02	AW896160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
9022	22101	35841	0.7	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC-4040
9103	22182	35727	7.44	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stralagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10299	23334	36939	4.06	1.1E-02	AA314865.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
11224	24283	37934	2.41	1.1E-02	11435505	NT	Homo sapiens T-box 5' (TBX5), mRNA
12185	25152		4.01	1.1E-02	AA668239.1	EST_HUMAN	ab57711.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
7	13245	26247	8.82	1.0E-02	AW846120.1	EST_HUMAN	Alu repetitive element
1552	14705	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111088-003-g10 CT0176 Homo sapiens cDNA
2638	15701		1.71	1.0E-02	AA606389.1	EST_HUMAN	GM2-HT0177-041089-017-h12 HT0177 Homo sapiens cDNA
3159	16334	29344	2.88	1.0E-02	BE835556.1	EST_HUMAN	oc22h08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3336	16509	29525	1.24	1.0E-02	BE968998.1	EST_HUMAN	RC0-FN0025-250500-021-002 FN0025 Homo sapiens cDNA
3598	16762		0.7	1.0E-02	AW845621.1	EST_HUMAN	G01648987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3886	17143	30148	0.85	1.0E-02	AI065086.1	EST_HUMAN	MR0-CT0060-081088-003-h10 CT0060 Homo sapiens cDNA
4002	17159	30165	0.99	1.0E-02	AL163302.2	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4899	18029	31017	5	1.0E-02	6753521	NT	Homo sapiens chromosome 21 segment HS21C102
4989	18096	31074	4.14	1.0E-02	R86567.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5116	18243	31208	0.83	1.0E-02	AL161583.2	NT	yq54h01.r1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:189633 5'
5242	18384	31332	1.96	1.0E-02	P06599	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5532	18729	31745	0.81	1.0E-02	H52681.1	EST_HUMAN	EXTENSIN PRECURSOR
							yq36h11.r1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

Page 175 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	19055	32362	0.66	1.0E-02	AF309888.1	NT	Mus musculus transcription complex subunit NF-A1C4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.29	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syn2) gene, complete cds
6310	19482	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6901	20216	33646	1.69	1.0E-02	Z29842.1	NT	Z. mays U3snRNA pseudogene
9593	22948	35219	6.34	1.0E-02	BF038331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9593	22948	35219	6.34	1.0E-02	BF038331.1	EST_HUMAN	601469570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Orithidia fasciculata 27 kDa guinea RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11873	24928		1.7	1.0E-02	AI417961.1	EST_HUMAN	ig55h07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:U15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER6 repetitive element
11649	24728	38420	1.95	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MOS Homo sapiens cDNA clone MDSBDC10 5'
12278	26208		1.76	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A6e)
12339	26941	31762	3.58	1.0E-02	AW635621.1	EST_HUMAN	RC2-DT0007-120200-016-H02 DT0007 Homo sapiens cDNA
12366	26902		4.31	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12764	25974		1.4	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12949	26060		2.91	1.0E-02	X62654.1	NT	H. sapiens gene for Me491/CD63 antigen
916	14061	27156	5.89	9.0E-03	AI796128.1	EST_HUMAN	WH4209.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1203	14449		1.66	9.0E-03	BE781886.1	EST_HUMAN	MER22 MER22 repetitive element
2489	15599	28721	2.64	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2971	16147	29166	0.81	9.0E-03	AI251744.1	EST_HUMAN	qh8009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3768	16919	28921	0.66	9.0E-03	J05184.1	NT	qh8009.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5931	19117		1.19	9.0E-03	AI809782.1	EST_HUMAN	S. acidocaldarius thermopain gene, complete cds
6768	19922		4.01	9.0E-03	BE746988.1	EST_HUMAN	wf7704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
7923	20693	34169	0.61	9.0E-03	AI242219.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7940	20709	34188	0.91	9.0E-03	8922570	NT	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
8059	21142		0.8	9.0E-03	AL039891.1	EST_HUMAN	Homo sapiens hypodermal protein FLJ10650 (FLJ10650), mRNA
8443	21624		0.54	9.0E-03	AF223391.1	NT	DKFZp434L0412.1 t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
10050	23088	36690	0.54	9.0E-03	P26011	SWISSPROT	Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
10068	23104	38707	1.47	9.0E-03	P20908	SWISSPROT	INTTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
							COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

Page 176 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.68	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11851	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11851	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281298-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE348385.1	EST_HUMAN	hw17509.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12838	25558	32016	1.21	9.0E-03	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.6	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281298-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains
1013	14185	27248	12.69	8.0E-03	AF106858.1	NT	Alu repetitive element
2228	16360	28489	1.87	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2617	15741	28853	3.05	8.0E-03	P10286	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3442	18610	28628	1.02	8.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
3766	16927	29930	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3766	16927	29931	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17515	30495	1.15	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4502	17842	30827	5.73	8.0E-03	BF383327.1	EST_HUMAN	CM4-NN0119-300800-223-505 NN0119 Homo sapiens cDNA
4838	17972	30951	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
4838	17972	30962	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLF1 PROTEIN
5271	18350	31358	0.94	8.0E-03	AU140281.1	EST_HUMAN	AU140281 PLACE2 Homo sapiens cDNA clone PLACE2000223 5'
5640	18834	31911	2.8	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RelGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6328	25823	32857	1.27	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
7069	20112		1.06	8.0E-03	V01109.1	NT	Human BK virus (strain NM) genome. (Closely related to SV40.)
7357	20436	33898	1.43	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neurotrophin gene (bag cell), exon 1, 5' end
7714	20779		1.8	8.0E-03	AB038287.1	NT	Turelops truncatus mRNA for p40-phox, complete cds
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9111	22160	35734	3.53	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
9180	22258	35801	0.68	8.0E-03	9789958	NT	MR1-ST0111-111199-011-H06 ST0111 Homo sapiens cDNA
10154	23191		4.75	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
							QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA

Page 177 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE788441.1	EST_HUMAN	601478619F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.78	8.0E-03	Z48852.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11683	24742	38433	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11683	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24988	38701	4.37	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
12205	25159		1.89	8.0E-03	M68035.1	NT	Cryptolegus cuniculus eIF-2a kinase mRNA, complete cds
12252	25191		7.14	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.16	8.0E-03	AI277806.1	EST_HUMAN	qm55a09.x1 Soares_placenta_8w8weeks_2NbHP8c6w Homo sapiens cDNA clone IMAGE:1892752 3'
712	13894	26930	12.35	7.0E-03	AF087183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF087183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
898	14170	27231	3.28	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27361	3.55	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1428	14980	27653	3.39	7.0E-03	AA688298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFX-2)
1522	14885	27784	3.28	7.0E-03	AW303599.1	EST_HUMAN	ab78b09.s1 Stratiogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:853148 3'
2332	16060	28598	2	7.0E-03	P04929	SWISSPROT	xc21b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2695	15815		0.98	7.0E-03	AW772192.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3848	16811	29824	0.65	7.0E-03	AI150273.1	EST_HUMAN	hm87h07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element
3863	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	qf34f02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751895 3'
3914	17073	30071	1.13	7.0E-03	AF189344.1	NT	UHH-B13-akb-o-10-UJ.at NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733681 3'
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4721	17856		0.98	7.0E-03	AW630888.1	EST_HUMAN	UHH-B13-akb-o-10-UJ.at NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733681 3'
5103	18231		6.54	7.0E-03	AL163278.2	NT	hb9a05.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868998 5'
5840	19126		0.72	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6258	25821		4.42	7.0E-03	AW881089.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6444	18811	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0288 Homo sapiens cDNA
6667	18828	33213	2.82	7.0E-03	AA327129.1	EST_HUMAN	zc531f0.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:342475 5'

Page 178 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6695	19853	33243	1.05	7.0E-03	BE657385.1	EST_HUMAN	Tg34b10.x1 NCI CGAP Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2, contains TAR1.12 TAR1 repetitive element;
7689	20754	34238	4.76	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7689	20754	34239	4.76	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34632	0.59	7.0E-03	AJ228043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34633	0.59	7.0E-03	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21384	34905	2.48	7.0E-03	BE175667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8813	21892	35433	0.58	7.0E-03	AF281074.1	NT	RC9-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9587	22652		0.64	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
							Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
							Homo sapiens fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9704	22834	36414	0.68	7.0E-03	N52378.1	EST_HUMAN	y49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9921	22861	36548	2.72	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
9921	22861	36549	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10513	23548		1.34	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10704	23737		0.82	7.0E-03	A1789734.1	EST_HUMAN	AV687379 GKG Homo sapiens cDNA clone GKCAFC07 5'
10800	23833	37456	0.47	7.0E-03	BE184643.1	EST_HUMAN	wc37609.x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:2320840 3'
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	PM3-HT0344-181189-002-g06 HT0344 Homo sapiens cDNA
11140	24212	37838	1.55	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
							Homo sapiens partial MUC5B gene, exon 1-29
12792	26189		1.95	7.0E-03	H94065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12800	25634		1.46	7.0E-03	BE263253.1	EST_HUMAN	y116101.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12808	25601		1.78	7.0E-03	Y17455.1	NT	Alu repetitive element;
13058	26188		1.68	7.0E-03	AL183300.2	NT	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
							Homo sapiens LSF2 gene, penultimate exon
1269	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
1269	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	h222a05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2831	15945	28054	0.94	6.0E-03	AF112374.1	NT	SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR;
2856	16133	28147	3.29	6.0E-03	AA759135.1	EST_HUMAN	h222a05.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2856	16133	28148	3.29	6.0E-03	AA759135.1	EST_HUMAN	SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR;
3318	16491		2.27	6.0E-03	H75690.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
							ah78a11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
							ah78a11.s1 Soares testis NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

Page 179 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF190338.1	NT	Ndorcus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	10636	29655	1.25	6.0E-03	U00880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3469	16636	29658	1.25	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3636	16800		1.11	6.0E-03	W37865.1	EST_HUMAN	2013a11.1 Scarses parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:332172 5'
3750	16911	29914	3.73	6.0E-03	BF510988.1	EST_HUMAN	U1H-B14-epm-c-06-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17038	30034	1.31	6.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
4032	17188	30189	0.6	6.0E-03	AW847284.1	EST_HUMAN	RC0-CT0204-240899-021-b10 CT0204 Homo sapiens cDNA
4087	17223		1.28	6.0E-03	BE280108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2898613 6'
4484	17624		1.54	6.0E-03	AI018833.1	EST_HUMAN	ov33c71.1 Scarses testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17650	30935	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST271718 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5305	18422	31382	0.6	6.0E-03	AA889072.1	EST_HUMAN	995509.s1 Scarses parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404266 3'
6281	25822	32803	0.88	6.0E-03	9627521	NT	Varola virus, complete genome
6956	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SVNAPSIN III
6984	18513	31505	0.87	6.0E-03	BE283748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3383172 5'
7399	20477	33944	0.65	6.0E-03	AA289442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7399	20477	33945	0.65	6.0E-03	AA289442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7824	20879	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-18 and complete cds
8042	21125	34646	6.71	6.0E-03	AI033980.1	EST_HUMAN	ov13a04.x1 Scarses parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element ;
8161	21243	34783	2.76	6.0E-03	AW799337.1	EST_HUMAN	RC0-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8238	21318		1.65	6.0E-03	BF038188.1	EST_HUMAN	601454915F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859626 5'
9784	22692	36282	7.03	6.0E-03	D10548.1	NT	Subcutaneous sclerosing panniculitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	AI432661.1	EST_HUMAN	t22e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AJ011846.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ; Bacillus subtilis fenD gene
10603	23538		0.91	6.0E-03	AF084555.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10816	23648	37258	0.64	6.0E-03	X68366.1	NT	M. thermophilum complete plasmid pFV1 DNA
10861	23685		0.54	6.0E-03	AF24505.1	NT	Homo sapiens adican mRNA, complete cds
10983	24082	37697	1.56	6.0E-03	AW982164.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
11049	24126		1.94	6.0E-03	11546814	NT	Homo sapiens hypodermal zinc finger protein FLJ14011 (FLJ14011), mRNA

Page 180 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14558.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37838	2.66	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	25232		2.04	6.0E-03	AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	25398		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	25926		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450288 (section 39 of 148) of the complete genome
12532	25993		2.49	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12690	26367		1.63	6.0E-03	Q62209	SWISSPROT	SYNAPTOMEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12644	26622		2.41	6.0E-03	AJ245480.1	NT	Brassica napus sld gene for S-locus glycoprotein, cultivar T2
13095	26018		1.61	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
13147	26746		1.19	6.0E-03	BF110296.1	EST_HUMAN	7935617.1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3566564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-lke protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-lke protein, complete cds
687	13871	26903	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-lke protein, complete cds
687	13871	26904	3.08	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-lke protein, complete cds
1136	14301	27357	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1601	14754		1.08	5.0E-03	A1138977.1	EST_HUMAN	q079005.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2746	15863	26974	2.43	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3206	16381	26392	3.87	5.0E-03	T87623.1	EST_HUMAN	yc81109.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y88602.s1 Soares breast 2NtHb1st Homo sapiens cDNA clone IMAGE:156666 3'
3351	16523		0.84	5.0E-03	AJ297357.1	EST_HUMAN	y88602.s1 Soares breast 2NtHb1st Homo sapiens cDNA clone IMAGE:156666 3'
3790	16951	29957	5.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 particillin-binding protein 15 (pbpB) gene, complete cds
3854	17014	30014	0.81	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.64	5.0E-03	AA299675.1	EST_HUMAN	EST112218 Uterus tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.65	5.0E-03	AJ002125.1	NT	Matrix domestica 2fx type gene
4421	17562	30546	0.71	5.0E-03	H78355.1	EST_HUMAN	y079010.r1 Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:240066 5'
4423	17014	30014	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17866	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30864	1.56	5.0E-03	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC, cn15c02 random
5286	18405		1.9	5.0E-03	4768747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBP2) mRNA
5816	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
6169	19346	32891	2.82	5.0E-03	O00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6204	19379		0.88	5.0E-03	AE002234.2	NT	Chlamydia pneumoniae AR39, section 62 of 94 of the complete genome
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	800644584.T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860871 3'
6888	18506	31520	7.22	5.0E-03	AB025024.1	NT	Mus musculus AVID1 gene for S-adenosylmethionine decarboxylase, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7237	20321	33765	0.61	5.0E-03	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahe11), mRNA
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	EST03012 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFB CR83 similar to EST containing Alu repeat
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-f07 CT0255 Homo sapiens cDNA
7944	20994	34505	7.18	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
8415	21496	35027	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8416	21496	35028	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8433	21514	35045	1.99	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8811	21860		5.83	5.0E-03	M91132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
9007	22086	35629	1.21	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4 min)
9140	22219	35763	0.52	5.0E-03	M25060.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
10044	23082	36684	1.03	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
10176	23213	36805	0.74	5.0E-03	AW821898.1	EST_HUMAN	RC0-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10360	23395	37006	0.56	5.0E-03	AA53143.1	EST_HUMAN	h46h10.s1 NCL CGAP_P16 Homo sapiens cDNA clone IMAGE:995587
10539	23574	37181	0.47	5.0E-03	7662667	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10696	23729		0.47	5.0E-03	AA653261.1	EST_HUMAN	sg48c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126280 3'
10959	24040		4.79	5.0E-03	T19586.1	EST_HUMAN	964F Heart Homo sapiens cDNA clone 694
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	hns6g05.x1 Soares_NHCoC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 t2 L1 repetitive element
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	hns6g05.x1 Soares_NHCoC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 t2 L1 repetitive element
11297	24363	38004	1.76	5.0E-03	T49153.1	EST_HUMAN	h09ed04.t1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 6'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11615	24666		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz4c04.y1 NCL CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12070	25051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	25051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12467	26144		11.86	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12616	25414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA456597.1	EST_HUMAN	z75603.s1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHEOL OXIDASE A2 COMPONENT ;
12802	25935		5.99	5.0E-03	BF57232.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4262002 5'
13002	26851	31951	2.86	5.0E-03	AW449109.1	EST_HUMAN	U1-H-B13-alc4-r-08-Q-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2794215 3'
242	13464	26493	1.54	4.0E-03	AW800186.1	EST_HUMAN	U1-HF-BN0-alc4-r-04-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
331	13545	26575	1.75	4.0E-03	R46482.1	EST_HUMAN	y51a04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
456	13651	26689	1.36	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE)(PTDINS-3-KINASE)(PI3K)
616	13805	26825	4.37	4.0E-03	AA938339.1	EST_HUMAN	on75g12.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1562568 3'
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	RC3-BT0333-110100-012-f01 BT0333 Homo sapiens cDNA
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	z81a08.r1 Stralagene cdon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
1174	14337	27393	34.06	4.0E-03	AA099777.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1198	14368	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	z559a01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1331	14486	27556	1.48	4.0E-03	AA284374.1	EST_HUMAN	
1783	14932	28026	2.68	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and oligodendrocyte associated protein A11-46 mRNA, complete cds
2075	15215	28334	17.33	4.0E-03	AA098777.1	EST_HUMAN	z81a08.r1 Stralagene cdon (#637204) Homo sapiens cDNA clone IMAGE:510998 5'
2321	15463		2.06	4.0E-03	BE410555.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2352	15483	28616	1.53	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28980	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2755	15872	28981	2.97	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15877	28984	0.97	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3267	16471	29491	1.08	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-r108 HT0340 Homo sapiens cDNA

Page 183 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3297	16471	29492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151298-003-108 HT0340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW189426.1	EST_HUMAN	X8804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3619	16783	29799	0.83	4.0E-03	AW189426.1	EST_HUMAN	X8804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3714	16875	29980	0.64	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29980	0.85	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17166	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tag101) gene, complete cds
4102	17258		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
5339	18452	31420	0.98	4.0E-03	AW500547.1	EST_HUMAN	UHF-BNO-ak-e-10-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468 5'
5390	18592	31564	1.98	4.0E-03	AF005859.1	NT	Drosophila melanogaster anan2D7 (anan2D7) mRNA, complete cds
5515	18713	31728	27.24	4.0E-03	AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5814	19102	32416	3.1	4.0E-03	P04196	SWISSPROT	(HPRG)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOBLAST ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7811014.1 J1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014 5'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW590572.1	EST_HUMAN	hg48c07.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2848652 3'
6439	19806	32969	1.78	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6809	19863	33367	1.07	4.0E-03	AA813222.1	EST_HUMAN	g32711.s1 Soares_Testis_NHT Homo sapiens cDNA clone 1392045 3'
6914	20229	33662	1.41	4.0E-03	U76408.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33496	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33889	3.73	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20950	34136	0.98	4.0E-03	AI681483.1	EST_HUMAN	h37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20962	34138	0.82	4.0E-03	BE670170.1	EST_HUMAN	7631502.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20758		0.85	4.0E-03	X92109.1	NT	H. sapiens hcgX gene
8128	21210	34731	0.57	4.0E-03	Q91T92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
8238	21210	34838	4.51	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8398	21479	35006	2	4.0E-03	7662067	NT	Dactyloctenium discoloratum AX4 development protein DG1122 (DG1122) gene, partial cds
8655	21745	35284	0.87	4.0E-03	AF139827.1	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8761	21840	35381	0.51	4.0E-03	Y12855.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
8911	21980	35529	7.06	4.0E-03	AI553983.1	EST_HUMAN	h48b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080013 3' similar to contains Alu repetitive element
9090	22169		3.24	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.78	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9826	22865	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9826	22865	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23169	36766	0.63	4.0E-03	H30664.1	EST_HUMAN	yp42g12.r1 Soares retina N2b5f1R Homo sapiens cDNA clone IMAGE:190150 5'
10587	23622	37229	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37966	1.36	4.0E-03		NT	Homo sapiens splicing factor, arginine/sarthe-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		5.84	4.0E-03	BE151173.1	EST_HUMAN	PMA4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12541	25367		1.95	4.0E-03	AW604279.1	EST_HUMAN	U1HF-BN0-01p-04-Q-UL11 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3080622 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element/contains element MER31 repetitive element
12856	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	h102c07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR6 repetitive element
12871	25581		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-103 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
382	13590	26626	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
902	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14848	27930	3.65	3.0E-03	AA468110.1	EST_HUMAN	nc73c03.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element
2367	15486		6.37	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triphosphate isomerase
2368	15486	28624	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15486	28625	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3056	16232		0.77	3.0E-03	Y08006.1	NT	Arabidopsis thaliana pck1t gene
3152	16327	29338	3.55	3.0E-03	BE379296.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009633 5'
3220	16394	29405	2.53	3.0E-03	AW802687.1	EST_HUMAN	IL2JUM0076-240300-056-P03 UM0076 Homo sapiens cDNA
3504	16671	29681	2.16	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3513	16679		7.5	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17299	30291	1.67	3.0E-03	AJ762278.1	EST_HUMAN	af04f09.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4641	17777	30759	4.62	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'

Page 185 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4888	17891	30878	0.89	3.0E-03	AL119087.1	EST_HUMAN	DKFZp761B0712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B0712 5'
4955	18085	31061	2.06	3.0E-03	AI732754.1	EST_HUMAN	ab18a08.x6 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4978	18107	31083	5.53	3.0E-03	BE787946.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5255	18375	31341	0.9	3.0E-03	4508414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5255	18375	31342	0.9	3.0E-03	4606414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5262	18381	31347	1.76	3.0E-03	AI168860.1	EST_HUMAN	q80b10.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1748276 3' similar to SW:AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17 ; contains MSR1.12 MER22 repetitive element ;
5380	18582	31451	3.36	3.0E-03	8022499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32153	1.09	3.0E-03	AJ249881.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18937	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	aa1310.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7188	20301	33744	0.75	3.0E-03	D37677.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7364	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcp3 gene for purine-cytosine permease
7691	20756	34241	3.71	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
8124	21206	34726	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-607 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-607 BT0812 Homo sapiens cDNA
8360	21431	34955	1.4	3.0E-03	N92580.1	EST_HUMAN	zb27b04.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8490	21571	35108	0.47	3.0E-03	AI866028.1	EST_HUMAN	wf24d06.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425841 3'
8510	21661		0.63	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35276	1.34	3.0E-03	P61989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8679	21759	35295	1.5	3.0E-03	AI163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8788	21865		1.45	3.0E-03	Q8QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9182	22270		10.8	3.0E-03	AW513774.1	EST_HUMAN	hh80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2668131 3' similar to contains L1.11 L1 repetitive element ;
9245	22322	35666	4.28	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9259	22345	35668	0.96	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI_CGAP_K183 Homo sapiens cDNA clone IMAGE:1836247 3' similar to gb:X67138_jmat
9290	22356	35906	0.53	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9608	22684		0.78	3.0E-03	D80801.1	NT	602035980F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4189936 5'
9648	21089	34604	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synochocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9836	22876		0.56	3.0E-03	P03355	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Page 186 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9808	22948		6.51	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
10099	23137	36738	2.31	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23378	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11085	24159		2.67	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38457	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinuclidide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24762	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinuclidide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24838	38532	1.36	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPYRROLINE [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	U1H-B12-eh1-d06-QJ1st NCI_CGAP_Sut4 Homo sapiens cDNA clone IMAGE:2726842 3'
12199	26048		1.62	3.0E-03	AI525056.1	EST_HUMAN	promna-5.E07.7 b1 tumor Homo sapiens cDNA 5'
12235	25179	38346	1.24	3.0E-03	AA933154.1	EST_HUMAN	c77b10.s1 Soares_t04a1 Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.03 MER26 repetitive element;
12296	26050		1.78	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12481	25333	32057	1.23	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
528	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	y415h03.l1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1394	14548	27624	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1397	14551	27626	1.42	2.0E-03	AA681805.1	EST_HUMAN	nu85f01.s1 NCI_CGAP_A1V1 Homo sapiens cDNA clone IMAGE:1217593
1406	14660	27634	20.85	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1519	14672	27754	1.1	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14698	27776	2.26	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (P1OD) mRNA
1546	14698	27777	2.28	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (P1OD) mRNA
1621	14773		6.17	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1811	14980	28053	1.27	2.0E-03	AA450138.1	EST_HUMAN	z42a10.1 Soares_t04a1 Homo sapiens cDNA clone IMAGE:789114 5'
1928	15071		1.05	2.0E-03	BE144908.1	EST_HUMAN	GM2-HT0183-061099-018-d03 H1T0183 Homo sapiens cDNA

Page 187 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	16192	28305	1.59	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	16456	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2847	15770		4.93	2.0E-03	AW137782.1	EST_HUMAN	UIH-B11-adj-g-10-o-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16670	29680	4.92	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3510	16676	29686	0.96	2.0E-03	BF568955.1	EST_HUMAN	602183660T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3756	16917	29919					H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4062	17218	30228	0.82	2.0E-03	XB7344.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17376	30364	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP36]
4280	17435	30423	1.02	2.0E-03	AA179893.1	EST_HUMAN	z013M01.r1 Stralagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:909361 5'
4336	17479		13.93	2.0E-03	U66491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17670		1.99	2.0E-03	L36079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4847	17685		1.22	2.0E-03	AW297390.1	EST_HUMAN	UIH-BW70-adj-g-03-o-U1.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17689	30670	1.05	2.0E-03	A1084748.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17603	30780	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4668	17603	30791	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17961	30949	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b-4HB65Y Homo sapiens cDNA clone IMAGE:180890 3'
4962	18081	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223					Homo sapiens X-linked arthralgia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18766	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	25610	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5828	18019	32325	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xefitin mRNA, complete cds
6208	19411	32758	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6236	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19643	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6476	19643	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6478	19645	33007	7.55	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19679	33049	2.16	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19680	33050	0.75	2.0E-03	AV709073.1	EST_HUMAN	AY709075 ADC Homo sapiens cDNA clone ADOAEF09 5'
6544	19706	33082	1.45	2.0E-03	XB4451.1	NT	L. seculentum mRNA for lysyl-tRNA synthetase (LysRS)

Page 188 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6736	19892		1.36	2.0E-03	AI991089.1	EST_HUMAN	wu38h09.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW_RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element MSRI repetitive element ;
6775	19830	33320	0.7	2.0E-03	AA677831.1	EST_HUMAN	213a1.1 s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430682 3'
7098	18625	31517	1.35	2.0E-03	AB038602.1	NT	Ceanorhabditis elegans mRNA for galectin LEC-11, complete cds
7231	20136	33554	3.3	2.0E-03	BE08786.1	EST_HUMAN	GM4-BT0368-061298-054-401 BT0368 Homo sapiens cDNA
7294	20376	33833	0.65	2.0E-03	AI298883.1	EST_HUMAN	gm98d11.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7444	20821	33984	0.8	2.0E-03	T88669.1	EST_HUMAN	y477g10.t1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7794	20850	34342	1.41	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
							h137b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q60978
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	Q60978 JERKY. ;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares_melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8459	21540	35059	0.64	2.0E-03	Q82350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C69.05 IN CHROMOSOME I
8481	21562	35097	1.08	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8536	21617	35153	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8536	21617	35154	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136878.1	EST_HUMAN	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
							Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8614	21694		0.9	2.0E-03	AJ400877.1	NT	MR2-UM0025-300300-102402 UM0025 Homo sapiens cDNA
9396	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102402 UM0025 Homo sapiens cDNA
9396	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9441	22515	36079	1.07	2.0E-03	AF224688.1	NT	y98a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194286 3'
9726	22791	36362	0.71	2.0E-03	H50832.1	EST_HUMAN	y98a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194286 3'
9726	22791	36363	0.71	2.0E-03	H50832.1	EST_HUMAN	YENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEIN) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
							225) (TENASCIN-C) (TN-C)
9758	22696	36264	3.33	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36483	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36494	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9924	22864	36552	0.6	2.0E-03	AF09732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

Page 189 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8924	22864	38553	0.8	2.0E-03	AF097732.1	NT	Homo sapiens cathepsin recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	38755	0.96	2.0E-03	AW594289.1	EST_HUMAN	QV3-OT0084-060400-144-a01 OT0084 Homo sapiens cDNA
10248	23283		6.28	2.0E-03	AA251376.1	EST_HUMAN	Zs10a08.s1 NCI CGAP_G081 Homo sapiens cDNA clone IMAGE:884764 3'
10828	23682	37270	0.49	2.0E-03	BF367386.1	EST_HUMAN	MR2-GN0030-140800-001-s03 GN0030 Homo sapiens cDNA
11265	24334		2.14	2.0E-03	MB6524.1	NT	Human dyetrophin gene
11778	20860	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330809.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11844	24833	38528	9.84	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	A1625745.1	EST_HUMAN	ly65h03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283888 3' similar to SW:VATG_MANSE
12198	25155	38833	4.31	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SELTL (SELTL) gene, partial cds
12222	25171	38836	1.71	2.0E-03	A1084325.1	EST_HUMAN	cy43g06.s1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P87535 P87535 PS-PLA1 PRECURSOR ;
12245	18497		4.86	2.0E-03	AJ245167.1	NT	Camelus dromedarius ehv19 gene for immunoglobulin heavy chain variable region
12462	28140		4	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 6'
12661	26383	32039	1.29	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	25594		1.38	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, C7, LST-1, LTB, TNF, and LTA genes, complete cds
13090	25927		2.48	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGXD05 5'
452	13648	26684	1.38	1.0E-03	H98471.1	EST_HUMAN	y68c08.r1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
852	14029	27091	1.55	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
852	14029	27092	1.55	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEINENOYL-COA HYDRATASE ;
1119	14284	27339	2.61	1.0E-03	A1665788.1	EST_HUMAN	wk66a06.x1 NCI CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2422268 3'
1139	14304	27360	1.61	1.0E-03	A1654572.1	EST_HUMAN	wx83e10.x1 NCI CGAP_Mel16 Homo sapiens cDNA clone IMAGE:2551242 3'
1182	14354	27412	0.85	1.0E-03	A1692616.1	EST_HUMAN	wd66a01.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2084	15224	28348	3.42	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMWMI)
2222	15356	28486	9.52	1.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
3044	18220	28241	1.37	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3260	18434	28451	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

Page 190 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3280	18434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3632	16796	20813	0.94	1.0E-03	U68061.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16796	29814	0.94	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
4034	17160	30200	0.98	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4044	17200	30211	0.91	1.0E-03	Z49489.1	NT	contains TAR1.11 TAR1 repetitive element;
4556	17694	30873	2.34	1.0E-03	BE939162.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR149w
4598	17735	30715	4.89	1.0E-03	BE246536.1	EST_HUMAN	RC1-TN0128-169800-021-g01 TN0128 Homo sapiens cDNA
4786	17920	30908	0.81	1.0E-03	U29449.1	NT	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4945	18075	31050	2.54	1.0E-03	A1073485.1	EST_HUMAN	Ceenorhabdites elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18075	31051	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4946	18076		6	1.0E-03	BE164087.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5188	18310	31276	15.5	1.0E-03	O46409	SWISSPROT	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5423	18624	31600	2	1.0E-03	AA280951.1	EST_HUMAN	hw51602.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178955 3'
5518	18716	31730	3.57	1.0E-03	AJ066346.1	NT	z44401.1 NCI CGAP_G0B1 Homo sapiens cDNA clone IMAGE:700345 5'
5572	18768	31809	1.64	1.0E-03	K03332.1	NT	Homo sapiens KVLQ11 gene
5572	18768	31810	1.64	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5690	18884	32176	0.95	1.0E-03	BE786491.1	EST_HUMAN	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5696	18880	32181	1.77	1.0E-03	Q02388	SWISSPROT	60158941F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h05.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
6033	19216		0.59	1.0E-03	BF541639.1	EST_HUMAN	yy07h05.r1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element;
6144	19322		2.75	1.0E-03	X07899.1	NT	60208042F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4066807 5'
6184	19360	32708	0.85	1.0E-03	BE96939.2	EST_HUMAN	Mouse nucleolin gene
6321	19483		8.77	1.0E-03	11526176	NT	601657616R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6464	19631	32992	1.11	1.0E-03	T87761.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6538	19702		1.68	1.0E-03	AW902585.1	EST_HUMAN	y493a11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6885	20046	33455	1.41	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7302	20384	33843	2.81	1.0E-03	D16825.1	NT	Human gene for fourth somatostatin receptor subtype
7856	20724		1.12	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7817	20872	34370	1.88	1.0E-03	U52111.2	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7885	20937	34443	3.44	1.0E-03	M63376.1	NT	601491081F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:383278 5'
7934	20984	34492	0.79	1.0E-03	BE880044.1	EST_HUMAN	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8073	21155	34874	0.66	1.0E-03	AF274581.1	NT	Homo sapiens partial stealin-1 gene
8138	21218	34738	5.02	1.0E-03	AJ251973.1	NT	z187c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:480768 3' similar to contains L1.1 L1 repetitive element;
8337	21418	34944	1.95	1.0E-03	AA122770.1	EST_HUMAN	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8438	21519	35048	2.35	1.0E-03	AF163980.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
8625	21705	35241	0.75	1.0E-03	U28397.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
8144	22223		1.48	1.0E-03	Y11204.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
8170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
							Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9281	22357		0.65	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9319	22385	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9798	22636		0.47	1.0E-03	AJ247482.1	EST_HUMAN	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Human class III alcohol dehydrogenase (ADH5) chl subunit mRNA, complete cds
10025	23063	36660	0.88	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10366	23401	37012	9.37	1.0E-03	AF003529.1	NT	Homo sapiens glycine 3 (GPC3) gene, partial cds and flanking repeat regions
10372	23407		0.75	1.0E-03	AF007485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10522	23557	37165	1.08	1.0E-03	AI024350.1	EST_HUMAN	047508.x1 Soares_basils_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1
10823	23556	37478	0.5	1.0E-03	AE004782.1	NT	MER39 MER39 repetitive element;
10823	23556	37479	0.5	1.0E-03	AE004782.1	NT	Pseudomonas aeruginosa PA01, section 323 of 528 of the complete genome
							Pseudomonas aeruginosa PA01, section 323 of 528 of the complete genome

Page 192 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10830	23983		0.53	1.0E-03	AA706202.1	EST_HUMAN	ag33112.s1 Strategene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:1142063 3' similar to contains Alu repetitive element;
10902	23986	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181089-011-a09 CT0279 Homo sapiens cDNA
10902	23986	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181089-011-a09 CT0279 Homo sapiens cDNA
10989	24088	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AI583847.1	EST_HUMAN	tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE.
11425	24486		2.63	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11924	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
11924	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	(TRANSCRIPTION FACTOR NTF-1)
12176	25136	38851	5.51	1.0E-03	BE594488.1	EST_HUMAN	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
12678	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	(TRANSCRIPTION FACTOR NTF-1)
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	PROTEIN GRANY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY)
12889	25590		1.17	1.0E-03	11465834	NT	(TRANSCRIPTION FACTOR NTF-1)
5327	18440	31408	0.7	9.0E-04	P08548	SWISSPROT	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3918524 5'
5789	18989		2.08	9.0E-04	P08727	SWISSPROT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
6388	19537		0.59	9.0E-04	AJ006345.1	NT	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3918524 5'
6615	19775	33166	1.27	9.0E-04	P02381	SWISSPROT	Nicotiana tabacum chloroplast, complete genome
6843	22883		1.46	9.0E-04	AB037203.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1517	14670		1.07	8.0E-04	X86469.1	NT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
4286	17439		4.4	8.0E-04	P08547	SWISSPROT	Homo sapiens KVLQ17 gene
4887	18017	31002	2.5	8.0E-04	U29185.1	NT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
11412	24473		2.59	8.0E-04	AA777084.1	EST_HUMAN	Glycylrhiza glabra GgbA1 mRNA for beta-amylin synthase, complete cds
11576	24631		1.87	8.0E-04	AI571099.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1874	15018	28127	1.11	7.0E-04	L41875.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2472	15599	28724	1.46	7.0E-04	U29185.1	NT	z24c10.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377674 3'
2778	15894	29004	1.33	7.0E-04	AL163210.2	NT	tr85a08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2176310 3'
3353	19526	29540	1.4	7.0E-04	4885170	NT	Homo sapiens CYP17 gene, 5' end
							Homo sapiens prion protein (PrP) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

Page 193 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6221	16398	32745	0.93	7.0E-04	AA516212.1	EST_HUMAN	ng55g12.s1 NCI_CGAP_L1p2 Homo sapiens cDNA clone IMAGE:339718 similar to contains L1.b3 L1 L1 repetitive element;
6642	19801		2.33	7.0E-04	AI769331.1	EST_HUMAN	wg35f09.x1 Soares NSF Fg_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367206 3'
7376	20455		0.72	7.0E-04	AK024446.1	NT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24853		1.7	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine Kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11883	24881	38578	3.78	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12723	25481		9.28	7.0E-04	BE077841.1	EST_HUMAN	GM1-BT0814-110302-142-b12 BT0814 Homo sapiens cDNA
13001	26650		2.68	7.0E-04	R17396.1	EST_HUMAN	yg13c06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32288 5'
13038	26682		5.43	7.0E-04	8005855	NT	Homo sapiens Ratina-derived POJ-domain factor-1 (RPF-1), mRNA
2760	16876		0.97	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4146287 5'
4069	17225	30232	1.64	6.0E-04	AJ862625.1	EST_HUMAN	w15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4201	17350	30341	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30342	0.65	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4301	17444	30430	3.81	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4665	17703	30683	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
4665	17703	30684	0.89	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
8050	21133		4.58	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
8205	21287		0.51	6.0E-04	H92947.1	EST_HUMAN	y84o11.o1 Soares_pithec_gland_N3HPG Homo sapiens cDNA clone IMAGE:231866 3' similar to contains LOR1 repetitive element;
10185	23222		3.26	6.0E-04	AL048507.2	EST_HUMAN	DKFZp666M2024_T1 588 (synonym: huter1) Homo sapiens cDNA clone DKFZp666M2024
10215	23251		0.53	6.0E-04	AJ858286.1	EST_HUMAN	w135g02.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2426830 3'
10285	23320	36922	2.29	6.0E-04	BE008850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10547	23582		0.84	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
11774	24766	38482	2.07	6.0E-04	AJ229042.1	NT	Homo sapiens 955 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11868	24854	38549	2.47	6.0E-04	AW013847.1	EST_HUMAN	UIH-B10-aab-e-09-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11937	24923		1.82	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
12363	26007		3.31	6.0E-04	AW380619.1	EST_HUMAN	RC1-HT0269-281189-012-008 HT0269 Homo sapiens cDNA
13226	25797		14.14	6.0E-04	AJ817088.1	EST_HUMAN	w176g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
668	13854	26882	7.88	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1531	14684		2.03	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3500	16667	29877	1.6	5.0E-04	AA548931.1	EST_HUMAN	h27e11.s1 NCJ_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16669	29872	0.94	5.0E-04	Q9JUP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6785	18921	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	zo33508.r1 Strategene colon (#337204) Homo sapiens cDNA clone IMAGE:589663 5'
7534	20607	34082	9.01	5.0E-04	M23604.1	NT	Gonilla grilla involucrin gene medium allele, complete cds
							q113106.x1 Soares_placenta_80weeks_2Nbr-IP806W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb-X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
8143	21225	34745	5.58	5.0E-04	AI189382.1	EST_HUMAN	cd96e02.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
8498	21579	35115	0.95	5.0E-04	AA814519.1	EST_HUMAN	q159h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9477	22534	36098	1.67	5.0E-04	AA846545.1	EST_HUMAN	KK2745F Human fetal heart_Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPEATITIVE ELEMENT
9574	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9718	22763	36354	0.64	5.0E-04	P28126	SWISSPROT	xe06e02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2788898 3'
9809	22849	36428	4.78	5.0E-04	AW270938.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10484	23519		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11220	24289		1.9	5.0E-04	AL048607.2	EST_HUMAN	DKFZp686M2024_J1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp686M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA568513.1	EST_HUMAN	tr18h02.s1 NCJ_CGAP_Prl Homo sapiens cDNA clone IMAGE:913875
12872	25961		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	601876334F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
690	13874	26907	1.36	4.0E-04	U52748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	AI720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
870	14046	27112	1.55	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE ;
1493	14846	27728	5.58	4.0E-04	AW753356.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOVYL-COA HYDRATASE ;
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2202	15337		1.1	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
							DKFZp434D059_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D059 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	O98615	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	16407	29420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16537	29583	0.69	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barslead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13823
3443	16611	29629	0.8	4.0E-04	AV696624.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN ENOYL-COA HYDRATASE. ;
4443	17583	30561	3.24	4.0E-04	AA576331.1	EST_HUMAN	AV696524 GKC Homo sapiens cDNA clone GKCFH07 5'
4443	17583	30562	3.24	4.0E-04	AA576331.1	EST_HUMAN	rh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:961930 3' similar to gb:M21121 T-CELL
4659	17795	30781	2.33	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5199	18320	31289	3.62	4.0E-04	BE560660.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7418	20466	33665	1.55	4.0E-04	P48442	SWISSPROT	rh10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
7705	20770		0.85	4.0E-04	AL161568.2	NT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7896	20948	34456	0.8	4.0E-04	AU122079.1	EST_HUMAN	CALCIUM-SENSING RECEPTOR)
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	AU122079 MAMMA1 Homo sapiens cDNA clone MAMMA1001920 5'
9892	22832	36515	3.37	4.0E-04	AI025696.1	EST_HUMAN	601876985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
10045	23083		1.12	4.0E-04	AF022855.1	NT	y439f12.t1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:284142 5'
12691	25008		1.56	4.0E-04	AF254822.1	NT	ov87f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
180	13365	26415	3.21	3.0E-04	AL119426.1	EST_HUMAN	Mus musculus neuropilin-2 (nt7) mRNA, alternatively spliced, complete cds
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
803	14078	27144	1.63	3.0E-04	U83991.1	NT	DKFZ761J221.J1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781J221 5'
1896	15030	28137	1.7	3.0E-04	AI262100.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
1901	15044		0.97	3.0E-04	AI399674.1	EST_HUMAN	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
3393	16554	29568	4.35	3.0E-04	P25147	SWISSPROT	gz28d03.y1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
4071	17227	30234	4.94	3.0E-04	P46448	SWISSPROT	h23a02.x1 NCL CGAP_P228 Homo sapiens cDNA clone IMAGE:2119082 3'
4187	17317		1.36	3.0E-04	AJ271735.1	NT	INTERNALIN B PRECURSOR
4205	17354		1.06	3.0E-04	BE140309.1	EST_HUMAN	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4635	17771		1.16	3.0E-04	BE148546.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
4937	18067		5.2	3.0E-04	BE163778.1	EST_HUMAN	RC0-HT0014-310599-028 HT0014 Homo sapiens cDNA
5004	18133	31107	0.65	3.0E-04	AW937723.1	EST_HUMAN	MFO-HT0241-030200-008-001 HT0241 Homo sapiens cDNA
8271	19445		5.58	3.0E-04	AL163281.2	NT	PMD-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
6959	20187	33611	1.54	3.0E-04	AL163278.2	NT	QV3-DT0045-221299-046-d08 DT0045 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C081
							Homo sapiens chromosome 21 segment HS21C078

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.87	3.0E-04	AW893981.1	EST_HUMAN	RC4-NN0027-060400-011-508 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	36065	2.16	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23182	36760	1.28	3.0E-04	AA454055.1	EST_HUMAN	zx4808.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10381	23416	37025	0.46	3.0E-04	AI992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN); wt75a11.x1 Soares_thymus_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
10676	23710	37318	1.99	3.0E-04	AA781201.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
12249	26164	31555	2.39	3.0E-04	AA228301.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN); nc38e04.r1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1 repetitive element
12646	25987	31769	2.54	3.0E-04	AB018292.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	DKFZp647L186_t1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp647L186 5'
180	13403	26432	1.33	2.0E-04	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
491	13686	26719	2.67	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
930	14105	27168	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
930	14105	27169	5.02	2.0E-04	M86524.1	NT	Human dystrophin gene
1208	14368		2.78	2.0E-04	AI286021.1	EST_HUMAN	q88e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.l2 MER3 repetitive element
1213	14374		2.6	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1679	15023		1.71	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Ptx3 gene
2257	15390		1.21	2.0E-04	AA478980.1	EST_HUMAN	zx39605.e1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element
2641	15764	28878	6.42	2.0E-04	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV15S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,> am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3052	16228	29248	1.23	2.0E-04	AI124628.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3415	16594	29600	0.82	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
3622	16688	29697	2.56	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4322	17178	30187	0.98	2.0E-04	U01029.1	NT	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4261	17408		5.5	2.0E-04	H96285.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17628	30914	1.76	2.0E-04	H96285.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4791	17628	30915	1.76	2.0E-04	H96285.1	EST_HUMAN	

Page 197 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	18046		1.22	2.0E-04	U09228.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31256	1.47	2.0E-04	AB037997.1	NT	Danio rerio heparinase gene, exons 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF067019.1	NT	Dicystellum discoidium Interleukin (abpD) gene, complete cds
5681	18855	32138	1.11	2.0E-04	AF654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLC01H10.3'
5674	18868	32154	1.83	2.0E-04	AF690662.1	EST_HUMAN	ig03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:220709.3'
5868	19058	32385	0.93	2.0E-04	AA296852.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' and similar to EST containing O family repeat
6058	18250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6398	18838	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20487		2.57	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798.5'
7478	20563		0.84	2.0E-04	AW860663.1	EST_HUMAN	QV0-GT0387-180300-167-e10 C10387 Homo sapiens cDNA
7798	20864		13.66	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20963	34367	1.45	2.0E-04	P64298	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (185 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21660	35084	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21660	35086	1.24	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8941	22020	35561	0.67	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
8935	22800	36173	0.58	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518.3'
8918	22874	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGZF28.1
10180	23217	36808	1.16	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-161099-011-b66 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	zu65c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864.5'
11088	24162	37798	3.88	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA401.5'
11585	24638	38318	2.88	2.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCI_CGAP_Gaas4 Homo sapiens cDNA clone IMAGE:2140289.3' similar to contains Alu repetitive element
11710	24750	38443	2.39	2.0E-04	AW136740.1	EST_HUMAN	UJH-B11-edm-c-04-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190.3'
11858	24847		2.71	2.0E-04	BE066781.1	EST_HUMAN	RC2-BT0317-150200-011-b04 BT0317 Homo sapiens cDNA
12106	25086	38760	32.04	2.0E-04	P21733	SWISSPROT	HYPOPHOSPHATASE 2B.1 KD PROTEIN IN CRYB1 REGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	26178		1.29	2.0E-04	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds

Page 198 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
788	13967	27018	0.86	1.0E-04	H89946.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2Nbl-IM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.t1 L1 repetitive element;
1100	14269	27322	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
1138	14303	27358	3.79	1.0E-04	AW013847.1	EST_HUMAN	UHH-B10-aab-e-09-Q-U1.s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	UHH-B10-aab-e-09-Q-U1.s1 NCI CGAP Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1363	14517		2.65	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1667	14810	27895	4.23	1.0E-04	AF148805.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	hw45c08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2752	15869	28978	1.08	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2752	15869	28978	1.08	1.0E-04	BE218833.1	EST_HUMAN	hw45c08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3356	16528	29543	1.18	1.0E-04	Q82203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3829	16989	29862	0.86	1.0E-04	AI440282.1	EST_HUMAN	g01f11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140268 3' similar to contains Alu repetitive element;
4171	17321	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB004 3'
5207	18328	31298	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5980	19185	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI CGAP_P73 Homo sapiens cDNA clone IMAGE:252
6977	20205	33653	0.68	1.0E-04	AA584581.1	EST_HUMAN	nl28a04.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb-M87252
7338	20417	33879	12.52	1.0E-04	A1251980.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN) contains Alu repetitive element;
7744	20417	33879	13.49	1.0E-04	A1251980.1	EST_HUMAN	q67d10.x1 NCI CGAP_Oy32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21266	34789	1.02	1.0E-04	AA630453.1	EST_HUMAN	q67d10.x1 NCI CGAP_Oy32 Homo sapiens cDNA clone IMAGE:1985683 3'
9538	22603	36175	2.76	1.0E-04	A1808220.1	EST_HUMAN	ab94q08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854664 3'
9548	22613	36182	1.54	1.0E-04	Q98959	SWISSPROT	wf25a08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9625	22880		0.76	1.0E-04	T77153.1	EST_HUMAN	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 6)
9846	22886	36486	1.06	1.0E-04	10863876	NT	y072a08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 6'
							Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24873		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24838	38637	1.81	1.0E-04	AB032868.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24978	38980	1.94	1.0E-04	AW269081.1	EST_HUMAN	xx49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	25008	38710	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13698	28938	2.44	9.0E-05	AA718933.1	EST_HUMAN	ah45c11.t1 Soares_testis_NHT Homo sapiens cDNA clone 1282468 3'
4198	17346	30338	1.13	9.0E-05	A1762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394088 3' similar to contains MER8.11 MER6 repetitive element;
6084	19268	32595	1.37	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34301	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1H-B11-aar-d-08-0-UI.t1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
7751	20811	34302	2.44	9.0E-05	AW204958.1	EST_HUMAN	U1H-B11-aar-d-05-0-UI.t1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2720289 3'
9877	22639		3.03	9.0E-05	D85608.1	NT	Homo sapiens gene for cholesteryloltrin type-A receptor, complete cds
9879	22641	36211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11402	24463	36127	2.31	9.0E-05	AW079078.1	EST_HUMAN	xa34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11518	24574	36251	1.61	9.0E-05	A1287878.1	EST_HUMAN	qv23f08.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element;
11916	19266	32595	3.41	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12469	26018		3.37	9.0E-05	AF129759.1	NT	Homo sapiens MSH55 gene, partial cds; and CLUC1, DDAH, G8b, G8c, G8d, G8e, G8f, BAT6, G8b, CSK25, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
887	14063		3.11	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
3015	16191		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4804	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8948	22027	35598	0.51	8.0E-05	Y11668.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11419	24480	38146	2.58	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13169	26001		1.79	8.0E-05	AA279333.1	EST_HUMAN	zs88i01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
357	13568	26506	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220699-011-E04 CT0208 Homo sapiens cDNA

Page 200 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
581	13773	28793	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HF0072014
581	13773	28794	1.14	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human foetus cDNA Homo sapiens cDNA clone EST HF0072014
1080	14246	27303	1.07	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2763	15899	29008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dicotyledonum discoidium gene for TRFA, complete cds
4188	17318		0.85	7.0E-05	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30814	1.88	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5041	18169	31144	0.68	7.0E-05	8945300	NT	Rat cytomegalovirus Maadricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505582.1	EST_HUMAN	rh93g01.s1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:988096 3'
9763	22691	36261	3.6	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragelene (cat#036206) Homo sapiens cDNA clone HFBED60
11430	24451		5.87	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	15223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	15223	28345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2656	15778	28892	1.58	6.0E-05	AI655241.1	EST_HUMAN	wb54f06.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:23095531 3' similar to gb.J03250 DNA TOPOISOMERASE I (HUMAN);
2875	13880	26912	2.54	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32538	3.28	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32539	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6533	19897	33070	1.6	6.0E-05	N72829.1	EST_HUMAN	y60g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA897680.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8276	21358	34876	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-106 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-106 BT0311 Homo sapiens cDNA
8638	21718	35255	0.62	6.0E-05	AA150482.1	EST_HUMAN	z08c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8643	21723	36260	2.62	6.0E-05	AW896629.1	EST_HUMAN	PM4-NN0050-310300-001-f10 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9452	22598	36134	1.99	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9452	22598	36135	1.55	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786	36357	1.77	6.0E-05	T94149.1	EST_HUMAN	y228c12.1 Stragelene lung (8937210) Homo sapiens cDNA clone IMAGE:119062 5'
9922	22982	36550	0.69	6.0E-05	AW627885.1	EST_HUMAN	hi37a03.x1 Soares_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10987	24066	37701	2.42	6.0E-05	R75639.1	EST_HUMAN	y159d08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38495	2.7	6.0E-05	AA044015.1	EST_HUMAN	2k8f02.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12899	25999	31773	9.37	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-09 NT0038 Homo sapiens cDNA
1435	14598	27681	20.87	5.0E-05	AW392083.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1812	15055		1.07	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
2824	16102	28118	0.64	5.0E-05	AJ251058.1	NT	Homo sapiens MIEP1A gene, promoter region and exon 1
4086	17243	30250	3.16	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X58855.1	NT	Human MLC1emb gene for embryonic myosin alkaline light chain, 3'UTR
6116	18295	32830	3.58	5.0E-05	AV693544.1	EST_HUMAN	AV693544 GLC Homo sapiens cDNA clone GLCMA06 3'
6297	19470	32825	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7486	20560		1.4	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
12466	25503		5.26	6.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	6.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2868	13457		2.73	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4605	17742	30720	0.78	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	17742	30721	0.76	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4897	18126		0.85	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18256	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
9723	22788		6.78	4.0E-05	AF202838.1	NT	Homo sapiens PP1200 mRNA, complete cds
10617	23651	37260	0.54	4.0E-05	P23760	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
11007	24086	37723	4.14	4.0E-05	AW627946.1	EST_HUMAN	h8607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12426	25302		1.47	4.0E-05	AW117590.1	EST_HUMAN	xd8a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
13186	25773		1.16	4.0E-05	AA417756.1	EST_HUMAN	z01e11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746252 3'
698	13881	28914	0.8	3.0E-05	AI248061.1	EST_HUMAN	qf64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849488 3' similar to contains Alu repetitive element/contains element KER repetitive element
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	xd24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1950	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3365	16537		0.7	3.0E-05	AI289919.1	EST_HUMAN	q01g11.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:008632
4501	17641	30625	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4501	17641	30626	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4586	17725	30707	1.11	3.0E-05	AA388679.1	EST_HUMAN	EST79996 Placenta Homo sapiens cDNA similar to similar to p53-associated protein

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4588	17725	30708	1.11	3.0E-05	AA368679.1	EST_HUMAN	EST176986 Placenta 1 Homo sapiens cDNA similar to similar to p63-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4959	13881	26914	0.7	3.0E-05	AI248061.1	EST_HUMAN	q964c10.x1 Scarsa fetal liver spleen INFILS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element contains element KER repetitive element;
5675	18669	32155	1.72	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2pl), mRNA
6897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21164	34681	2.26	3.0E-05	BE733167.1	EST_HUMAN	607567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8547	21628	35186	1.55	3.0E-05	AA284049.1	EST_HUMAN	zs60005.s1 Stralagene schizop brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
9004	22173	35718	1.56	3.0E-05	AW770982.1	EST_HUMAN	h94e08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
9098	22177	35721	1.63	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (IMAGE-8 ANTIGEN)
9331	22407		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22588	36154	1.4	3.0E-05	AA372562.1	EST_HUMAN	EST164475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22803		3.62	3.0E-05	A1786331.1	EST_HUMAN	wg36f09.x1 Scarsa NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367208 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10755	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12553	26255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12551	26374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12913	26106		1.29	3.0E-05	AW518889.1	EST_HUMAN	xs89d06.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2778811 3'
2400	15531	26658	1.49	2.0E-05	AI286021.1	EST_HUMAN	q986f1.x1 Scarsa NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;
2650	15773	26896	14.63	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2777	16893		6.99	2.0E-05	AA160562.1	EST_HUMAN	zq48a12.r1 Stralagene hNT neuron (8937233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element;
3207	16382	26393	1.29	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3428	16597	29613	1.04	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NGF1) gene, complete cds
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3583	16748		0.87	2.0E-05	X95485.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3909	17068		0.81	2.0E-05	AL038107.1	EST_HUMAN	DKFZp5661064.r1 566 (synonym: hfdk2) Homo sapiens cDNA clone DKFZp5661064 5'
6003	18132	31106	0.9	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5878	18068	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6039	19222		0.87	2.0E-05	AF023308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Page 203 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6286	19459	32811	0.79	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NHP80c9W Homo sapiens cDNA clone IMAGE:1718114 3'
6780	19916	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element:
7042	20095	33511	1.69	2.0E-05	Y08926.1	NT	nm00812.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
7054	20107	33523	1	2.0E-05	A1492360.1	EST_HUMAN	P.falcipterus mRNA for AARP1 protein, partial
7062	20115		7.24	2.0E-05	A1991025.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:20300003 3' similar to TR:O02711
7303	20385	33844	2	2.0E-05	AF224262.1	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN:
7303	20385	33845	2	2.0E-05	AF224262.1	NT	wu35h07.x1 Soares_Dickgraeffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7524	20597		0.77	2.0E-05	AF128947.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
8069	21151	34671	1.58	2.0E-05	A1381040.1	EST_HUMAN	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
9467	22524	36087	0.56	2.0E-05	P49457	SWISSPROT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
9467	22524	36088	0.56	2.0E-05	P49457	SWISSPROT	ig20h05.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2105369 3'
10127	23165	36784	0.6	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10339	23174	36984	0.94	2.0E-05	BF055639.1	EST_HUMAN	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	7175p09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'
10881	20115		2.66	2.0E-05	A1991025.1	EST_HUMAN	wu91a06.r1 Soares_placenta_8to9weeks_2NHP80c9W Homo sapiens cDNA clone IMAGE:259570 5'
11738	23824	37549	1.55	2.0E-05	BE175801.1	EST_HUMAN	wu91a06.r1 Soares_placenta_8to9weeks_2NHP80c9W Homo sapiens cDNA clone IMAGE:259570 5'
11981	24988	38688	5.74	2.0E-05	A1912713.1	EST_HUMAN	wu35h07.x1 Soares_Dickgraeffe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
12477	25921		3.7	2.0E-05	BE348229.1	EST_HUMAN	RC6-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
12592	28104		8.13	2.0E-05	AW074604.1	EST_HUMAN	wu12h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340621 3'
							hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2:
							xe69a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.13 L1 repetitive element:

Page 204 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12850	25905		3.24	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25951	32014	2.01	2.0E-05	AU131513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13208	25787		1.64	2.0E-05	AI200970.1	EST_HUMAN	qf69g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2759	16071	28983	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	29905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lambo 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4286	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17635	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	zx69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781484 5'
4975	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	yx49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5079	18207	31179	0.66	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.64	1.0E-05	Z18943.1	NT	H.sapiens repeat region
6891	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20135	33553	4.24	1.0E-05	AA641846.1	EST_HUMAN	rs18g02.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.it L1
7232	20316	33759	5.19	1.0E-05	4805844	NT	L1 repetitive element
7837	20892	34394	0.73	1.0E-05	BF222846.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	7p57d01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3649945 3' similar to contains MER10.53
9116	22165		2.39	1.0E-05	AL163227.2	NT	MER10 repetitive element
9280	22337	35887	2.59	1.0E-05	AA452578.1	EST_HUMAN	62 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9487	22544	36107	12.29	1.0E-05	AA236110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9566	22708	36275	0.81	1.0E-05	AV732190.1	EST_HUMAN	z35h12.s1 Soares_total_fetus_NE2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gbl02332 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
10043	23081	36682	0.79	1.0E-05	AW510902.1	EST_HUMAN	z505e11.r1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element
10043	23081	36683	0.79	1.0E-05	AW510902.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element
10120	23156	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element
10120	23156	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element
10387	23422		2.04	1.0E-05	AW468895.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11159	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11159	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	28096	31663	1.4	1.0E-05	AL163303.2	NT	Human sapiens chromosome 21 segment HS21C103
2737	18854	28968	5.83	9.0E-06	AI583811.1	EST_HUMAN	tt73a05.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2243386 3'
3165	16340	29348	6.11	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8b5weeks_2NbHP8b5W Homo sapiens cDNA clone IMAGE:1759191 3'
3698	16859		2.59	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6025	19208	32528	2.48	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33657	0.82	9.0E-06	BE085042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7698	20668	34144	2.82	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7953	21003	34515	12.35	9.0E-06	AI034370.1	EST_HUMAN	cc20g01.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1686912 3' similar to contains Alu repetitive element:
8668	21739	35280	1.17	9.0E-06	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
9183	22261	36803	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22261	36604	3.3	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8423	22497	36063	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24249	37863	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2596	16065	28839	2.01	8.0E-06	AW382539.1	EST_HUMAN	RC3-CT0283-201196-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33276	2.75	8.0E-06	AA284847.1	EST_HUMAN	z22a05.e1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:713865 3' similar to contains MER9.t1 MER9 repetitive element:
10761	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	a630f10.e1 Stragene_lung (#937210) Homo sapiens cDNA clone IMAGE:854261 3' similar to contains MER20.t1 MER20 repetitive element:
1470	14624	27708	3.12	7.0E-06	7682177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2936	16113		10.99	7.0E-06	AI368252.1	EST_HUMAN	qiv16g09.x1 NCI_CGAP_Uf3 Homo sapiens cDNA clone IMAGE:1891296 3' similar to contains Alu repetitive element:
3654	18817		0.85	7.0E-06	AA385542.1	EST_HUMAN	EST198205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat

Page 206 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062:250400-173-h01 OT0062 Homo sapiens cDNA
5926	19112	32424	0.93	7.0E-06	NB8845.1	EST_HUMAN	Y65607.1 Soares_multiple_sclerosis_2NBHMSIP Homo sapiens cDNA IMAGE:278412 5'
8989	22068	35608	0.83	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF6BS1E), mRNA
10104	23142		0.52	7.0E-06	Q81147	SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31647	1.68	7.0E-06	BF215972.1	EST_HUMAN	60188192F-1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4093972 5'
2984	16160	29177	1.17	6.0E-06	BE069188.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
3784	16945	28952	1.02	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4876	16183	29206	2.13	6.0E-06	Q01468	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4883	18013	30997	2.19	6.0E-06	A1040099.1	EST_HUMAN	α08402.x1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element:
5465	18685	31844	2.20	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5525	18722	31739	1.16	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
10060	23098		1.98	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
13142	26742	31948	2.39	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
6186	19362	32710	3.74	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8487	19834	32995	1.84	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20480	33923	1.18	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
8654	21734	35274	0.58	5.0E-06	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35278	0.58	5.0E-06	AW856872.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23342	36947	6.96	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
10731	23764	37372	0.61	5.0E-06	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25686	31957	5.49	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
684	13850	28877	5.47	4.0E-06	R16287.1	EST_HUMAN	y448c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element:
869	14045	27110	4.73	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element:
1365	14519	27593	3.18	4.0E-06	A1334928.1	EST_HUMAN	tb33c09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1365	14519	27594	3.18	4.0E-06	A1334928.1	EST_HUMAN	tb33c09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1503	14656	27736	1.45	4.0E-06	BF365912.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
2338	15470	28605	1.56	4.0E-06	AW015401.1	EST_HUMAN	UJH-B10-eatf-05-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3131	16307	29321	0.89	4.0E-06	AF198349.1	NT	Gallus gallus Daech2 protein (Daech2) mRNA, complete cds
4000	17157	30163	0.99	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

Page 207 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4829	18059	31041	1.89	4.0E-06	AI889839.1	EST_HUMAN	wf94c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
8896	21776	36308	0.68	4.0E-06	OT5393	SWISSPROT	MER22 repetitive element;
9000	22079	35620	4.49	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9809	22949	36535	1.28	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11735	23921	37546	3.99	4.0E-06	AB007955.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
13148	28152		1.33	4.0E-06	AW298734.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	xs53601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773368 3'
2232	15369	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	234b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1; L1 repetitive element;
2340	15471		1.48	3.0E-06	AF202635.1	NT	234b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1; L1 repetitive element;
2988	16164	29180	0.84	3.0E-06	AA868218.1	EST_HUMAN	Homo sapiens PP1200 mRNA, complete cds
3339	16512		2.67	3.0E-06	AI857779.1	EST_HUMAN	ak48911.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
3883	17042	30040	1.47	3.0E-06	BE047094.1	EST_HUMAN	LTR1 repetitive element;
3883	17042	30041	1.47	3.0E-06	BE047094.1	EST_HUMAN	wf22a05.x1 NCI_CGAP_U01 Homo sapiens cDNA clone IMAGE:2425816 3' similar to TR:O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	h964d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4684	17819	30807	5.52	3.0E-06	X54816.1	NT	h964d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6289	19462	32814	0.82	3.0E-06	AU189412.1	EST_HUMAN	h978b10.r1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
7377	20456		2.14	3.0E-06	P08548	SWISSPROT	Homo sapiens gene for alpha-1-microglobulin-bikunlin, exons 1-6 (encoding alpha-1-microglobulin, N-terminus.)
8274	21366	34874	0.81	3.0E-06	BE592964.1	EST_HUMAN	AU196412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
8883	21962	35496	0.75	3.0E-06	P07743	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12656	25435		12.07	3.0E-06	AW385282.1	EST_HUMAN	601339213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680314 5'
207	13430		2.22	2.0E-06	P54366	SWISSPROT	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
1599	14752		6.39	2.0E-06	P21414	SWISSPROT	RCO1.T0001-261199-011-A03 L.T0001 Homo sapiens cDNA
2451	15378	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	HOMEOBOX PROTEIN GOOSECOID
2537	15962	28785	1.66	2.0E-06	P04929	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2632	15755	28670	1.81	2.0E-06	P06719	SWISSPROT	wf04a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1
3607	18771	29786	0.9	2.0E-06	AV667555.1	EST_HUMAN	MER30 repetitive element;
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
							KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
							AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3858	17018	30017	1.54	2.0E-06	AA173518.1	EST_HUMAN	z027e05.t1 Stralagene ovarian cancer (#93/219) Homo sapiens cDNA clone IMAGE:595232 5'
3868	17027	30026	0.68	2.0E-06	AW450215.1	EST_HUMAN	U14-B13-alky-g-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
3876	17035	30033	1.7	2.0E-06	AB030868.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6214	18369		0.92	2.0E-06	AA974932.1	EST_HUMAN	or34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6248	19420	32768	0.62	2.0E-06	A1539448.1	EST_HUMAN	te51f05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
6571	19733	33112	5.64	2.0E-06	A1819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7635	20704	34183	0.63	2.0E-06	AA698423.1	EST_HUMAN	W90604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184		1.02	2.0E-06	AW686228.1	EST_HUMAN	nv59c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1.13 L1
8281	21363	34882	0.76	2.0E-06	T12238.1	EST_HUMAN	repetitive element ;
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	MR3-SN0067-120400-002-102 SN0067 Homo sapiens cDNA
9049	22128	35872	1.59	2.0E-06	H62051.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9417	22481	36058	0.9	2.0E-06	AF003529.1	NT	zh27c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9417	22481	36057	0.9	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9436	22570		0.46	2.0E-06	A1473450.1	EST_HUMAN	y37c04.t1 Soares_ovary_tumor_NH0T Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:U74929
9902	22942	36927	0.86	2.0E-06	N30576.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10123	23181		0.7	2.0E-06	AV748999.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
12548	26135	31549	1.34	2.0E-06	P23249	SWISSPROT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
12711	25473		5.94	2.0E-06	BE328232.1	EST_HUMAN	U16g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
34	13272	26276	1.16	1.0E-06	O76082	SWISSPROT	yw68e03.s1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:257212 3'
674	13880	26891	1.8	1.0E-06	AF084394.1	NT	AV748999 NPC Homo sapiens cDNA clone NPOX005 5'
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	PROTEIN MOV-10
1553	14708	27786	1	1.0E-06	AL163278.2	NT	hs92f02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1
1603	14756	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	repetitive element ;
1603	14756	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
							Mus musculus D6MMSE protein (D6Mm59) mRNA, complete cds
							MEROZOITE SURFACE PROTEIN CMZ-8
							Homo sapiens chromosome 21 segment HS21C078
							z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;
							z08a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;

Page 209 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	14768		0.99	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	15191	28303	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2050	15191	28304	4.49	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4489	17029	30610	15.97	1.0E-06	U07661.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5215	18336	31308	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18336	31309	1.18	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-06	N65946.1	EST_HUMAN	za27a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283750 3'
5405	18607	31579	6.14	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-008 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31608	0.94	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-06	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6915	19103		0.72	1.0E-06	BE063527.1	EST_HUMAN	CMD-BT0281-031198-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHA1/ALPHA-E CHAIN PRECURSOR
7923	26223		0.73	1.0E-06	BE185330.1	EST_HUMAN	IL5-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8100	21272		0.99	1.0E-06	AA912023.1	EST_HUMAN	q28c08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8468	21549	35079	1.12	1.0E-06	A1347010.1	EST_HUMAN	qp54e02.x1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8685	21765	35297	1.31	1.0E-06	A1287878.1	EST_HUMAN	q23f06.x1 NCL CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element ;
8504	22770	36341	0.91	1.0E-06	N74635.1	EST_HUMAN	za65e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'
9578	22721	36291	0.61	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-06	U82685.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-06	U82685.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22669	36558	5.22	1.0E-06	AA132811.1	EST_HUMAN	zo17e08.l1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9991	23030		3.55	1.0E-06	AA449257.1	EST_HUMAN	zo04d11.s1 Soares fetal Tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785493 3' similar to
10705	23738		2.19	1.0E-06	AL163203.2	NT	gibD26128 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11849	24935		3.1	1.0E-06	AW1860941.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12569	25396	32041	8.24	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
371	13580	26613	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8802	21883		0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38257	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
4893	18023	31008	4.23	8.0E-07	A1286566.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081 ql82g07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878878 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4893	18023	31009	4.23	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6007	19192		8.17	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8181	21273		8.44	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11021	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST036800 Fetal brain, Stragelene (cat#332006) Homo sapiens cDNA clone HFBEN89
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1914	15057	28167	0.97	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5636	18830	31906	0.86	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31907	0.86	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1962	15105	28205	3.47	6.0E-07	AW85558.1	EST_HUMAN	CM3-CT0277-221099-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKIZW), RD, complement factor B (Bf), and complement component C2 (C2) genes>
2561	16686	28812	2.43	6.0E-07	AF019413.1	NT	HYPOPHYSICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
4090	17236		1.74	6.0E-07	P41479	SWISSPROT	7p84f07.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 456L.
9342	22418	35972	1.31	6.0E-07	BF001867.1	EST_HUMAN	GM0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
12115	25095	38600	1.45	6.0E-07	BE063509.1	EST_HUMAN	GM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
12444	26067		1.72	6.0E-07	AW903222.1	EST_HUMAN	hu11h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3196329 3' similar to contains L1.b2 L1 L1 repetitive element.
13229	25992		1.32	6.0E-07	BE222390.1	EST_HUMAN	repetitive element.
336	13549		1.04	5.0E-07	AI831893.1	EST_HUMAN	wn64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14243		2.39	6.0E-07	AA380630.1	EST_HUMAN	EST183615 Supt cells Homo sapiens cDNA 5' and
3096	16272		0.73	5.0E-07	AI831893.1	EST_HUMAN	wn64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4769	17904	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	19421	32767	1.33	5.0E-07	U65067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
							Ig080505.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element contains element A3R repetitive element.
7210	20075	33487	1.71	5.0E-07	AI93981.1	EST_HUMAN	Ig080505.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu repetitive element contains element A3R repetitive element.
7210	20075	33488	1.71	5.0E-07	AI93981.1	EST_HUMAN	repetitive element contains element A3R repetitive element.
7503	20578	34050	15.93	5.0E-07	AW070885.1	EST_HUMAN	xb31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gbX15341 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAMTS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
8687	21767		0.88	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

Page 211 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23612	37217	5.47	5.0E-07	AI808537.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
11805	24795	38493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11860	24868		2.08	5.0E-07	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12366	25668			5.0E-07	AL163285.2	NT	Homo sapiens chromosome 21, segment HS21C085
12918	25966		3.06	5.0E-07	AW862537.1	EST_HUMAN	QV0-CT0383-210400-204-B12 CT0383 Homo sapiens cDNA
4108	17280	30261	1.68	4.0E-07	AW009602.1	EST_HUMAN	ws84105.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:2504697.3
7328	20410		0.8	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20495	33983	0.97	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7471	20495	33984	0.97	4.0E-07	Q8Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21, segment HS21C007
9251	23228	35875	4.9	4.0E-07	AW418134.1	EST_HUMAN	xy49g11.x1 NCI CGAP_L334.1 Homo sapiens cDNA clone IMAGE:2856548.3
10332	23367	36976	0.53	4.0E-07	BE001075.1	EST_HUMAN	60150748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959851.5
10332	23367	36977	0.53	4.0E-07	BE001076.1	EST_HUMAN	60150748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959851.5
10531	23366	37174	0.55	4.0E-07	AL163218.2	NT	Homo sapiens chromosome 21, segment HS21C018
11179	24248	37881	3.88	4.0E-07	AJ765528.1	EST_HUMAN	wf81b08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11179	24248	37882	3.88	4.0E-07	AJ765528.1	EST_HUMAN	wf81b08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2399703.3
11495	24553		1.69	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
11919	24905		1.32	4.0E-07	BE067557.1	EST_HUMAN	60164903F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3632824.5
13207	25788		1.71	4.0E-07	11437074	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26686	5.38	3.0E-07	U19719.1	NT	Human microfilin-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
586	13786	26806	3.59	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1405	14559	27633	1.43	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1635	14908		3.62	3.0E-07	M64857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2104	15243		2.32	3.0E-07	AA528763.1	EST_HUMAN	n156b09.at NCI CGAP_Oy2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.13 L1 repetitive element;
2361	15492	28621	1.14	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3099	16275	29289	0.87	3.0E-07	T84704.1	EST_HUMAN	yd5012.1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:111605.6
3228	16402	20414	1.78	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT-TRIM INTERGENIC REGION PRECURSOR
4802	17937		0.64	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVONACROGLOBULIN)
4849	17982	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCDD01.3
4885	18015	30999	0.7	3.0E-07	AI787238.1	EST_HUMAN	w886b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347987.3

Page 212 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5175	18287	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5175	18287	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5783	18975	32281	12.39	3.0E-07	O88907	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6095	19276	32605	0.7	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	18985		5.09	3.0E-07	AA815175.1	EST_HUMAN	cc04c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338890 3'
7678	20743	34224	3.53	3.0E-07	AW797168.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7841	20888		1.3	3.0E-07	AI591065.1	EST_HUMAN	tw28f11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2281037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9330	22408	35959	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9330	22406	35960	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13194	25777		4.26	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
28	13267	26270	7.32	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26413	6.08	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
158	13383	26414	6.08	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vesicular) actin gene, complete cds
787	13948	26995	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
787	13948	26996	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
966	14139	27200	2.32	2.0E-07	AA223280.1	EST_HUMAN	zr08b07.s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:850869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
967	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc16g04.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element ;
1189	14361	27409	1.55	2.0E-07	Q26768	SWISSPROT	I/6 AUTOANTIGEN
1530	14782	27868	2.06	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3708	18888		0.63	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3779	18940	28946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-290400-188-h11 NN1023 Homo sapiens cDNA

Page 213 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6460	18680	31638	1.52	2.0E-07	AW898066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6681	26629	33229	0.73	2.0E-07	AW448968.1	EST_HUMAN	UHH-B12-ale-b-01-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734008 3'
6802	19957	33357	3.39	2.0E-07	AI208715.1	EST_HUMAN	cg56405.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8684	21744		3.87	2.0E-07	AV728390.1	EST_HUMAN	AV728390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8893	21972	35508	1.11	2.0E-07	AA035198.1	EST_HUMAN	z427g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
8983	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW892507.1	EST_HUMAN	GM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA
10706	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12138	26655		2.96	2.0E-07	BE163717.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12228	25987		2.38	2.0E-07	AI732462.1	EST_HUMAN	PM0-HT0338-280100-008-H07 HT0338 Homo sapiens cDNA
1128	14291		0.76	1.0E-07	AL163282.2	NT	zn85h11.x5 Stralagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR.b2 THR repetitive element;
2888	14704	27784	2.08	1.0E-07	P09258	SWISSPROT	Homo sapiens chromosome 21 segment HS21C082
3838	14291		1.24	1.0E-07	AL163282.2	NT	GLYCOPROTEIN GPV
4408	17550	30534	2.91	1.0E-07	AV718682.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
4408	17550	30535	2.91	1.0E-07	AV718682.1	EST_HUMAN	AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
							AV718682 GLC Homo sapiens cDNA clone GLCFNF04 5'
6632	19791	33180	0.8	1.0E-07	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
7006	20142	33590	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7006	20142	33561	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291339 5'
7662	20729	34205	7.6	1.0E-07	IN55081.1	EST_HUMAN	yv43c07.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7826	20881	34382	0.69	1.0E-07	BF376909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7828	20881	34383	0.69	1.0E-07	BF376909.1	EST_HUMAN	PM4-TN0024-030800-002-b06 TN0024 Homo sapiens cDNA
7854	20909	34413	1.24	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8410	21491	35020	2.76	1.0E-07	P07435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8410	21491	35021	2.76	1.0E-07	P07435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9155	22233	35778	2.7	1.0E-07	AA693576.1	EST_HUMAN	z151e10.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:434346 3'
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAM-TS8) (METH-2)

Page 214 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36438	0.6	1.0E-07	BE327843.1	EST_HUMAN	hu28h08.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36776	2.35	1.0E-07	BF674824.1	EST_HUMAN	MER18 repetitive element ;
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10682	23718		1.22	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12085	25065	38771	2.35	1.0E-07	AI341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12506	25639	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	6889e03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2008692 3'
12859	25438		1.45	1.0E-07	X64487.1	NT	hs55c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:O85722 O85722
12852	25568		2.1	1.0E-07	X51755.1	NT	DJ1163J1.1 ;
7433	20510	33982	0.75	9.0E-08	AI63962.1	EST_HUMAN	H. sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	9.0E-08	AV734819.1	EST_HUMAN	Human lambdaIda-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891052.1	EST_HUMAN	hs1b06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11865	24950	38556	2.38	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABFB08 5'
12456	25320		2.51	9.0E-08	AJ251973.1	NT	ws30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element ;
1075	14241		1.01	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3634	16798		1.57	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
8837	22016	35557	5.35	8.0E-08	AI752367.1	EST_HUMAN	wd18b05.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22016	35558	5.35	8.0E-08	AI752367.1	EST_HUMAN	601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8827	22867	36449	3.03	8.0E-08	AW970693.1	EST_HUMAN	601560133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11523	24578		1.73	8.0E-08	AF263417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
82	13317	26345	3.91	7.0E-08	Q02357	SWISSPROT	EST382776 MAGC resequences; MAGK Homo sapiens cDNA
1392	14546	27622	19.51	7.0E-08	X04809.1	NT	Homo sapiens Jun dimerization protein gene, partial cds; efos gene, complete cds; and unknown gene
3666	16826	29839	0.88	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3666	16826	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
5332	18445	31413	0.62	7.0E-08	T65891.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI535743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11970	24955	38658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)

Page 215 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12978	16829	29839	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16829	29840	1.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15564	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MR0-HT0168-161199-004-q09 HT0166 Homo sapiens cDNA
3129	16305	29319	0.68	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074) mRNA
4383	17608	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9529	22594		0.55	6.0E-08	AA827076.1	EST_HUMAN	cb56c06.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335388 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24698	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11823	24812		1.43	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
87	13322	26360	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2309	16441	28576	3.93	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P05681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12382	25271	32077	1.77	5.0E-08	AW861878.1	EST_HUMAN	QV0-CT0225-131099-034-e12 CT0225 Homo sapiens cDNA
1798	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-1D PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-1D PROTEIN PRECURSOR
2950	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426.t1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434J0426 5'
3132	16308		1.01	4.0E-08	AI078417.1	EST_HUMAN	cd05e02.x1 Sceres_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
4024	17180	30189	0.65	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6535	19698	33071	1.07	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8998	22077	35617	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9340	22416	35969	1.13	4.0E-08	L42571.1	NT	Cricetus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9845	22885		1.58	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10356	23871		0.85	4.0E-08	AI016342.1	EST_HUMAN	cl78d12.s1 Sceres_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622803 3'
10597	23632	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	en22d10.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1689411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
11328	24391	38037	5.16	4.0E-08	AA3593627.1	EST_HUMAN	z176b08.r1 Sceres_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/CA, K-EXCHANGER. ;

Page 218 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11328	24391	38038	5.16	4.0E-08	AA393627.1	EST_HUMAN	z76508.r1 Soares testis NIH Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11349	24411	38064	11.86	4.0E-08	BF692493.1	EST_HUMAN	G605579 NA/CA,K-EXCHANGER. ;
11349	24411	38065	11.86	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	26108		1.93	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12804	26598		2.01	4.0E-08	AI343953.1	EST_HUMAN	z456p03.r1 Soares fetal heart_Nb2H19W Homo sapiens cDNA clone IMAGE:345656 5' similar to contains L1.1 L1 repetitive element ;
5728	18921	32215	2.27	3.0E-08	BE018348.1	EST_HUMAN	1b95a11.x1 NCJ CGAP_C016 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.B3
7115	18541	31498	6.01	3.0E-08	AI792737.1	EST_HUMAN	MER18 MER18 repetitive element ;
7111	20776	34262	1.43	3.0E-08	AL163246.2	NT	1b678a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
7928	20978		3.32	3.0E-08	AI436352.1	EST_HUMAN	q97811.y5 NCJ CGAP_P128 Homo sapiens cDNA clone IMAGE:1944045 5'
10102	23140		0.63	3.0E-08	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C046
11278	24343	37883	1.84	3.0E-08	AI218001.1	EST_HUMAN	1b83h09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
11957	24942	38646	1.32	3.0E-08	AF111167.2	NT	Homo sapiens MHC class 1 region
12156	25123		33.85	3.0E-08	R18420.1	EST_HUMAN	q121a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845284 3'
211	13434		4.16	2.0E-08	AW302998.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene y902f04.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element ;
236	13458		5.76	2.0E-08	AA425598.1	EST_HUMAN	xr87f06.x1 NCJ CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
509	13703	26732	4.46	2.0E-08	AF198349.1	NT	z448f07.r1 Soares fetal_fetus_Nb2Hf8_9W Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER16 repetitive element ;
677	13863	26893	9.7	2.0E-08	AW866438.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
677	13863	26894	9.7	2.0E-08	AW866438.1	EST_HUMAN	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1014	14186		7.75	2.0E-08	BE280477.1	EST_HUMAN	MFR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	607155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1774	14923	28017	0.98	2.0E-08	AW841890.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G047
1780	14929		2.08	2.0E-08	BE734871.1	EST_HUMAN	IL5-CN0024-030300-028-C01 CN0024 Homo sapiens cDNA
1802	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3945189 5'
2608	15732		1.86	2.0E-08	K00216.1	NT	xp43f11.x1 NCJ CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
3279	16453	29474	5.61	2.0E-08	O42280	SWISSPROT	Sheep His-IRNA-GUG WNT-14 PROTEIN PRECURSOR

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3279	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3982	17120		1.83	2.0E-08	AW813820.1	EST_HUMAN	RC3-STO197-TG1098-O12-B03 ST0197 Homo sapiens cDNA
4189	17359	30332	0.62	2.0E-08	UB2668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17694		1.48	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17h08.x2 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2819327 3' similar to contains Alu repetitive element
5753	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	a80h11.a1 Scores testis_NHT Homo sapiens cDNA clone 1377189 3'
5955	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2698462 3' similar to contains MER18.b3
8193	21275	34788	1.11	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element ;
8301	21363	34804	1.5	2.0E-08	AA480121.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9286	22362		0.89	2.0E-08	AU139978.1	EST_HUMAN	ab02g06.e1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838674 3'
10738	23771	37381	0.83	2.0E-08	N78097.1	EST_HUMAN	AU139978.PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10738	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	yw7202.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
12478	26328		1.77	2.0E-08	AL163284.2	NT	yw7202.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element;
13085	28159		1.8	2.0E-08	I1431678	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1672	14824	27907	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT BINDING ACTIVITY)
1872	14824	27908	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT BINDING ACTIVITY)
1816	14965	28058	1.66	1.0E-08	AF125348.1	NT	(TRANSCRIPTION FACTOR NTF-1)
2110	15248		2.97	1.0E-08	BE141959.1	EST_HUMAN	Homo sapiens cavedin 1 (CAV1) gene, exon 3 and partial cds
3261	16435	29453	0.85	1.0E-08	BE246944.1	EST_HUMAN	PM2-HT1030-150999-001-F12 HT1030 Homo sapiens cDNA
3261	16435	29454	0.95	1.0E-08	BE246944.1	EST_HUMAN	TGBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAEP5232
5716	18009	32204	4.51	1.0E-08	AJ010770.1	NT	TGBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAEP5232
7948	20998	34507	0.94	1.0E-08	P18474	SWISSPROT	KMO KMO RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8224	21308	34828	0.62	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102

Page 218 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8320	21402	34927	0.54	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35359	2.27	1.0E-08	A015304.1	EST_HUMAN	alpha05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22478		0.56	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10778	23811	37434	0.87	1.0E-08	P88063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11598	24848	38332	3.55	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12581	25391		3.08	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
13137	25825		1.26	1.0E-08	BF375398.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10287	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7414	20492	33950	8.1	8.0E-09	AH183500.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
8189	21271	34796	2.54	8.0E-09	AW900159.1	EST_HUMAN	q442e07.x1 Soares fetal heart_NbhH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element:
9189	22267		2.53	8.0E-09	AA838892.1	EST_HUMAN	CM0-NN1004-100300-273-e06 NN1004 Homo sapiens cDNA
3695	16856		1.98	7.0E-09	D96842.1	NT	op74008.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1682575 3'
4115	17269		0.98	7.0E-09	U50871.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3 Human familial Alzheimer's disease (STM2) gene, complete cds
8088	21188		0.58	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element:
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr80c05.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element:
9460	22517	36080	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3351834 5'
10554	23589		0.76	7.0E-09	AA058626.1	EST_HUMAN	zf59e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element:
10910	23983		2.01	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2221	13355		0.95	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0514 5'
5085	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-r05 HT0527 Homo sapiens cDNA

Page 219 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5486	18695	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8776	21854	35396	1.11	6.0E-09	BE161663.1	EST_HUMAN	MR3-HT0446-260300-201-h12 HT0446 Homo sapiens cDNA
9377	22452	36014	2.18	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10969	24049	37882	1.66	6.0E-09	BF108755.1	EST_HUMAN	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to
12089	25069	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	contains MER29.b2 MER28 repetitive element;
1447	14800	27877	3.47	5.0E-09	BE149284.1	EST_HUMAN	H-UMGS0003762 Human adult (K Okubo) Homo sapiens cDNA
1900	15043	28154	7.4	5.0E-09	AL163284.2	NT	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
6540	19703	33075	2.22	5.0E-09	AA359454.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
							EST168746 Fetal Lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV7S2A1N4T, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2P, TCRBV7S2A1N4T, TCRBV13S913S>
6988	18507	31523	0.66	5.0E-09	U65059.1	NT	
8785	21864	35407	0.63	6.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10300	23335	36940	3.25	5.0E-09	AW799867.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
11944	24930	38632	1.87	5.0E-09	AA460142.1	EST_HUMAN	z680e09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795680 3'
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1497	14850	27732	1.86	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038199), mRNA
2500	15627	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	EST166395 Infant brain Homo sapiens cDNA 5' end similar to
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	z604c06.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8719	21789	35334	1.02	4.0E-09	T64942.1	EST_HUMAN	ydt1a07.s1 Soares_fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:66804 3'
11330	24393	38041	9.51	4.0E-09	A1886401.1	EST_HUMAN	wm94f10.x1 NCI_CGAP_U22 Homo sapiens cDNA clone IMAGE:2443627 3'
							zr34e12.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:565278 5' similar to gb.L07807
11379	24440		1.44	4.0E-09	AA196142.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
							hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.i3
2427	15558	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2619	15742	28856	1.06	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.i3
2716	16834	28844	0.99	3.0E-09	P23249	SWISSPROT	MER18 repetitive element; PROTEIN MOV-10
3408	16578	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.i3 MER18 repetitive element;

Page 220 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3464	16631		0.7	3.0E-09	AA442272.1	EST_HUMAN	zr64a04.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17361		0.62	3.0E-09	X16674.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4546	17694	30668	3.47	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF-4A1) gene, partial cds
4634	17770	30751	1.19	3.0E-09	Q973R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0863)
8084	21166	34882	1.1	3.0E-09	BE465780.1	EST_HUMAN	h80a02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN. ;
10792	23825	37448	0.46	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37978	3.15	3.0E-09	BF109943.1	EST_HUMAN	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37978	3.15	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.98	2.0E-09	X16674.1	NT	7172c08.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1237	14443	27511	4.7	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1591	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2403	15534	28661	2.24	2.0E-09	Q9Y3R5	SWISSPROT	DKFZp761B1710_r1 781 (synonym: hemy2) Homo sapiens cDNA clone DKFZp761B1710 5'
4048	17204	30214	3.01	2.0E-09	C60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0863)
4119	17273	30272	0.9	2.0E-09	AI263479.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5264	18363	31348	0.82	2.0E-09	M23161.1	NT	q107d09.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5837	19027	32333	0.67	2.0E-09	AI004062.1	EST_HUMAN	Human transposon-like element mRNA
6278	19452		0.75	2.0E-09	AL163249.2	NT	cl47609.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST166142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7692	20757	34242	0.66	2.0E-09	W28834.1	EST_HUMAN	z63h106.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:756187 5' similar to contains Alu repetitive element;
7971	21021	34534	0.59	2.0E-09	AI243732.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8909	21988	35528	1.2	2.0E-09	AJ271735.1	NT	cl48g10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1864114 3'
10824	23857	37460	0.85	2.0E-09	AV688942.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
12745	14013		20.06	2.0E-09	X16674.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12830	26188		1.89	2.0E-09	AA226070.1	EST_HUMAN	AV688942 GKC Homo sapiens cDNA clone GKACACAT11 5'
1019	14180		1.19	1.0E-09	W78152.1	EST_HUMAN	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1133	14258	27353	1.43	1.0E-09	5031624	NT	nc11c02.r1 NCI CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1133	14258	27353	1.43	1.0E-09	5031624	NT	z479d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:346853 3' similar to gb:U02932 PEROMYSE Proliferator Activated Receptor Alpha (HUMAN);
1133	14258	27353	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1133	14258	27353	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

Page 221 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	15698		1.15	1.0E-09	AI356086.1	EST_HUMAN	g6-611.x1 NCJ_CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2016812 3' similar to contains MER12.12 MER12 repetitive element ;
2954	18131	28148	2.02	1.0E-08	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
2992	16168	28184	6.17	1.0E-08	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2992	16168	29185	6.17	1.0E-08	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16278	28283	0.99	1.0E-08	BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4920	18950		6.15	1.0E-09	AA719287.1	EST_HUMAN	zh35b03.s1 Soares_pithecus_gland_N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
5341	18454		0.8	1.0E-09	AA921958.1	EST_HUMAN	cm44g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942 3'
5820	18814	31882	0.85	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5862	18138	32454	1.29	1.0E-09	U07008.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19448	32784	3.34	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8584	21685	35206	0.82	1.0E-08	AI688474.1	EST_HUMAN	wd39005.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains MER25.11 MER25 repetitive element ;
10620	23555		2.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12842	28120	31668	1.71	1.0E-08	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12787	25510		1.42	1.0E-08	T57360.1	EST_HUMAN	y651gt12.s1 Sitratigene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74758 3'
13132	28020		1.68	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14494	27584	1.62	9.0E-10	AW867740.1	EST_HUMAN	MRQ-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2895	18074	28092	3.74	9.0E-10	AI870071.1	EST_HUMAN	we78h03.x1 Soares_Deckgraele_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
6973	20201	33627	4.98	9.0E-10	AI452982.1	EST_HUMAN	i46b08.x1 Soares_NSIF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372 000372 PUTATIVE P150 ;
151	13376	28408	9.26	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	28007	0.66	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0831-150200-071401 BT0831 Homo sapiens cDNA
4318	17491	30446	5.45	8.0E-10	AA376832.1	EST_HUMAN	EST89564 Small intestine I Homo sapiens cDNA 5' end
10170	23207		2.51	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	28641	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51898), mRNA
719	13901	28642	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51898), mRNA
1651	14804	27890	2.58	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2628	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3157	16332	28841	2.25	7.0E-10	X00865.1	NT	H. sapiens DHFR gene, exon 3

Page 222 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6314	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST161247 Gall bladder II Homo sapiens cDNA 5' end
7574	20846	34124	1.37	7.0E-10	BF352883.1	EST_HUMAN	IL3-UT0619-110700-208-D12 HT0819 Homo sapiens cDNA
7834	20889		1.65	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8163	21245	34765	1.54	7.0E-10	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
936	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
2742	15859	28971	1.63	6.0E-10	AH424405.1	EST_HUMAN	h02407.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4615	17752	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17994		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031099-012-g12 CT0254 Homo sapiens cDNA
8963	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8963	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
9834	22874	36458	0.48	6.0E-10	P98073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
780	13980		5.29	5.0E-10	AL046804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3564	16729	29745	1.14	5.0E-10	Q01033	SWISSPROT	EST384012 MAGI2 sequences, MAGL Homo sapiens cDNA
5105	18233	31202	1.4	5.0E-10	AF181897.1	NT	DKFZp434N219.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
7475	20550		1.85	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	25021	38725	1.31	5.0E-10	AF091415.1	NT	Macaca tonkeana isolate 568tonkeana NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
114	13345		1.09	4.0E-10	A1221083.1	EST_HUMAN	qg0909.x1 Soares_placenta_866weeks_ZNBP86c9W Homo sapiens cDNA clone IMAGE:1795049 3' similar to contains LTR.b2 LTR8 repetitive element:
2052	15193	28306	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg58g03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element:
2040	15763	28877	6.79	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7327	20409	33871	17.76	4.0E-10	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	UI-H-B12-ant-a-07-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
10662	23696	37305	1.12	4.0E-10	AI267342.1	EST_HUMAN	eq63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653

Page 223 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37460	0.54	4.0E-10	BE199208.1	EST_HUMAN	PM1-HT0521-120200-001-008 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE199208.1	EST_HUMAN	PM1-HT0521-120200-001-008 HT0521 Homo sapiens cDNA
939	14112	27173	2.24	3.0E-10	N36113.1	EST_HUMAN	y93206.s1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.11 L1 repetitive element;
1392	14637		5.3	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4657	17753	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17753	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5350	18463	31428	0.89	3.0E-10	L34076.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18767	31808	0.78	3.0E-10	N50709.1	EST_HUMAN	yz11g08.s1 Soares multiple sclerosis 2N6HMSP Homo sapiens cDNA clone IMAGE:282782 3'
6332	19503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBOLD PROTEIN (VEINLET PROTEIN)
6481	19648	33010	3.62	3.0E-10	BE302970.1	EST_HUMAN	ba76d08.y1 NIH JMG 20 Homo sapiens cDNA clone IMAGE:2906319 5'
7637	20687	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone C8FBGD08 5'
7637	20687	34496	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone C8FBGD08 5'
8928	22007	35546	1.57	3.0E-10	H87208.1	EST_HUMAN	y674b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
9249	22326	35972	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22326	35973	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22808		0.78	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10679	23713		1.95	3.0E-10	T65991.1	EST_HUMAN	yc11e12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
10820	23853		0.96	3.0E-10	AA769284.1	EST_HUMAN	nz36g03.s1 NCJ CGAP GC81 Homo sapiens cDNA clone IMAGE:1289908 3'
12941	25619	31977	1.87	3.0E-10	BE176517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
36	13274	26278	2.08	2.0E-10	P49888	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
36	13274	26279	2.08	2.0E-10	P49888	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1946	15089		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF876047.1	EST_HUMAN	602136640F1 NIH JMG 83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	19111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.56	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7537	20610	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	607586208F1 NIH JMG 7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34807	0.58	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8203	21285	34808	0.58	2.0E-10	P28809	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Page 224 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
9502	22568		1.06	2.0E-10	EST_HUMAN	7c78d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1
11609	24652		1.33	2.0E-10	EST_HUMAN	repetitive element;
1538	14691		3.09	1.0E-10	EST_HUMAN	la10f12.x1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2043695 3'
1637	14769	27874	3.37	1.0E-10	EST_HUMAN	MRO-SN0038-280300-001-101 SN0038 Homo sapiens cDNA
2649	15772		2.16	1.0E-10	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
3589	16763	29768	0.9	1.0E-10	EST_HUMAN	QV0-CT0225-191199-05B-608 CT0225 Homo sapiens cDNA
3829	16793		0.67	1.0E-10	EST_HUMAN	QV2-TT0003-181189-013-010 TT0003 Homo sapiens cDNA
3947	16793		0.76	1.0E-10	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	NT	DKFZp434N1317_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N1317 5'
4245	17391	30378	16.24	1.0E-10	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30379	16.24	1.0E-10	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4253	17399	30388	1.76	1.0E-10	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4285	17430		2.28	1.0E-10	NT	Homo sapiens PCCX1 mRNA for protein containing CXX domain 1, complete cds
5277	18386		1.01	1.0E-10	EST_HUMAN	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
7644	20713		0.58	1.0E-10	SWISSPROT	we82f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains
7860	20914	34419	0.69	1.0E-10	EST_HUMAN	MER31.11 MER31 repetitive element;
8434	21515	35046	1.14	1.0E-10	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8855	21924		1.62	1.0E-10	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
10406	23441		6.24	1.0E-10	EST_HUMAN	FB_5A4 Feal brain library Homo sapiens cDNA
11154	24225	37854	3.5	1.0E-10	EST_HUMAN	qno04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1
12165	18503		1.8	1.0E-10	NT	repetitive element;
272	13490	26521	0.87	9.0E-11	EST_HUMAN	zn23p06.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
2171	15306	28433	6.02	9.0E-11	EST_HUMAN	cy85f03.x1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
2171	15306	28434	6.02	9.0E-11	EST_HUMAN	H_sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
					NT	
					EST_HUMAN	IL2-HT0203-281099-016-c08 HT0203 Homo sapiens cDNA
					EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
					EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

Page 225 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	AL134395.1	EST_HUMAN	DKFZp647D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp647D225.1
3470	16637	29658	2.88	9.0E-11	AL134395.1	EST_HUMAN	DKFZp647D225.1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp647D225.1
4622	17759	30741	0.8	9.0E-11	AA775985.1	EST_HUMAN	ae78f01.s1 Stratiene ichizo brain S11 Homo sapiens cDNA clone DKFZp647D225.1
5692	18886		3.05	9.0E-11	BE078780.1	EST_HUMAN	RC8-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25378	32072	2.45	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN:608808.6
3185	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	Yn53f1.1 s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172173.3 similar to contains L1 repetitive element;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Walzmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298.3
5913	19101	32415	0.66	8.0E-11	AW674318.1	EST_HUMAN	ba66g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900982.3
5811	19935		0.82	8.0E-11	AW166158.1	EST_HUMAN	x445h11.x1 NCI_CGAP_Bm50 Homo sapiens cDNA clone IMAGE:2621061.3 similar to contains MER10.t1
1478	14632	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	MER10 repetitive element;
8695	21775	35307	2.61	7.0E-11	AF163864.1	NT	EST34392 Embryo, 6 week 1 Homo sapiens cDNA 5' end
10434	23469		1.37	7.0E-11	P11369	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
425	13620	26661	6.19	8.0E-11	M55270.1	NT	RETRONIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
425	13620	26662	6.19	8.0E-11	M55270.1	NT	ENDONUCLEASE]
							Human matrix Gla protein (MGP) gene, complete cds
							Human matrix Gla protein (MGP) gene, complete cds
							Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds
6962	20014	33424	0.91	6.0E-11	L44140.1	NT	(G6PD) gene, complete cds
7870	20924	34431	3.5	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8559	21640	35179	0.99	6.0E-11	AV727856.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC08.5
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	GM0-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12	13250	26250	1	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6645	18804	33191	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7659	20764	34248	11.57	6.0E-11		NT	Homo sapiens prolactin beta 3 (PCHB3), mRNA
1433	14586		1.39	4.0E-11	AA436042.1	EST_HUMAN	zu01b12.11 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559.5
2851	15995	28074	8.94	4.0E-11	BE859800.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906295.5
3034	16210	26233	1.26	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17975	30858	0.81	4.0E-11	D44696.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6005	19765	33154	3.29	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

Page 226 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33718	0.82	4.0E-11	AA442630.1	EST_HUMAN	z55f10.r1 Soares, testis, NHT: Homo sapiens cDNA clone IMAGE:757863 5' similar to TR:G1055250
7532	20805		3.66	4.0E-11	AF224689.1	NT	G1055250 PHEROMONE RECEPTOR VN4. ;
9595	22650		1.56	4.0E-11	BE149425.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9862	22802	36487	0.79	4.0E-11	AI609753.1	EST_HUMAN	RC1-HT0256-210100-013-038 HT0256 Homo sapiens cDNA
10856	23822	37513	0.94	4.0E-11	BF367283.1	EST_HUMAN	h82g12.x1 NCI CGAP_Brm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
12794	25530	32008	1.71	4.0E-11	11545732	NT	CE00385 ;
1521	14674	27756	4	3.0E-11	6879077	NT	MRO-GN0024-180900-008-h09 GN0024 Homo sapiens cDNA
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
982	14165	27215	1.43	2.0E-11	AI150502.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	q36c04.x1 Soares, testis, NHT: Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1644	14796	27880	4.44	2.0E-11	L17432.1	NT	MER10 repetitive element ;
1644	14796	27881	4.44	2.0E-11	L17432.1	NT	Y943e12.r1 Soares Infant brain: INIB Homo sapiens cDNA clone IMAGE:35144 5'
2823	15937	29047	1.09	2.0E-11	AF087913.1	NT	Y943e12.r1 Soares Infant brain: INIB Homo sapiens cDNA clone IMAGE:35144 5'
3266	16440	29401	5.56	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector-like protein
3403	16573	29568	0.92	2.0E-11	AI478917.1	EST_HUMAN	COR3bela (COR3'bela) genes, complete cds
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and effector-like protein
							COR3'bela (COR3'bela) genes, complete cds
							Human endogenous retrovirus HERV-P-T47D
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							h54c09.x1 NCI CGAP_K611 Homo sapiens cDNA clone IMAGE:2101936 3'
							POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC-POLYPEPTIDE, N-
							ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3448	16618	29634	0.67	2.0E-11	Q10473	SWISSPROT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3586	16760		1.01	2.0E-11	AF020503.1	NT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
3797	16958	29882	0.64	2.0E-11	P70213	SWISSPROT	RC3 BT0316-170200-014-e05 BT0316 Homo sapiens cDNA
4568	17704		1.07	2.0E-11	BE085537.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21 C027
4728	17863		0.8	2.0E-11	AL163227.2	NT	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
5051	18179		1.86	2.0E-11	BE082568.1	EST_HUMAN	EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-macroglobulin
6142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	QV2-P10073-280300-109-h09 PT0073 Homo sapiens cDNA
6263	19437	32784	1.23	2.0E-11	AW877808.1	EST_HUMAN	

Page 227 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6440	19807	32970	2	2.0E-11	AA591028.1	EST_HUMAN	nc80h05.t1 NCL CGAP_GC1 Homo sapiens cDNA clone IMAGE:787433 5' similar to SW:PR18_YEAST
7345	20425	33888	0.85	2.0E-11	BF582945.1	EST_HUMAN	PI5938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP18.1
8066	21148		0.69	2.0E-11	P37072	SWISSPROT	787c03.t1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:3442685 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10491	23526	37135	5.13	2.0E-11	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.09	2.0E-11	AW885874.1	EST_HUMAN	RG4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW885874.1	EST_HUMAN	RG4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.84	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:471784 3'
11375	24436	38095	1.84	2.0E-11	AA035369.1	EST_HUMAN	zk27g02.s1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:471784 3'
11408	24469	38133	1.4	2.0E-11	AA261956.1	EST_HUMAN	z018b04.t1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:685518 5'
12122	25102	38807	12.19	2.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	26105		1.85	2.0E-11	AA704195.1	EST_HUMAN	zk77g03.s1 Soares_fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12328	25237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RG4-OT0072-210100-011-c01 CN0027 Homo sapiens cDNA
12354	26258	32115	2.15	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12841	25431		1.43	2.0E-11	D26217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25542		3.62	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	25767		2.5	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
693	13878	28909	1.67	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
808	13886	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27464	2.81	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C076
1528	14881		1.82	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2095	16235	28356	0.94	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2185	15330	28455	3.59	1.0E-11	AF000873.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
2229	15363	28482	1.1	1.0E-11	AA30918.1	EST_HUMAN	EST180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3598	16762	29767	0.86	1.0E-11	BE004315.1	EST_HUMAN	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5447	18947	31625	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
5953	19139	32455	0.78	1.0E-11	BF222846.1	EST_HUMAN	7c57d01.t1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3
8396	21477	35004	2.65	1.0E-11	4985546	NT	MER10 repetitive element
8781	21880	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9246	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	y773d08.t1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28166 5'
							QV4-NN1149-250900-423-e03 NN1149 Homo sapiens cDNA

Page 228 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9248	22325	35871	1.49	1.0E-11	BF365118.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NNT149 Homo sapiens cDNA
10626	23660		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	1.0E-11	BF680078.1	EST_HUMAN	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
12603	26879		1.37	1.0E-11	Z30377.1	EST_HUMAN	HSAAAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3017	16193	29216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	6.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9639	22604		0.88	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-038-G12 BT0578 Homo sapiens cDNA
12408	26287		4.68	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4793	17918	30905	1.57	7.0E-12	Q06904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	423g01.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18	7.0E-12	D16473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.96	6.0E-12	AV730594.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW.F06 5'
4468	17608	30586	9.23	6.0E-12	AA732516.1	EST_HUMAN	nc88f11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
5336	18449	31418	5.12	6.0E-12	AH59161.1	EST_HUMAN	ij65g12.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2146438 3' similar to contains MER10.12 MER10 MER10 repetitive element;
9196	22274	35811	1.09	6.0E-12	AF003249.1	NT	Marone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9675	22637		1.81	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367883 similar to contains MER29.12 MER29 repetitive element;
13205	25786		1.25	6.0E-12	AW886846.1	EST_HUMAN	RC4-OT0072-050400-012-f11 OT0072 Homo sapiens cDNA
1068	14234	27293	2.37	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HF8DV33
3477	16644	28663	1.28	5.0E-12	BE047778.1	EST_HUMAN	tz42b05.y1 NCL_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2291217 5'
3821	16981	29084	7.44	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32666	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32667	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19760	33168	9.98	5.0E-12	AW974780.1	EST_HUMAN	EST366860 MAGC resequences; MAGN Homo sapiens cDNA
7176	20032	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615 s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615 s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21905	36038	1.28	5.0E-12	AA093745.1	EST_HUMAN	z07g12.s1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8867	21948		0.55	5.0E-12	AW887037.1	EST_HUMAN	RC1-OT0088-220300-011-507 OT0088 Homo sapiens cDNA
9195	22273		0.77	5.0E-12	AL076581.1	EST_HUMAN	DKFZp434J0426 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9308	22384	35636	2.52	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

Page 229 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9623	22878	36247	1.22	5.0E-12	P34882	SWISSPROT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21G103
10573	23608	37213	0.69	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
10793	23828	37449	0.6	5.0E-12	6878754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	26505	3.29	4.0E-12	AA700328.1	EST_HUMAN	274g1.1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
255	13474	26505	3.42	4.0E-12	AA700328.1	EST_HUMAN	274g1.1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4742	17877	30860	0.88	4.0E-12	AI688984.1	EST_HUMAN	h28h05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270748 3' similar to TR:Q13639 Q13639
7797	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	MARINER TRANSPOSASE. ;
8437	21519		4.81	4.0E-12	AF109907.1	NT	h221b03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2
11338	24401	38050	4.33	4.0E-12	AJ229043.1	NT	MER7 repetitive element ;
12684	25468		2.11	4.0E-12	U78027.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
631	13818	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
631	13818	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5276	18395	31363	0.78	3.0E-12	AL163288.2	NT	h213d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517 O14517 SMRP ;
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	h213d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808377 3' similar to TR:O14517 O14517 SMRP ;
8570	21651	35193	0.5	3.0E-12	O35453	SWISSPROT	Homo sapiens chromosome 21 segment HS21C068
10891	23975	37606	2.32	3.0E-12	U37672.1	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10891	23975	37607	2.32	3.0E-12	U37672.1	NT	SERINE PROTEASE HEPSEN
1685	14837	27921	1.24	2.0E-12	AW802131.1	EST_HUMAN	Human prostate specific antigen gene, 5' flanking region
3556	16721	29736	0.93	2.0E-12	6754485	NT	Human prostate specific antigen gene, 5' flanking region
4230	17377	30365	1.29	2.0E-12	J01894.1	NT	IL5-UM0071-120400-065-ac05 UM0071 Homo sapiens cDNA
4230	17377	30366	1.29	2.0E-12	J01894.1	NT	Mus musculus keratin-associated protein 6.2 (Krtap6.2), mRNA
4841	17679		2.03	2.0E-12	BE063509.1	EST_HUMAN	Rat U3A small nuclear RNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	Rat U3A small nuclear RNA
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	CM6-BT0281-031199-087-ac03 BT0281 Homo sapiens cDNA
6606	18766		2.08	2.0E-12	AW971857.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)
7326	20408	33870	3.85	2.0E-12	T08169.1	EST_HUMAN	TBX15 PROTEIN (T-BOX PROTEIN 15)

Page 230 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MRO-HT0559-200400-015-608 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF166864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10181	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.78	2.0E-12	AI334130.1	EST_HUMAN	q07702.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538
12129	25109	38813	1.53	2.0E-12	AW242934.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN ;
12133	25228		1.34	2.0E-12	AL163283.2	NT	hm27h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694965 3'
12516	25352		1.48	2.0E-12	11418248	NT	Homo sapiens chromosome 21 segment HS21C083
125	13354	26385	1.64	1.0E-12	AW627674.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
2044	15185		1.78	1.0E-12	AI871728.1	EST_HUMAN	hm51r07.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.03 L1
3138	16314	29328	1.04	1.0E-12	AF000991.1	NT	repetitive element ;
3138	16314	29327	1.04	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30138	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6088	19269		1.6	1.0E-12	U82828.1	NT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6188	19342		1.62	1.0E-12	Q9Y2G7	SWISSPROT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6282	19455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	HYPOPHOSPHATASE 1 (HPP1) gene, complete cds
6282	19455	32805	0.59	1.0E-12	BF642800.1	EST_HUMAN	EST000008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
							EST000008 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
6682	19821	33208	0.63	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds, and unknown gene
7285	20348	33800	2.53	1.0E-12	AF166864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							qf68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element ;
7300	20382	33940	10.78	1.0E-12	AI249533.1	EST_HUMAN	qf68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element ;
7300	20382	33841	10.78	1.0E-12	AI249533.1	EST_HUMAN	qf68a04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8686	21768	35298	0.59	1.0E-12	U6059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
8902	21981	35521	1.25	1.0E-12	AA782323.1	EST_HUMAN	ec26d05.s1 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
12215	25166	38835	2.32	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGE resequences, MAGE Homo sapiens cDNA
12437	25310		1.54	1.0E-12	AI739592.1	EST_HUMAN	w433108.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2392095 3'
12600	26068		1.93	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS210068
12788	26168		1.19	1.0E-12	P44838	SWISSPROT	PROBABLE TONB-DEPENDENT RECEPTOR H0712 PRECURSOR
12951	26661		2.82	1.0E-12	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4059	17212	30223	1.21	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
8901	22841		2.81	9.0E-13	N89653.1	EST_HUMAN	za28506.s1 Soares fetal liver opion 1NLS Homo sapiens cDNA clone IMAGE:293851 3'
735	13917	26957	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26956	5.03	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1885	16029	28136	2.73	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8303	21385	34907	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.63	8.0E-13	AI884398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437601 3'
10360	23385		2.82	8.0E-13	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
8429	21510		0.77	7.0E-13	Q95166	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	501463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868613 5'
12976	25635		1.63	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
2168	15303	28430	5.85	6.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS210007
5239	18361	31329	0.83	6.0E-13	AI267928.1	EST_HUMAN	qq44a09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1811352 3'
3399	15569		1.15	6.0E-13	R76336.1	EST_HUMAN	y82104.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145769 5'
3484	16662		1.56	5.0E-13	AA435773.1	EST_HUMAN	z177e12.s1 Soares testis NIH Homo sapiens cDNA clone IMAGE:728350 3' similar to containo Alu repetitive element contains element MER23 repetitive element;
7016	20152	33672	0.99	6.0E-13	P08983	SWISSPROT	GAP JUNCTION PROTEIN (CONNEXIN 30) (CX30)
11100	24173	37808	2.84	5.0E-13	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1918	15059		4.86	4.0E-13	AW378814.1	EST_HUMAN	FM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA

Page 232 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15556		1.61	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4869	18002		1.08	4.0E-13	AA454054.1	EST_HUMAN	z48607.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
5704	18897	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PN3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33698	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	z478g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
7898	20950		2.62	4.0E-13	N44291.1	EST_HUMAN	G452763 COR1 MRNA ;
9042	22121	35683	1.38	4.0E-13	AL043810.1	EST_HUMAN	y33g05.r1 Soares_melanocytes 2NbtHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
9702	22751	36821	0.47	4.0E-13	AA076907.1	EST_HUMAN	A32995 t complex sterility protein - mouse ;
10228	23262	36850	4.44	4.0E-13	AI289831.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	q32d05.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899845 3' similar to contains Alu repetitive element
184	13408		4.35	3.0E-13	AF003528.1	NT	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
888	14064		1.81	3.0E-13	AA430310.1	EST_HUMAN	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
1502	14855	27737	0.86	3.0E-13	AI904151.1	EST_HUMAN	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
2443	15571	28700	1.53	3.0E-13	AI271738.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2648	15673		2.28	3.0E-13	AL163210.2	NT	z478g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2729	15847	28957	3.69	3.0E-13	BF372862.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 2/2
3592	16756	29771	9.73	3.0E-13	P18616	SWISSPROT	Homo sapiens chromosome 21 segment HS21C010
3592	16756	29772	9.73	3.0E-13	P18616	SWISSPROT	GM3-F10100-140700-242-A08 FT0100 Homo sapiens cDNA
5657	18851	32133	0.68	3.0E-13	AA134017.1	EST_HUMAN	GM3-F10100-140700-242-A08 FT0100 Homo sapiens cDNA
5657	18851	32134	0.68	3.0E-13	AA134017.1	EST_HUMAN	z488h10.r1 Stragogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
6114	19204	32828	0.73	3.0E-13	AW005639.1	EST_HUMAN	z488h10.r1 Stragogene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR.12 THR repetitive element ;
							w288c02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
							O75139 KIAA0644 PROTEIN ;
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
8067	21149	34869	7.1	3.0E-13	U62111.2	NT	

Page 233 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8288	21350	34865	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST80487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
8288	21350	34865	0.5	3.0E-13	AA352487.1	EST_HUMAN	EST80487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Re- reactive factor
10401	23436	37043	0.58	3.0E-13	AW855487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10916	23998		3.1	3.0E-13	AJ064768.1	EST_HUMAN	HAQ636 Human fetal liver cDNA library Homo sapiens cDNA
11301	24967	38008	3.41	3.0E-13	BE063509.1	EST_HUMAN	CM0-BT0281-031199-087-403 BT0281 Homo sapiens cDNA
11898	24886	38585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
134	13379	28411	3.52	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1289	14455	27521	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16243	28266	0.81	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16246	29287	0.81	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3596	16760	29776	1.88	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	19424	32770	4.34	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		0.58	2.0E-13	X78417.1	NT	S. scrofa rps12 mRNA for ribosomal protein S12
6854	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7189	20084	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
7189	20084	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
10875	23709	37317	2.41	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12388	23274		22.49	2.0E-13	AW882155.1	EST_HUMAN	CM0-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
302	13519	26551	1.34	1.0E-13	S74128.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1367	14521	27596	1.4	1.0E-13	X87344.1	NT	H. sapiens DMA, DME, HLA-Z1, IPP2, LMP2, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes
2079	15219	28339	2.81	1.0E-13	AA720574.1	EST_HUMAN	rw21 g02, s1 NCL CGAP_G060 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element;
4715	17850	30833	1.32	1.0E-13	BF340887.1	EST_HUMAN	602038009F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4165888 5'

Page 234 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8094	21176	34691	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element ;
8094	21176	34692	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24c01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element/contains element MER24 repetitive element ;
10295	23330		1.04	1.0E-13	O13481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (IMAGE-B4 ANTIGEN)
10508	23543	37154	0.8	1.0E-13	AF300701.1	NT	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11661	24740	38431	0.74	1.0E-13	BF108755.1	EST_HUMAN	746910.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
12206	25160		1.38	1.0E-13	AV716377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DOBAIE03 5'
12920	25605		3.46	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13077	25708		1.85	1.0E-13	X87578.1	NT	H.sapiens CD4 gene
343	13554	26583	3.76	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
2569	15694		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2811	15925	29036	7.9	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	29360	7.5	9.0E-14	AW513286.1	EST_HUMAN	xc64h05.x1 NCI_CGAP_UHT Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element ;
3898	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	16010	30994	2.23	9.0E-14	AJ002153.1	NT	Saguinus oedipus gene for seminal vesicle secreted protein semenogelin I
3587	16751		1.17	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4068	17222		3.64	8.0E-14	R76269.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
9647	21090	34605	38.93	8.0E-14	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
9760	22698	36266	3.22	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629970 3'
11717	24757		1.79	8.0E-14	BE062568.1	EST_HUMAN	QV2-BT0258-267099-014-e01 BT0258 Homo sapiens cDNA
12611	25410	32048	2.43	8.0E-14	AI688118.1	EST_HUMAN	wo92h08.x1 NCI_CGAP_Cc3 Homo sapiens cDNA clone IMAGE:2326743 3'
1668	16044		4.76	7.0E-14	AW151673.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9120	22189		0.73	7.0E-14	AL163285.2	NT	MER10 repetitive element ;
378	13586	26620	12.43	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10027	23066	36682	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10027	23065	36683	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
633	13818	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5166	18288	31254	1.32	6.0E-14	AW073791.1	EST_HUMAN	X03065.x1 NCL_CGAP_GU11 Homo sapiens cDNA clone IMAGE:2676186 3' similar to contains L1.12 L1 repetitive element;
5650	18844	32125	5.28	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	18030		1.81	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1926	15069	28174	10.15	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	AA046502.1	EST_HUMAN	Z037a06.11 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487658 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	Y073c12.81 Soares_multiple_sclerosis_2NbHMSF Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
8145	21227		0.71	4.0E-14	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12043	25024	38720	5.5	4.0E-14	BE242468.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470
12966	26203		5.69	4.0E-14	AJ86224.1	EST_HUMAN	W08003.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element
972	14145	27204	1.66	3.0E-14	X85496.1	NT	R.norvegicus mRNA for GRC2 protein
6873	20025	33434	0.93	3.0E-14	A1420786.1	EST_HUMAN	t691c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
6873	20025	33435	0.93	3.0E-14	A1420786.1	EST_HUMAN	t691c12.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
7173	20308	33749	0.6	3.0E-14	AA388311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
8987	22066	35606	0.86	3.0E-14	N42185.1	EST_HUMAN	Y07b10.11 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:270523 5' repetitive element;contains element MER9 repetitive element;
11612	18495	31533	5.87	3.0E-14	AW265354.1	EST_HUMAN	Xp45f12.x1 NCL_CGAP_JN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element;contains element MER9 repetitive element;
12894	26041		1.88	3.0E-14	AL162852.2	NT	Homo sapiens chromosome 21 segment HS21C086
13212	26684	31863	1.61	3.0E-14	BE891650.1	EST_HUMAN	G01435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920169 5'
401	13598	26634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
708	16019	26925	11.36	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2461	15588		1.04	2.0E-14	AW372898.1	EST_HUMAN	RC5-BT0377-091299-031-D12 3T0377 Homo sapiens cDNA
2535	15660		0.99	2.0E-14	7657528	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
2583	15718	28835	1.63	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31912	0.97	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	AI312351.1	EST_HUMAN	ta78n01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.t3 L1 repetitive element;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20159		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-408 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.46	2.0E-14	BE168761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.46	2.0E-14	BE168761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36758	0.56	2.0E-14	AI978795.1	EST_HUMAN	wf58g10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23664	37273	0.51	2.0E-14	AV741848.1	EST_HUMAN	AV741848 CB Homo sapiens cDNA clone CBFBBF04 5'
11019	24098	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	U1-H-B11-edw-a-10-0-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15860		1.26	2.0E-14	7657528	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1092	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1438	14591	27684	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27685	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	16198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	6.44	1.0E-14	AF001889.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16188	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30155	1.69	1.0E-14	AA682984.1	EST_HUMAN	ae89c12.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17733	30713	2.01	1.0E-14	AW276862.1	EST_HUMAN	xp39h10.x1 NCI_CGAP_Luz28 Homo sapiens cDNA clone IMAGE:2753059 3'
							Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5930	19116	32429	1.98	1.0E-14	AF126145.1	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6813	25834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6813	25834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
1607	14760	27839	1.81	9.0E-15	7427622	NT	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	16376		1.38	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM6 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel.
7665	20732	34207	4.24	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P16, P12, P30, P10]
8206	21288	34810	1.24	9.0E-15	BE903569.1	EST_HUMAN	60187750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960156 5'
13066	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
7331	20412	33874	1.13	7.0E-15	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
10650	23684		2.34	7.0E-15	AW241896.1	EST_HUMAN	xt77402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR.12 THR repetitive element;
12270	25203		1.44	7.0E-15	AA284485.1	EST_HUMAN	zs57408.11 NCI_CGAP_OCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gb.L21834 STEROL O-ACYL TRANSFERASE (HUMAN); contains L1, L1, repetitive element;
1018	14189	27250	7.51	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5263	18382		0.98	6.0E-15	AW901266.1	EST_HUMAN	CM4-NN1011-T00300-110-410 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
11583	28231		1.54	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-160200-070-c10 LT0036 Homo sapiens cDNA
423	13618	26658	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2818	15933	29044	1.76	5.0E-15	U91326.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
440	13240	26240	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	19959	33359	0.9	4.0E-15	AB007670.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11316	21065	34677	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11316	21065	34676	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17478		7.67	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANFCARDIODILATIN
5141	18264	31232	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.67	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.11	3.0E-15	Q84825	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33976	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20507	33976	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds

Page 238 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10129	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	cc36807.s1 NCJ_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element ;
11033	24112	37748	8.11	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12620	26081		65.8	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
260	13479	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13987	26621	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13987	26622	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1559	14712		0.99	2.0E-15	8823201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17980		2.76	2.0E-15	A1806335.1	EST_HUMAN	wf0706.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR.Q61043 Q61043 NINEIN. ;
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	G01344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	G01344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7263	20946		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20498	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	z77903.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3' WP:F44F4.8 CE02227 TRANSPOSASE ;
7554	20526	34102	5.05	2.0E-15	W05064.1	EST_HUMAN	z77903.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3' WP:F44F4.8 CE02227 TRANSPOSASE ;
9107	22186	35730	2.88	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9273	22949	35899	0.91	2.0E-15	AA397758.1	EST_HUMAN	z77908.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9273	22949	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	z77908.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9804	22659	36231	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201095-079-a12 HT0244 Homo sapiens cDNA
9804	22659	36232	1.18	2.0E-15	AW379465.1	EST_HUMAN	CM0-HT0244-201095-079-a12 HT0244 Homo sapiens cDNA
11077	24162		3.69	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Page 239 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13016	18763	28779	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exon 7-49, and partial cds, alternatively spliced
2834	15948		3.09	1.0E-15	AI689984.1	EST_HUMAN	h28h05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539
3077	16253	29275	1.42	1.0E-15	BE043584.1	EST_HUMAN	MARINER TRANSPOSASE ;
3211	16385	29398	1.18	1.0E-15	P08547	SWISSPROT	h44b02.y1 NCL CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2989162 5'
4479	17819	30601	0.61	1.0E-15	BE182698.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6502	18668	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	RC3-H10649-100500-022-b05 HT0849 Homo sapiens cDNA
7149	20284		1.98	1.0E-15	BE074217.1	EST_HUMAN	ye40e10.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER6 repetitive element ;
7184	20049	33480	0.78	1.0E-15	P39057	EST_HUMAN	QV3-BT0569-270100-074-g03 BT0569 Homo sapiens cDNA
8427	21508	35040	0.99	1.0E-15	AL163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8616	21696	35232	4.84	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35233	4.94	1.0E-15	AI200976.1	EST_HUMAN	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9239	22316	35858	0.78	1.0E-15	AL163207.2	NT	q68h06.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9242	22319	35862	0.98	1.0E-15		NT	Homo sapiens chromosome 21 segment HS21C007
9448	22564	38127	0.89	1.0E-15	Q39575	SWISSPROT	Homo sapiens spermidine synthase (SRM) mRNA
9832	22872	38465	0.94	1.0E-15	AA864653.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
11057	24134	37770	3.04	1.0E-15	AF044083.1	NT	ch37c03.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459872 3' similar to contains L1.13 L1 repetitive element ;
13104	25892	31856	13.05	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4628	17782	30744	0.93	9.0E-16	4503188	NT	t31c05.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216912 3' similar to contains Alu repetitive element ;
11241	24310	37947	1.41	9.0E-16	F08688.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
11985	24980	38685	1.48	9.0E-16	AI244341.1	EST_HUMAN	HSC2F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11985	24980	38685	1.48	9.0E-16	AI244341.1	EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11985	24980	38685	1.48	9.0E-16	AI244341.1	EST_HUMAN	MER10 repetitive element ;
5819	19009	32315	0.85	7.0E-16		EST_HUMAN	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
7498	20571	34043	1.3	7.0E-16	O88807	SWISSPROT	MER10 repetitive element ;
7498	20571	34044	1.3	7.0E-16	O88807	SWISSPROT	q76a02.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
13043	25995		38.08	7.0E-16	T94149.1	EST_HUMAN	MER10 repetitive element ;
							Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							ye28c12.r1 Stragene lung (R837210) Homo sapiens cDNA clone IMAGE:118082 5'

Page 240 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2208	15342		9.12	6.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1522	14876	27757	0.86	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
2745	15862	28973	2.21	5.0E-16	AA992178.1	EST_HUMAN	cd90c04.s1 Soares fetal_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
11809	24799	38498	2.68	5.0E-16	BF217368.1	EST_HUMAN	contains element L1 repetitive element;
13152	25749		14.16	5.0E-16	11418127	NT	60188573AF1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2463	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2463	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3546	16711	29722	5.29	4.0E-16	Q16853	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30391	8.68	4.0E-16	BE083975.1	EST_HUMAN	PM4-BT0650-010400-002-g03 BT0650 Homo sapiens cDNA
4260	17405	30392	8.68	4.0E-16	BE083975.1	EST_HUMAN	PM4-BT0650-010400-002-g03 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	36114	0.72	4.0E-16	11423191	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12393	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.68	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12682	25277	32078	3.23	4.0E-16	6912469	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12682	25494		1.33	4.0E-16	R18591.1	EST_HUMAN	y98b11.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	d445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
135	13361	26398	1.09	3.0E-16	AW022862.1	EST_HUMAN	d445c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13673		1.58	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
486	13682		2.33	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14636	27720	2.73	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
3041	16217	29237	4.71	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
4711	17846	30830	0.59	3.0E-16	AW160828.1	EST_HUMAN	aw78b06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to
5057	18195	31160	1.32	3.0E-16	AV661383.1	EST_HUMAN	SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
5392	18594		0.98	3.0E-16	AA077225.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLOCSA01 3'
5734	18927	32223	1.67	3.0E-16	AF003529.1	NT	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
8858	21837	35473	4.25	3.0E-16	AI002836.1	EST_HUMAN	Homo sapiens glycoprotein 3 (GPC3) gene, partial cds and flanking repeat regions am38405.a1 Striatagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR, b2 THR repetitive element;

Page 241 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	BF600617.1	EST_HUMAN	602246538F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23369	36969	2.69	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	26171	31557	3.62	3.0E-16	AL043268.2	EST_HUMAN	DKFZp434L1623.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L1623 5'
904	14168		1.03	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS210079
2459	15586		0.98	2.0E-16	AA621761.1	EST_HUMAN	af06ad04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030885 3'
2763	15870		1.14	2.0E-16	J03081.1	NT	Human SSV4-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	A1208733.1	EST_HUMAN	gq56103.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER29.13
6299	18416	31385	0.64	2.0E-16	BE081178.1	EST_HUMAN	MER29 repetitive element;
6880	20032	33442	0.68	2.0E-16	Q31125	SWISSPROT	RC3-BT0046-131199-003-H12 BT0046 Homo sapiens cDNA
7893	20945	34451	0.96	2.0E-16	A1470723.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
							g16e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
8154	21236	34757	1.87	2.0E-16	A1732837.1	EST_HUMAN	nz47106.x5 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:054849 084849
8352	21433	34957	0.81	2.0E-16	BE658026.1	EST_HUMAN	HYPOTHETICAL 42.8 KD PROTEIN, [2] TR:008905; contains MER711 MER7 repetitive element;
8352	21433	34958	0.81	2.0E-16	BE658026.1	EST_HUMAN	782h09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303621 3'
8724	21804	35340	0.76	2.0E-16	AW877214.1	EST_HUMAN	782h09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303621 3'
8724	21804	35341	0.76	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	AF200718.1	NT	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
393	13630		22.69	1.0E-16	AA628592.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
2028	15169	28276	3.42	1.0E-16	BF327942.1	EST_HUMAN	er39g11.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1034084 3' similar to
6839	19029	32335	0.6	1.0E-16	AF163884.1	NT	contains ORF 12 ORF repetitive element;
6565	19727		18	1.0E-16	U45983.1	NT	QV0-BN0148-070700-293-at10 BN0148 Homo sapiens cDNA
8704	19882	33252	2.96	1.0E-16	Q02779	SWISSPROT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7728	19727		5.39	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9483	22540	36103	0.81	1.0E-16	AW875851.1	EST_HUMAN	QV2-PT0012-040400-124-605 PT0012 Homo sapiens cDNA
3832	18992	29994	2.08	9.0E-17	AW800048.1	EST_HUMAN	GM1-NN1003-200300-153-e01 NN1003 Homo sapiens cDNA
6864	20016		2.15	9.0E-17	A1392964.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_C11.1 Homo sapiens cDNA clone IMAGE:2109824 3' similar to contains MER28.12
							MER28 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8299	21381		3.56	9.0E-17	AW150257.1	EST_HUMAN	xq49g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element:
10428	23464		2.35	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1043	14209		2.43	8.0E-17	AW860701.1	EST_HUMAN	QV6-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
3998	17155		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C980
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
7425	20502		1.73	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1487	14640		2.58	7.0E-17	8753097	NT	Mus musculus adiponectin B editing complex 2 (Apobec2), mRNA
5438	18638		3.11	7.0E-17	AF216850.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6826	19979	33987	7.91	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
208	13431	26463	5.62	6.0E-17	AW963880.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
6443	19610	32973	2.06	6.0E-17	AW662772.1	EST_HUMAN	H81-d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878595 3' similar to contains L1.12 L1 repetitive element:
10499	23634	37144	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
434	13234	26234	2.37	6.0E-17	T64110.1	EST_HUMAN	y605h08.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79839 5'
7759	20818	34308	1.81	5.0E-17	T81043.1	EST_HUMAN	y428b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9582	22704	38270	1.32	4.0E-17	AW129165.1	EST_HUMAN	x220e04.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element:contains MER19.b1 MER19 repetitive element:
11783	24773	38469	2.51	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12308	25226		1.82	4.0E-17	AI073546.1	EST_HUMAN	ov45604.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR.Q16530
2165	16300	28428	1.85	3.0E-17	AW119123.1	EST_HUMAN	Q16530 PMS3 MRNA ; contains MER10.12 MER10 repetitive element:
3263	16437		1.17	3.0E-17	P35410	SWISSPROT	x489c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3732	16853	29897	1.91	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	16853	29898	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8463	21544	36074	1.12	3.0E-17	N68451.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
9903	22843	36528	5.19	3.0E-17	AB026898.1	NT	z814602.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.13 P TR5 repetitive element:
10591	23626	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10591	23626	37235	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12268	25201		4.2	3.0E-17	11417968	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA

Page 243 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	EST_HUMAN	AV720204 GLC Homo sapiens cDNA clone GLC01F08 5'
363	13574	26803	2.65	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element
364	13574	26805	2.78	2.0E-17	A1270080.1	EST_HUMAN	q163a06.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA722832.1	EST_HUMAN	z981d04.s1 Scarses_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:368751 3'
2518	15844	28765	2.59	2.0E-17	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
2518	15844	28766	2.59	2.0E-17	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
2996	16172	29191	6.96	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	18681	31698	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
5482	18681	31697	1.75	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19553		1.92	2.0E-17	AF059068.1	NT	Homo sapiens MHC class 1 region
6819	19779		1.39	2.0E-17	AL134881.1	EST_HUMAN	DKFZp762J0610.J1 762 (synonym: Imel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8006	21056	34568	0.89	2.0E-17	AB037839.1	NT	Homo sapiens mRNA for KIAA1418 protein, partial cds
8275	21357	34876	1.24	2.0E-17	Q86156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to similar to glycogenin
10073	23111	36715	2.71	2.0E-17	BE298888.1	EST_HUMAN	600944630.Ft NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860615 5'
10108	23148	36744	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10108	23148	36745	3.53	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10468	23501	37114	5.02	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10590	23625	37232	0.87	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625	37233	0.97	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.83	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23652	37262	0.93	2.0E-17	A1798902.1	EST_HUMAN	we94b04.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	13850	26998	2.79	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1746	14894		2.01	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
1807	14958	28050	4.83	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15319	28445	2.05	1.0E-17	P02481	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15542	28689	3.16	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3657	16820		1.03	1.0E-17	AF224698.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4256	17401		9.42	1.0E-17	R05942.1	EST_HUMAN	y30a07.r1 Scarses fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'

Page 244 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6791	19946	33344	1.62	1.0E-17	A185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6791	19946	33346	1.62	1.0E-17	A185642.1	EST_HUMAN	q65505.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33766	1.33	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE082744.1	EST_HUMAN	QV0-BT0263-101289-072-407 BT0283 Homo sapiens cDNA
10210	23246	36836	1.04	1.0E-17	AW99538.1	EST_HUMAN	QV3-BN0046-220300-128-c10 BN0046 Homo sapiens cDNA
11703	24700	38383	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
9698	22747	34146	3.05	9.0E-18	A1472167.1	EST_HUMAN	q85403.x1 Soares_NSF_F8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:2148389 3'
3886	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26599	16.47	7.0E-18	AW316976.1	EST_HUMAN	xx10504.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7601	20671	34146	1.09	7.0E-18	AW887642.1	EST_HUMAN	xx10504.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
12826	13570	26599	10.65	7.0E-18	AW316976.1	EST_HUMAN	RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA
12826	13570	26600	10.65	7.0E-18	AW316976.1	EST_HUMAN	xx10504.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
3367	16539	29552	1.23	6.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn/Pr-1 gene for glia-derived neurotrophic factor, enhancer region
4868	18001		3.99	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE)
8444	21525		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8543	21624	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	A1608256.1	EST_HUMAN	RC-BT168-020469-014 BT166 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	A1608256.1	EST_HUMAN	RC-BT166-020469-014 BT166 Homo sapiens cDNA
11399	24460	38124	3.63	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24664	38351	1.69	6.0E-18	X67344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
12634	25364	32068	3.91	6.0E-18	U87929.1	NT	Human acylate hydratase (ACO2) gene, exon 4
1171	14394	27390	12.48	5.0E-18	AI280214.1	EST_HUMAN	q65511.x1 Soares_placenta_86weeks_2NBHP8169W Homo sapiens cDNA clone IMAGE:1883668 3' similar to contains Alu repetitive element
4433	17573	30553	0.59	5.0E-18	10946865	NT	Mus musculus galectin (Gsdm), mRNA
5387	18569	31561	1.29	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8917	21996	35635	3.47	5.0E-18	BE143312.1	EST_HUMAN	MRO-HT0161-221039-002-c06 HT0161 Homo sapiens cDNA

Page 245 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24292	37932	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24292	37933	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12875	25450		6.29	5.0E-18	AW587182.1	EST_HUMAN	MR1-SN0035-060-000-001-g11 SN0035 Homo sapiens cDNA
13063	26698		28.98	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGGA02 3'
127	13355	26386	0.91	4.0E-18	BE044076.1	EST_HUMAN	h038h04.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	h038h04.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1754	14903	27998	52.62	4.0E-18	AA621814.1	EST_HUMAN	h024f11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144848 3' similar to gb:M28328
1838	15081		1.05	4.0E-18	AI738592.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
2274	15407	28538	1.26	4.0E-18	Q06430	SWISSPROT	h033h08.x1 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2392095 3'
2274	15407	28537	1.26	4.0E-18	Q06430	SWISSPROT	N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
3892	17051	30060	0.61	4.0E-18	AI581596.1	EST_HUMAN	N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
5479	18878	31691	2.47	4.0E-18	AI017565.1	EST_HUMAN	ar93b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element
5479	18878	31692	2.47	4.0E-18	AI017565.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
8029	21112		0.52	4.0E-18	AA746811.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
11264	24323	37964	7.69	4.0E-18	AA371807.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
872	14048	27114	3.81	3.0E-18	AA814166.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
953	14126	27187	2.25	3.0E-18	BE088634.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
4080	17216	30226	1.06	3.0E-18	AL163247.2	NT	repetitive element
6988	20186	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	repetitive element
11767	24238	37689	1.99	3.0E-18	BF218650.1	EST_HUMAN	EST83683 Pituitary gland, subcloned (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
12832	25554		4.56	3.0E-18	AW022015.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
291	13460	28612	4.2	2.0E-18	AW836820.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
1176	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
3193	18988	28374	0.94	2.0E-18	Q39576	SWISSPROT	ou23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'

Page 246 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA868610.1	EST_HUMAN	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408652 3' similar to TR:O14577
5623	18817	31896	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;
5623	18817	31897	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5999	18184		1.64	2.0E-18	BF347229.1	EST_HUMAN	602021164F1 NCL CGAP_Brm07 Homo sapiens cDNA clone IMAGE:4196670 5'
6284	18467	32820	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6284	18467	32821	0.91	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	18577	32838	0.9	2.0E-18	BF352940.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
8448	18915	32979	2.93	2.0E-18	AW665853.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978984 3' similar to contains
7594	20665	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	MER19.12 MER19 repetitive element;
8341	21422	34947	0.6	2.0E-18	BE439524.1	EST_HUMAN	ae89d1.1.r1 Stratiagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838485 5' similar to
10253	23288	36884	0.95	2.0E-18	AW151673.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
10253	23288	36885	0.95	2.0E-18	AW151673.1	EST_HUMAN	x67e10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
11217	24286	37925	2.91	2.0E-18	AW470791.1	EST_HUMAN	MER10 repetitive element;
12031	25014	38716	4.46	2.0E-18	AW151289.1	EST_HUMAN	x67e10.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
12465	14339		12.67	2.0E-18	BE256097.1	EST_HUMAN	h63306.x1 NCL CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
4837	17876		0.76	1.0E-18	T85406.1	EST_HUMAN	THR repetitive element;
5471	18671	31651	2.64	1.0E-18	AV653405.1	EST_HUMAN	xg47e09.x1 NCL CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	MER8 repetitive element;
5688	18882	32175	3.08	1.0E-18	D00099.1	NT	601114332F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3355044 5'
6584	19746	33128	1.31	1.0E-18	AL163280.2	NT	yed3g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1205336 5' similar to contains
8637	21717	35254	1.05	1.0E-18	AI148288.1	EST_HUMAN	L1 repetitive element;
10103	23141	38740	4.93	1.0E-18	U91328.1	NT	AV653405 GLC Homo sapiens cDNA clone GLCDE11 3'
12416	25294	32084	4.65	1.0E-18	AF003529.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens chromosome 21 segment HS21C080
							cc69d09.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680393 3' similar to contains L1.H L1 repetitive element;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13762	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	z11d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
560	13762	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	z11d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
8032	21115		3.69	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8886	21965	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21966	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24463	38118	3.16	9.0E-19	AB032869.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13762	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	z11d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
1073	14239		1.88	8.0E-19	AW874902.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158936.1	EST_HUMAN	MRO-HT0404-210200-001-g08 HT0404 Homo sapiens cDNA
2319	16461	26583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kd) [DDX6] mRNA
6686	19747	33129	2.11	7.0E-19	AF092090.1	NT	Rattus norvegicus opt51 mRNA, partial cds
7452	20528	34002	0.94	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.84	7.0E-19	A1344951.1	EST_HUMAN	1b01c08.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2092302 3'
12318	26183		1.72	7.0E-19	AA705684.1	EST_HUMAN	z180501.s1 Soares fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3878	17038		1.18	6.0E-19	AW852830.1	EST_HUMAN	PMO-CT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4685	17722	30705	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5978	19163	32483	6.17	6.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6346	19516	32873	0.89	5.0E-19	AW693302.1	EST_HUMAN	hh77608.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868787 5'
10639	23673	37263	1.18	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11829	24818	38509	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element MSR1 repetitive element:
							Human gamma T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S6A3N2T, TCRBV13S6A2T, TCRBV6S8P, TCRBV6S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV6S2, TCRBV6S6A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV6S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
13083	25895		1.34	5.0E-19	U68060.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
568	13760	26784	0.96	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15864	26975	1.15	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

Page 248 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224688.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17543	30528	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)
4400	17543	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 8 (TRIPLE LIM DOMAIN PROTEIN 8)
4569	17707	30686	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18596		0.89	3.0E-19	AF223487.1	NT	Homo sapiens NP0008 protein (NP0008) mRNA, complete cds
7543	20615		1.88	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9658	21101	34614	1.09	3.0E-19	X89685.1	NT	M.musculus mRNA for TPCR33 protein
12563	25385		16.36	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2627	15750	28865	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 cognate HS21C001
4568	17706		1.34	2.0E-19	AI311783.1	EST_HUMAN	q691e02X1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386 POL/ENV GENE:
6179	18355	32703	0.91	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63	2.0E-19	7657286	NT	Mus musculus karatin-associated protein 9-1 (Krtap9-1), mRNA
8525	21606	39149	10.24	2.0E-19	AA012854.1	EST_HUMAN	z63409.r1 Soares relina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	56753	0.64	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13689		1.86	1.0E-19	BE408611.1	EST_HUMAN	601304125F-1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:368310 5'
2233	15357	28496	1.94	1.0E-19	H30795.1	EST_HUMAN	yp78p07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2782	18898		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	15087		6.72	1.0E-19	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16655	29669	1.18	1.0E-19	AA834987.1	EST_HUMAN	q449b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:193631 3' similar to contains MER37.12
6452	18652	31631	0.73	1.0E-19	AI890866.1	EST_HUMAN	wm91b08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16530 Q16530 PMS3 mRNA:
6169	19374	32725	2.6	1.0E-19	U12196.1	NT	Oryzias latipes sodiumdicarboxylate cotransporter mRNA, partial cds
6337	26213		0.63	1.0E-19	AA595527.1	EST_HUMAN	nm22403.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:963083 similar to contains L1.1 L1 repetitive element;
7806	20862	34355	1.05	1.0E-19	U08813.1	NT	Oryzias latipes Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20862	34356	1.05	1.0E-19	U08813.1	NT	Oryzias latipes Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

Page 248 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8844	21724	35261	1.94	1.0E-19	M64657.1	NT	Rabbit phosphatase kinase beta subunit mRNA, complete cds
8939	22018		2.72	1.0E-19	T98920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains ORF repetitive element;
8950	22989		0.69	1.0E-16	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23425	37032	25.12	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191086-031-005 S10174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-18	N44631.1	EST_HUMAN	Y931e08.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37888	1.87	1.0E-19	BE616026.1	EST_HUMAN	601270882F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611483 5'
6784	19939	33336	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
6784	19939	33337	2.4	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
7687	20752	34234	1.48	8.0E-20	A1221371.1	EST_HUMAN	qg88109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34235	1.48	8.0E-20	A1221371.1	EST_HUMAN	qg88109.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	16521	29537	0.71	7.0E-20	BF328455.1	EST_HUMAN	PNM4-AN00096-050900-003-004 AN00096 Homo sapiens cDNA
7134	18560	31474	5.68	7.0E-20	AL138120.1	EST_HUMAN	DKFZ5547D092_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZ5547D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	n146c04.s1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
12014	24968		2.89	7.0E-20	6912633	NT	MER29 repetitive element;
3645	16808	26822	3.64	6.0E-20	P39186	SWISSPROT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
4367	17530	30511	4.58	6.0E-20	BE622434.1	EST_HUMAN	ALL SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
7264	20347	33789	1.42	5.0E-20	AF075301.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBA01 5'
8131	21213	34733	6.96	5.0E-20	W90525.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
8131	21213	34734	6.96	5.0E-20	W90525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
8295	21377	34898	0.79	5.0E-20	BE165980.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1N1FLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element;
9035	22114	35657	1.28	5.0E-20	AB028174.1	NT	MIR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9035	22114	35658	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9944	21087		1.13	5.0E-20	O60609	SWISSPROT	Mus musculus MMAN-g mRNA, complete cds
1849	14802	27889	0.94	4.0E-20	AL163247.2	NT	HYPOTHETICAL PROTEIN DJ845024.1
5765	18957		1.13	4.0E-20	Q69880	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
8110	21192		5.61	4.0E-20	AI874352.1	EST_HUMAN	HISTONE H2B C (H2B/C)
10717	23750	37357	1.13	4.0E-20	AW897469.1	EST_HUMAN	ts84g03.x1 NCL_CGAP_Ox35 Homo sapiens cDNA clone IMAGE:2283398 3'
							QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17488	30455	1.28	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4747	17862	30894	1.08	3.0E-20	AA037618.1	EST_HUMAN	2k38b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
9135	22214		2.69	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10627	23562	37198	0.47	3.0E-20	BF185294.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12331	25239	32109	6.09	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S5 ;
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	ng98h09.s1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
2878	14030		5.32	2.0E-20	AW303868.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ;
5061	18189	31163	5.15	2.0E-20	Q28983	SWISSPROT	ng98h09.s1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN ;
5256	18376		0.9	2.0E-20	6174538	NT	xr24e10.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2781098 3' similar to SW:RS5_MOUSE
8309	21391	34915	0.87	2.0E-20	AA308467.1	EST_HUMAN	ZONADHESIN PRECURSOR
9391	22466	36030	2.65	2.0E-20	D10083.1	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9391	22466	36031	2.65	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
12743	28878	31852	2.17	2.0E-20	H55371.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
2070	15995	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
4560	17698	30879	1.02	1.0E-20	BF115158.1	EST_HUMAN	CHFR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_381 5'
7034	20170	33592	0.74	1.0E-20	AF049507.1	EST_HUMAN	z111008.11 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
9364	22439	35998	2.08	1.0E-20	11418491	NT	MER19 repetitive element ;
11847	24836	38530	2.03	1.0E-20	AF223391.1	NT	h184b06.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element ;
12461	25323		2.81	1.0E-20	AA420453.1	EST_HUMAN	AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
							Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							ne60g08.11 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1 repetitive element ;

Page 251 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2578	16155		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-8J21
12174	25135		3.98	9.0E-21	AW898189.1	EST_HUMAN	RC3-NN0068-09050-021-503 NN0068 Homo sapiens cDNA
6011	22090		0.98	8.0E-21	AW874891.1	EST_HUMAN	b330a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11830	24819	38510	3.91	8.0E-21	AA808411.1	EST_HUMAN	O95168 NADH-UBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
12345	25250		3.8	8.0E-21	O21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 8)
2130	16266	28385	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2130	16266	28386	3.85	7.0E-21	P15800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	16933	29958	1.38	7.0E-21	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4369	17612		6.28	7.0E-21	AA046502.1	EST_HUMAN	2k67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
5564	19726	33104	0.94	7.0E-21	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8582	21653	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-8
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10319	23354	36963	1.07	7.0E-21	AW856922.1	EST_HUMAN	RCO-CT0301-271169-031-F03 CT0301 Homo sapiens cDNA
10634	24016	37648		7.0E-21	AA723404.1	EST_HUMAN	zp73d03.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:396981 3' similar to
4220	17369	30358	0.75	6.0E-21	BE408611.1	EST_HUMAN	gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR 13 OFR
9336	22412		1.39	6.0E-21	BE192737.1	EST_HUMAN	repetitive element ;
947	14120	27181	1.34	5.0E-21	5802031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
2364	15485	28617					on23d03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541808 3' similar to TR:002711
4493	17623	30804	1.23	5.0E-21	AA928194.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4809	14120	27181	1.16	5.0E-21	5802031	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4923	18053	31039	8.33	5.0E-21	4885474	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
6902	20217		0.77	5.0E-21	AW40864.1	EST_HUMAN	Homo sapiens melanoma antigen, family G, 1 (MAGEC1), mRNA
7137	20291	33734					7d05e10.x1 NCI_CGAP_C181 Homo sapiens cDNA clone IMAGE:2818154 3'
10801	23834	37457	1	5.0E-21	BE856505.1	EST_HUMAN	OFR repetitive element ;
10801	23834	37458	0.54	5.0E-21	O81690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
12259	25186		1.28	5.0E-21	O91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
1772	14921	28015	1.86	4.0E-21	AA970713.1	EST_HUMAN	cc08e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:727878 5'
							PM53 MRNA ;contains OFR.11 OFR repetitive element ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7011	20147	33588	2.61	4.0E-21	AB019578.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
9983	23022	36614	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10010	23048	36642	0.51	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1894	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	zq15d06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15479	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3148	16324	28335	6.41	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5616	18810	31879	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3)-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5866	19046		0.9	3.0E-21	AV681044.1	EST_HUMAN	AV681044 GLC Homo sapiens cDNA clone GLCGOAT0 3'
6308	19480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844469F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
7215	20080	33493	7.52	3.0E-21	BF361083.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9894	22834	36518	0.92	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-h08 NN0063 Homo sapiens cDNA
12879	28099	31665	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13375		24.5	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-080-g12 HT0458 Homo sapiens cDNA
958	14131	27189	0.51	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27180	0.61	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141109-011-h08 BT0311 Homo sapiens cDNA
2703	15821	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15821	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18796	31846	1.66	2.0E-21	A1624582.1	EST_HUMAN	ts30f03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q98854 Q98854
5604	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN;
5694	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
6157	19333	32678	0.74	2.0E-21	W44493.1	EST_HUMAN	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8467	21548	35078	0.58	2.0E-21	AJ010770.1	NT	z897a12.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8568	21639	35178	8.13	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hyperion gene, exons 1-50
9023	22102	35842	3.27	2.0E-21	AU196779.1	EST_HUMAN	QV0-HT0103-091109-060-g11 HT0103 Homo sapiens cDNA
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	AU138779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11599	24652	38335	2.88	2.0E-21	BE973829.1	EST_HUMAN	H09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MIER28 b3
							MER29 repetitive element;
							601880369F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

Page 253 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11599	24652	38336	2.88	2.0E-21	BE973829.1	EST_HUMAN	601880636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	25339		6.44	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1284	14440	27609	1.89	1.0E-21	AA557657.1	EST_HUMAN	h46c04.s1 NCL_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1434	14687		4.93	1.0E-21	AI601284.1	EST_HUMAN	at88d12.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
6616	19776		2.73	1.0E-21	AL078752.1	EST_HUMAN	DKFZp43410830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43410830 5'
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	qq47e05.x1 Soares_beds_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M84241 QM
10448	23483	37082	0.47	1.0E-21	AL163203.2	NT	PROTEIN (HUMAN);
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
13014	25667		1.67	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22.410-8
4530	17698	30654	2.38	9.0E-22	AI702498.1	EST_HUMAN	b24a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266204 3' similar to TR:Q1540R Q1540R
8803	21882	35420	2.02	9.0E-22	AL163201.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT ;
8803	21882	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37748	3.1	9.0E-22	AV761874.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCG05 5'
12007	24962	38696	1.39	9.0E-22	AU140368.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE200394 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	CMO-HT0179-281086-078-105 HT0179 Homo sapiens cDNA
8080	21162		3.36	8.0E-22	AA046502.1	EST_HUMAN	z687a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487868 5'
682	13867	26898	3.78	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
4398	17841	30522	3.27	7.0E-22	O61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5150	18272	31241	0.91	7.0E-22	AB008861.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8888	21967		1.24	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
9032	22111	35653	2.77	7.0E-22	M78990.1	EST_HUMAN	EST00738 Fetal brain, Stratagene (calf036206) Homo sapiens cDNA clone HFBCF07
9802	22842	36419	2.05	7.0E-22	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8438	21517		1.25	6.0E-22	AW028123.1	EST_HUMAN	w08g07.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2642812 3'
6846	19805	33192	3.27	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10525	23560	37167	2.98	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12833	25655		1.63	5.0E-22	BF476511.1	EST_HUMAN	nae27b06.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:3265888 3' similar to contains Alu
3726	16887		0.77	4.0E-22	AJ271735.1	NT	repetitive element;
8608	28224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10961	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096434 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	25672		3.85	4.0E-22	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C009
881	14154		1.34	3.0E-22	AI469679.1	EST_HUMAN	hm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L18593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1 L1 repetitive element;
2636	15759	28873	1.33	3.0E-22	AI859038.1	EST_HUMAN	wl66b04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428639 3' similar to SW:RL21_HUMAN
3763	16924		1.55	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21;
4922	16052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
8011	21081	34573	0.8	3.0E-22	P11369	SWISSPROT	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697380 3' similar to contains MER12.12 MER12 repetitive element;
8425	21506		1.11	3.0E-22	BE156613.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
8430	21511	35042	1.88	3.0E-22	BE089841.1	EST_HUMAN	ENDONUCLEASE]
8555	21636	35172	1.14	3.0E-22	X60680.1	NT	QV0-HT0369-090200-099-f12 HT0368 Homo sapiens cDNA
8555	21636	35173	1.14	3.0E-22	X60680.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	R.rattus RY2G5 mRNA for a potential ligand-binding protein
2560	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
3507	16674	29684	3.98	2.0E-22		SWISSPROT	Yr73d05.s1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:267369 3'
4341	17484	30466	1.41	2.0E-22	AW817794.1	EST_HUMAN	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
5973	28814	32476	1.47	2.0E-22	W39453.1	EST_HUMAN	Homo sapiens protein kinase AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
6308	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	PM1-ST0282-261199-001-d12 ST0282 Homo sapiens cDNA
9904	22944	36529	1.78	2.0E-22	AI276522.1	EST_HUMAN	zc20101.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
10001	23039	36630	0.85	2.0E-22	AA715315.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
10001	23039	36631	0.85	2.0E-22	AA715315.1	EST_HUMAN	q78h08.x1 Soares_NHHMPu_ST Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.13 MER29 repetitive element;
12056	25037	38745	1.52	2.0E-22	AW418960.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219289 3'
12139	26656	31964	2.33	2.0E-22	AL163280.2	NT	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219289 3'
1927	15070	28175	2.05	1.0E-22	AW865317.1	EST_HUMAN	ha24f04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
2651	15774	28887	2.38	1.0E-22	U50871.1	NT	Homo sapiens chromosome 21 segment HS21C080
3497	19684	29676	1.53	1.0E-22	D14547.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
7820	20971	34478	1.09	1.0E-22	BE084667.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
10776	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	Human DNA, SINE repetitive element
							MIR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
							qz09b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
							MER29 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23809	37433	1.05	1.0E-23	AI365435.1	EST_HUMAN	q209b07.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2 MER29 repetitive element ;
13078	26707		12.31	9.0E-23	AW802801.1	EST_HUMAN	I2-UM0078-070400-061-F11 UM0078 Homo sapiens cDNA
3661	16824	29833	0.74	8.0E-23	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3386	16555		2.21	7.0E-23	AV647246.1	EST_HUMAN	AV647246 GLC Homo sapiens cDNA clone GLCAW037 3'
11283	24359	38000	3.74	7.0E-23	5031952	NT	Homo sapiens Nci58 (D. melanogaster)-like protein (NOT58L) mRNA
3520	16686		1.83	6.0E-23	AF189333.1	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
4383	17626	30507	1.15	6.0E-23	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
12283	25211	32097	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12283	25211	32098	4.93	6.0E-23	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12483	25335	32058	3.18	6.0E-23	AI209130.1	EST_HUMAN	qg58c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to SW:MW10_MOUSE P23249 PROTEIN MOV-10 ;
5560	18767	31798	4.01	5.0E-23	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
6369	25824	32898	3.69	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
7695	25824	32898	2.78	5.0E-23	AF179818.1	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
6570	19732	33110	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6570	19732	33111	0.67	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8022	21105	34622	3.26	3.0E-23	AA130195.1	EST_HUMAN	238g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:603988 5' similar to contains MER28.12 MER29 repetitive element ;
9450	22666	36130	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
9450	22666	36131	3.72	3.0E-23	Z70664.1	NT	Human endogenous retroviral element HC2
10523	23558		1.42	3.0E-23	AW897627.1	EST_HUMAN	RC3-NIN0066-270400-011-101 NN0066 Homo sapiens cDNA
11372	24433		1.35	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
683	13668	26599	3.69	2.0E-23	AL289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZ1FL1 gene
1168	15988		3.46	2.0E-23	IM55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2856	15970	29078	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2856	15970	29080	1	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

Page 256 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
3457	16324		1.11	2.0E-23	AI201458.1	EST_HUMAN	q573f11.x1 NCJ CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3810	16970		3.53	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4085	17240	30246	4.43	2.0E-23	HS9931.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
4085	17240	30247	4.43	2.0E-23	HS9931.1	EST_HUMAN	Y18a02.L1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:205418 5'
							Y18a02.L1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
8057	21140		6.28	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
9044	22123	35865	0.95	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
1265	25199		6.7	2.0E-23	MS2688.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12844	25561		3.68	2.0E-23	AF009680.1	NT	AUT33831 OVARC1 Homo sapiens cDNA clone OVARC1000846 5'
12863	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
4650	17786	30769	1.57	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
4888	18018		5.42	1.0E-23	AL163210.2	NT	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	z682c06.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12
8551	21632	35169				EST_HUMAN	PTR5 repetitive element ;
10909	23992	37625	4.61	1.0E-23	AA448097.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
10909	23992	37625	2.19	1.0E-23	BE409643.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
13082	26074	31654	2.19	1.0E-23	BE409643.1	EST_HUMAN	QVO-NN1020-170400-195-at11 NN1020 Homo sapiens cDNA
			1.35	1.0E-23	AW901816.1	EST_HUMAN	ab75a08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852759 3' similar to
596	13759					EST_HUMAN	TR:E1982Z E1982Z CA PROTEIN. ;
4771	17906	30888	1.87	9.0E-24	AA663213.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN B3
4771	17906	30889	1.12	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN B3
6578	19740	33121	1.12	8.0E-24	P23269	SWISSPROT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3976	17133		0.95	8.0E-24		NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
5281	18400		0.94	7.0E-24	AW937954.1	EST_HUMAN	QVO-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
			18.79	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434A2311 5'
10876	23861		1.81	7.0E-24	AW303317.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element ;
724	13906		2.21	8.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4078	17234	30241	9.39	5.0E-24	AJ228043.1	NT	Homo sapiens 850 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
						NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
7935	20885	34493	1.27	5.0E-24	AF23391.1	NT	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17614		0.9	4.0E-24	BF369469.1	EST_HUMAN	RC0-GN0390-250300-022-109 GN0390 Homo sapiens cDNA
6052	18234	32559	2.77	4.0E-24	AA584178.1	EST_HUMAN	hm31h06.s1 NCL_CGAP_Gae1 Homo sapiens cDNA clone IMAGE:1085529 3' similar to SW:POL_MLVK
8890	21959	35494	0.71	4.0E-24	AW813711.1	EST_HUMAN	P31795 POL_POLYPROTEIN ;
11454	24514	38182	2.06	4.0E-24	BE544822.1	EST_HUMAN	RC3-ST0197-130100-014-108 ST0197 Homo sapiens cDNA
12668	25446	32054	4.02	4.0E-24	AB028016.1	NT	801078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498 5'
							Homo sapiens mRNA for KIAA1083 protein, partial cds
7228	20134	33551	0.73	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
7229	20134	33552	0.73	3.0E-24	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
8618	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	hm6608.x1 NCL_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2967850 3' similar to contains MER28.82
8873	21753		1.24	3.0E-24	AW662076.1	EST_HUMAN	MER29 repetitive element ;
9665	22627	36198	3.79	3.0E-24	AL163252.2	NT	EST374149 IMAGE sequences, MAGG Homo sapiens cDNA
12796	25501	32034	1.34	3.0E-24	BF12762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
2422	15351	28678	2.55	2.0E-24	AA197639.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053306 5'
3899	17058		0.82	2.0E-24	AW898189.1	EST_HUMAN	zp1108.r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:909161 5'
7515	26219		0.63	2.0E-24	AL163209.2	NT	RC3-NN0068-090500-021-103 NN0068 Homo sapiens cDNA
7643	20712	34191	0.9	2.0E-24	AF088824.1	NT	Homo sapiens chromosome 21 segment HS21C009
7648	20717	34194	0.58	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rhofac-interacting citron kinase (Chik) mRNA, complete cds
8938	22017	35559	3.81	2.0E-24	AL119158.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIpl12-5H13
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	DKFZp781L1712_r1 781 (synonym: hary2) Homo sapiens cDNA clone DKFZp781L1712 5'
10058	23096	36698	1.06	2.0E-24	AI521759.1	EST_HUMAN	ly92d08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains
10098	23096	36699	1.06	2.0E-24	AI521759.1	EST_HUMAN	MER28 repetitive element ;
12580	26153		21.43	2.0E-24	M28877.1	NT	EST_HUMAN
1731	14881	27872	4.81	1.0E-24	7706340	NT	MER28 repetitive element ;
2738	15855		1.65	1.0E-24	AW920104.1	EST_HUMAN	Human O family dispersed repeat element
3085	16261	29278	0.72	1.0E-24	D86423.1	NT	Homo sapiens CGI-127 protein (LOC51649). mRNA
4385	17628		1.93	1.0E-24	AF143313.1	NT	QV6-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
							Mus musculus mRNA for HGT keratin, partial cds
							Homo sapiens PTEN (PTEN) gene, exon 2

Page 258 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	19695	33088	1.13	1.0E-24	7106336	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7720	20784	34272	4.95	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20959	34465	5.07	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0168-271189-005-d09 HT0168 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901184.1	EST_HUMAN	OM0-NN1010-130900-281-d07 NN1010 Homo sapiens cDNA
11999	24984	38689	1.37	9.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG1), mRNA
5111	18239	31206	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne2e10.s1 NCL_CGAP_Kld1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8413	21494	35025	3.7	7.0E-25	AA468846.1	EST_HUMAN	MER1 repetitive element: ne06a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
12003	24988	38638	3.64	7.0E-25	AA583540.1	EST_HUMAN	repetitive element: nt25r08.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST
7899	20951	34458	5.04	6.0E-25	W87623.1	EST_HUMAN	P31015 PROBABLE 60S RIBOSOMAL PROTEIN L14EA ;
1683	14835	27820	1.61	5.0E-25	AW850271.1	EST_HUMAN	z165107.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
11598	24649	38333	3.12	5.0E-25	AW979107.1	EST_HUMAN	Mus musculus diogenin (Odog), mRNA
1478	14631	27716	2.66	4.0E-25	T98107.1	EST_HUMAN	IL3-CT0219-161199-031-D04 CT0219 Homo sapiens cDNA
3489	16856		2.81	4.0E-25	AW887671.1	EST_HUMAN	ye56h04.r1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
4436	17576		4.06	4.0E-25	BE170657.1	EST_HUMAN	PM3-OT0033-280200-001-g07 OT0093 Homo sapiens cDNA
10144	23182	36779	0.83	4.0E-25	AA388873.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
2266	15399	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	EST97317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
3396	16566	29581	3.12	3.0E-25	8923321	NT	RCS-BT0377-131289-031-F02 BT0377 Homo sapiens cDNA
3396	16566	29582	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	P29622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
8532	21613	35149	5.42	3.0E-25	AL163210.2	NT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
11287	24353	37993	2.7	3.0E-25	AA879013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1378	14533	27607	4.9	2.0E-25	5032158	NT	repetitive element: nt30h10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.L1 L1
2382	15513	28641	7.33	2.0E-25	BE888016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2893	15731	28848	3.71	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9967	23006	36601	2.13	2.0E-25	AL449573.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
375	13583	26617	0.81	1.0E-25	AL040229.1	EST_HUMAN	AL449573 Homo sapiens Testis (Starvies GS) Homo sapiens cDNA
1277	14434		2.07	1.0E-25	9635487	NT	DKFZp434f0313_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434f0313 5'
							Human endogenous retrovirus, complete genome

Page 259 of 550

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-109 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	19855		0.95	1.0E-25	AA198080.1	EST_HUMAN	z043b05.s1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to
6830	25938	33686	2.95	1.0E-25	AA682660.1	EST_HUMAN	contains Alu repetitive element;
8098	21180	34698	3.66	1.0E-25	AA706079.1	EST_HUMAN	nm54r11.s1 NCLCGAP Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8748	22810	36388	1.32	1.0E-25	X60660.1	NT	z06g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains
9748	22810	36389	1.32	1.0E-25	X60660.1	NT	PTR5.13 PTR5 repetitive element;
11212	24261	37920	3.11	1.0E-25	U63163.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
12280	25209	38364	1.62	1.0E-25	D14547.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
12280	25209	38365	1.62	1.0E-25	D14547.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
2563	16678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens (MAGE-B1) genes, complete cds
11252	24321		2.35	9.0E-26	AI905368.1	EST_HUMAN	Human DNA, SINE repetitive element
12140	25901		5.33	9.0E-26	AL163285.2	NT	Human DNA, SINE repetitive element
5811	18001		1.51	8.0E-26	D14547.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
1808	14761	27840	5.61	7.0E-26	AF003528.1	NT	regions
4089	17244	30251	1.68	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340163.1	EST_HUMAN	hd02e12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808369 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11966	24551		6.85	7.0E-26	AA115895.1	EST_HUMAN	z030d08.r1 Stragene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:648943 6'
12901	25936		5.49	7.0E-26	AW864559.1	EST_HUMAN	similar to gb:MI4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
2300	15432	28565	3.83	6.0E-26	AF028308.1	NT	EST366629 MAGE resequences, MAGE Homo sapiens cDNA
3427	16595	29611	0.69	6.0E-26	AA206131.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10753	23766	37400	0.62	6.0E-26	AL163202.2	NT	z052h04.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:648271 6'
10753	23766	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24964	38666	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C002
1204	14366	27426	0.89	5.0E-26	AI708295.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
							as38h08.x1 Bershead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to
							WP:F49C12.11 CE03371;

Page 260 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318519 3' similar to
9612	22667		3.29	4.0E-26	7657670	NT	WP.F49C12.11 CE03371 ;
10897	23981	37613	2.84	4.0E-26	BE260187.1	EST_HUMAN	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
11604	24667	38342	1.38	4.0E-26	AL163246.2	NT	00191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3635210 5'
1797	14946	28038	1.25	3.0E-26	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C048
2059	15200	28314	1.14	3.0E-26	AL045885.2	EST_HUMAN	Human DNA, SINE repetitive element
2088	16228		3.34	3.0E-26	AA115895.1	EST_HUMAN	DKFZp434i066_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434i066 5'
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zn30d08.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	G695374 STRATAGENE COLON (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
7051	20104	33521	6.09	3.0E-26	BF245438.1	EST_HUMAN	zn30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
11867	24855	38550	1.97	3.0E-26	AW187565.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11867	24855	38551	1.97	3.0E-26	AW187565.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11902	24890	38591	7.79	3.0E-26	AA593173.1	EST_HUMAN	zn30f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
699	13882	26915	6.84	2.0E-26	AL163282.2	NT	G695374 THYROID RECEPTOR INTERACTOR ;
1917	16060		3.07	2.0E-26	AL038099.2	EST_HUMAN	601864663F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
3303	16477	29489	5.22	2.0E-26	X86694.1	NT	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
10991	24070		1.93	2.0E-26	D87675.1	NT	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11493	24551	38226	2.96	2.0E-26	AI801412.1	EST_HUMAN	hm37405.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
11704	24701		2.06	2.0E-26	AF055086.1	NT	OFR repetitive element ;
12389	25276		1.76	2.0E-26	AB037869.1	NT	Homo sapiens chromosome 21 segment HS21C082
12604	26088	31658	2.33	2.0E-26	BE170371.1	EST_HUMAN	DKFZp566L171_e1 568 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566L171 3'
139	13365	26398	8.96	1.0E-26	AL039363.2	EST_HUMAN	Musculus mRNA for astrocytic phosphoprotein, PEA-15
2105	15244	28365	1.42	1.0E-26	AL039363.2	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
2751	15668		6.28	1.0E-26	AF261085.1	NT	hs89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element/contains element MER20 MER20 repetitive element ;
6880	20208		2.89	1.0E-26	BE165980.1	EST_HUMAN	Homo sapiens MHC class 1 region
11131	24203		1.96	1.0E-26	AL039487.1	EST_HUMAN	Homo sapiens mRNA for KIAA1439 protein, partial cds
12855	28178		2.77	1.0E-26	H55083.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
							DKFZp434H1910_r1_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434H1910 5'
							Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
							DKFZp566C2148_r1 568 (synonym: htkd2) Homo sapiens cDNA clone DKFZp566C2148 5'
							CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
							UHFH-BM0-adw-d-10-0-U1.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

Page 261 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-402 FN0138 Homo sapiens cDNA
9503	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12143	25118		6.5	9.0E-27	BF445555.1	EST_HUMAN	ncs03c07.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:3253044 3' similar to contains OFR.11 OFR repetitive element ;
11	13248	28249	4.22	8.0E-27	AL831482.1	EST_HUMAN	w49c04.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
571	13763		4.67	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783299 3' similar to gb:K00658 TUBULIN ALPHA-1 CHAIN (HUMAN);
1448	14601	27679	23.84	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783299 3' similar to gb:K00658 TUBULIN ALPHA-1 CHAIN (HUMAN);
2286	15369	28499	1.82	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-407 SN0018 Homo sapiens cDNA
3254	16428	29446	1.8	8.0E-27	P12238	SWISSPROT	ADP ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3434	16602	29821	0.75	8.0E-27	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
5812	18002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 6'
7117	18543		2.65	8.0E-27	BE928560.1	EST_HUMAN	MR4-BT0398-260800-204-406 BT0398 Homo sapiens cDNA
7192	20057	33467	2.49	8.0E-27	N84870.1	EST_HUMAN	J1761F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1761 5' similar to REPETITIVE ELEMENT L1
9410	22484	36048	1.63	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091289-063-407 CT0315 Homo sapiens cDNA
9410	22484	36049	1.63	8.0E-27	AW857579.1	EST_HUMAN	CM1-CT0315-091289-063-407 CT0315 Homo sapiens cDNA
701	13884		1.77	7.0E-27	Z70084.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	h51h12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:076040
8058	22137		0.97	7.0E-27	D86984.1	NT	Q76040 ORF2: FUNCTION UNKNOWN. ;
10988	24087		3.7	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
10994	24046	37679	3.21	6.0E-27	M26697.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2 Human nuclear protein (B23) mRNA, complete cds
12094	25074	38781	1.55	6.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
7854	21004		0.73	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37081	3.21	5.0E-27	BF66681.4	EST_HUMAN	60212149T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10442	23477	37082	3.21	5.0E-27	BF66681.4	EST_HUMAN	60212149T1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6883	20035	33444	1.65	4.0E-27	9910569	NT	Mus musculus sperm tail associated protein (Slap), mRNA

Page 262 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	21207		0.98	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9945	22984	36577	0.61	4.0E-27	AW880559.1	EST_HUMAN	QVQ-OT0033-07030-152-b10 OT0033 Homo sapiens cDNA
11903	24891	38592	2.62	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
2099	15239	28361	7.1	3.0E-27	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4386	17529	30510	1.55	3.0E-27	BE071924.1	EST_HUMAN	PMO-BT0527-080100-001-d11 BT0527 Homo sapiens cDNA
5462	18932	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9605	22771	36342	3.49	3.0E-27	BF035327.1	EST_HUMAN	60148531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3652086 5'
42	13280	26286	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1944	15087		24.24	2.0E-27	AA565345.1	EST_HUMAN	h01b10.a1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000698 similar to gb:M17886 60S
3178	16353		13.34	2.0E-27	AW629172.1	EST_HUMAN	h151h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040
3296	16470	29489	1.45	2.0E-27	AF111187.2	NT	O76040 ORF2: FUNCTION UNKNOWN.;
3296	16470	29490	1.45	2.0E-27	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19987	33373	0.79	2.0E-27	H02655.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
8282	21364	34883	1.17	2.0E-27	A1866347.1	EST_HUMAN	Y36601.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:160840 5' similar to SP:HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;
9469	22526		2.6	2.0E-27	AA551527.1	EST_HUMAN	w128g07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9995	23033	36625	0.83	2.0E-27	X60658.1	NT	h01b10.a1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
10241	23276	36888	1.45	2.0E-27	M78590.1	EST_HUMAN	repetitive element ;
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
11197	24266	37801	3.61	2.0E-27	AU121685.1	EST_HUMAN	ESTT00738 Fetal brain, Striatogene (caif836206) Homo sapiens cDNA clone HFBCF07
11777	15087		6.43	2.0E-27	AA565345.1	EST_HUMAN	ESTT00738 Fetal brain, Striatogene (caif836206) Homo sapiens cDNA clone HFBCF07
12107	26087	36701	1.64	2.0E-27	AF218650.1	NT	ESTT00738 Fetal brain, Striatogene (caif836206) Homo sapiens cDNA clone HFBCF07
449	13645		2.34	1.0E-27	AL163246.2	NT	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
1021	14192	27251	4.97	1.0E-27	AB026898.1	NT	AU121685 MAMMA1 Homo sapiens cDNA clone IMAGE:1000698 similar to gb:M17886 60S
6874	18833	33222	6.51	1.0E-27	6005855	NT	h01b10.a1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000698 similar to gb:M17886 60S
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
							Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

Page 263 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33568	1.85	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000086C10
7010	20146	33567	1.85	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000086C10
8809	21888	35430	1.16	1.0E-27	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9186	22284		1.69	1.0E-27	BE076780.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
9223	22863	36551	2.85	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12005	24690	38694	3.05	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant b5ah mRNA, complete cds
144	13368		2.26	9.0E-28	BE348396.1	EST_HUMAN	hwt7c11.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	28567	2.17	9.0E-28	AU126280.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313
10601	23636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	zsl18g12.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
12224	25173		3.04	9.0E-28	BF377889.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12565	26003		13.39	8.0E-28	AW167571.1	EST_HUMAN	eu83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782811 3' similar to TR:O60302 KIAA0656 PROTEIN, contains element MER22 repetitive element;
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y78AA1 Homo sapiens cDNA clone Y78AA1000824 5'
11483	24522	38192	1.85	7.0E-28	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12181	25141		5.04	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
9119	22188		1.28	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF181 (ZNF181) gene, complete cds
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCL CGAP_GC81 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu repetitive element; contains element PTR8 repetitive element;
328	13542		2.75	5.0E-28	A1921003.1	EST_HUMAN	wo18c07.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1 THR repetitive element;
4116	17270	30269	38.94	5.0E-28	R70762.1	EST_HUMAN	y89f10.r1 Soares placenta N02HP Homo sapiens cDNA clone IMAGE:146443 5'
2889	15808	28928	1.46	4.0E-28	AW195095.1	EST_HUMAN	xn33e09.x1 NCL CGAP_KiH1 Homo sapiens cDNA clone IMAGE:2885604 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95;
3177	16352	28358	1.34	4.0E-28	BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
7483	20558	34030	3.55	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
11105	24177		4.19	4.0E-28	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
11253	24324		14.89	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
11278	20558	34030	4.34	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12622	26418		1.7	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0264 Homo sapiens cDNA
12773	28069		1.82	4.0E-28	AW862360.1	EST_HUMAN	RC0-CT0379-070100-031-r01 CT0379 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1312	14488		2.29	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
5227	18349		0.94	3.0E-28	AF009650.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
9027	22106	35347	2.28	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-03 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12653	25433		3.77	3.0E-28	AI831991.1	EST_HUMAN	w98907.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element
12803	25536		3.29	3.0E-28	BE092801.1	EST_HUMAN	RC2-BT0642-210200-013-03 BT0642 Homo sapiens cDNA
12855	25576	31993	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12855	25576	31994	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
81	13326	26354	12.79	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1191	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI548634.1	EST_HUMAN	q35506.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.B2 L1 repetitive element
3446	16614	28632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	19604	32968	1.48	2.0E-28	BF224402.1	EST_HUMAN	h76603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element
6460	19627		3	2.0E-28	BF212905.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.53	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGE resequences, MAGL Homo sapiens cDNA
11913	24900	38603	2.52	2.0E-28	AF224686.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424	H06376.1	1.74	2.0E-28	H06376.1	EST_HUMAN	y76c09.r1 Soares Infant brain 1 INIB Homo sapiens cDNA clone IMAGE:44300 5'
1508	14661	27744	2.85	1.0E-28	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2294	15426	28560	3.91	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120500-360-b03 BT0821 Homo sapiens cDNA
4691	17826		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8044	21127		1.95	1.0E-28	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC635091), mRNA
8208	21260		3.03	1.0E-28	8922763	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36099	4.75	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36720	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
12186	25145		7.66	1.0E-28	AA054182.1	EST_HUMAN	z51c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
13013	25881		4.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	26122	31643	1.8	9.0E-29	AW663987.1	EST_HUMAN	h179g06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2678266 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1632	14784	27870	1.98	7.0E-29	AW968447.1	EST_HUMAN	EST378521 MAGI resequences, MAGI Homo sapiens cDNA
13197	25779		9.03	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	6.0E-29	A038748.1	EST_HUMAN	wc89b01.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12495	25342		5.19	6.0E-29	BE940436.1	EST_HUMAN	O16475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
12587	25395		2.1	6.0E-29	BF568087.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-29	AL163203.2	NT	602184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 6'
8829	22008		8.35	5.0E-29	AW887641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12785	26531		1.49	5.0E-29	BE612446.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3304	16478		2.28	4.0E-29	AJ752357.1	EST_HUMAN	601481827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855728 5'
6133	19312		7.06	4.0E-29	BE104600.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnl5c02 random
8272	21354	34870	0.84	4.0E-29	A1678101.1	EST_HUMAN	QV1-HT0471-280300-121-405 HT0471 Homo sapiens cDNA
8272	21354	34870	0.84	4.0E-29	A1678101.1	EST_HUMAN	wd35g06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8272	21354	34870	0.84	4.0E-29	A1678101.1	EST_HUMAN	MER29.12 MER29 repetitive element;
8944	22023	35563	3.59	4.0E-29	J04988.1	NT	Human 80 kD heat shock protein gene, complete cds
4536	17674	30658	1.31	3.0E-29	AB042267.1	NT	Homo sapiens PTS gene for 5-pyruvylaldehyde dehydrogenase, complete cds
4855	17988	30976	1.1	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-170900-360-B03 BT0821 Homo sapiens cDNA
6053	19235	32560	0.83	3.0E-29	BE314018.1	EST_HUMAN	601152857F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508627 5'
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	Human gene for AII-receptor, exon 7-9
9500	22558	38119	1.22	3.0E-29	AW303317.1	EST_HUMAN	xv1703.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu
9731	22796		1.49	3.0E-29	AL163248.2	NT	repetitive element; contains MER19.12 MER19 repetitive element;
10164	23201		0.61	3.0E-29	BE350127.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
11546	24602	38278	2.26	3.0E-29	AA403053.1	EST_HUMAN	h099g01.x1 NCL CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146258 3' similar to contains MER29.b3
12365	25272		1.36	3.0E-29	D63882.1	NT	MER29 repetitive element;
13092	26132		1.62	3.0E-29	D63882.1	NT	262501.1 Scores_Teasta_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
505	13699	26727	0.98	2.0E-29	AF084869.1	NT	G1335769 GAG-POL POLYPROTEIN;
505	13699	26728	0.98	2.0E-29	AF084869.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
						NT	Human HsLIM15 mRNA for HsLIM15, complete cds
						NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
						NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds

Page 286 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1663	14716	27794	7.8	2.0E-29	AB93804.1	EST_HUMAN	w65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
1503	14716	27796	7.8	2.0E-29	AB93804.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN ;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	w65d10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	HERV-E ENVELOPE GLYCOPROTEIN ;
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	H.sapiens mRNA for laminin-5, alpha3b chain
5946	19132	32446	0.78	2.0E-29	AB082459.1	EST_HUMAN	H.sapiens mRNA for laminin-5, alpha3b chain
6309	19481	32835	1.49	2.0E-29	AB08418.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C068
7732	19481	32835	1.28	2.0E-29	AB08418.1	EST_HUMAN	os71e04.x1 NCI_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1
8164	21246	34766	1.16	2.0E-29	BE887157.1	EST_HUMAN	repetitive element ;
8777	21856	35398	0.81	2.0E-29	10567821	NT	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23566860 3' similar to contains
8777	21856	35398	0.81	2.0E-29	10567821	NT	element MERG repetitive element ;
9708	22757	36327	2.76	2.0E-29	AL163248.2	NT	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3846648 5'
9708	22757	36328	2.76	2.0E-29	AL163248.2	NT	element MERG repetitive element ;
10444	23479	37084	3.85	2.0E-29	AL163248.2	NT	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5'
10444	23479	37085	3.85	2.0E-29	AL163248.2	NT	Homo sapiens DNA-binding protein (LOC58242), mRNA
11767	24760	37085	1.87	2.0E-29	11425108	NT	Homo sapiens chromosome 21 segment HS21C048
8992	22071	35611	8.27	1.0E-29	AW198380.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
10860	23883	37503	2.81	1.0E-29	X60688.1	NT	Homo sapiens chromosome 21 segment HS21C048
6712	19870	33281	3.53	9.0E-30	AA781215.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
12266	25200		4.55	9.0E-30	11422746	NT	Homo sapiens chromosome 21 segment HS21C048
6449	19616		10.5	8.0E-30	F08688.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
8485	21546	35076	2.26	8.0E-30	AA383873.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
1646	14697		1.07	7.0E-30	BE091133.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
1814	14963	28056	1.57	6.0E-30	D28303.1	NT	Homo sapiens chromosome 21 segment HS21C048
3259	16433	29450	3.15	6.0E-30	BE008026.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4881	16433	29450	1.02	6.0E-30	BE008026.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
10760	23793	37412	0.76	6.0E-30	AF177227.1	NT	Homo sapiens chromosome 21 segment HS21C048

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17275	30274	43.22	6.0E-30	A1999992.1	EST_HUMAN	ig2g03.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5353	25928		5.79	5.0E-30	U87931.1	NT	Human acetylcholinesterase (ACO2) gene, exon 7
11126	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.78	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38149	2.78	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	15344	28470	2.38	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
2210	15344	28471	2.38	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-090200-080-c08 DT0043 Homo sapiens cDNA
9106	22185	35728	1.55	4.0E-30	AW612488.1	EST_HUMAN	CM1-ST0181-091198-035-08 ST0181 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	A133851.1	EST_HUMAN	qq83c05.x1 Soares [etal] fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29.b2 MER29 repetitive element;
3853	17013	30013	1.15	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
8138	21220		0.63	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8853	21763		0.45	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10849	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3 MER29 repetitive element;
11482	24541	38211	1.52	3.0E-30	P34059	SWISSPROT	TRANSCRIPTION FACTOR AP-2
692	13875	26908	1.42	2.0E-30	AW857315.1	EST_HUMAN	CM0-CT0307-310100-198-003 CT0307 Homo sapiens cDNA
1108	14273		2.53	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1509	14862	27745	6.5	2.0E-30	BE175977.1	EST_HUMAN	RG5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2779	15895	29005	9.93	2.0E-30	BE765232.1	EST_HUMAN	IL2-NT0101-280700-118-E04 NT0101 Homo sapiens cDNA
2988	16162	29179	6.93	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZF1) gene, complete cds
3889	17048	30048	1.95	2.0E-30	AW208681.1	EST_HUMAN	U1-H-B11-af0-c-12-Q-U1 st NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4900	18030	31018	2.02	2.0E-30	BE268845.1	EST_HUMAN	607119860FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4900	18030	31019	2.02	2.0E-30	BE268845.1	EST_HUMAN	607119860FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
8734	21814	35349	4.89	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFulwara) Homo sapiens cDNA clone GEN-670C01 5'
8836	21915	35452	1.71	2.0E-30	BE670817.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284692 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
8836	21915	35453	1.71	2.0E-30	BE670817.1	EST_HUMAN	7e37c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284692 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
10201	23238	36828	3.78	2.0E-30	AW971958.1	EST_HUMAN	EST1383557 MAGE resequences, MAGL Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	23322	36924	6.31	2.0E-30	AW470791.1	EST_HUMAN	h33306.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
297	13514	26548	10.87	1.0E-30	C18939.1	EST_HUMAN	THR repetitive element 1; C18939 Human placenta cDNA (Tfujiiwara) Homo sapiens cDNA clone GEN:570C01 5'
551	13744	26769	1.62	1.0E-30	AW468897.1	EST_HUMAN	h33004.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains MER1.3 MER1 MER1 repetitive element 1;
734	13916	26956	5.15	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2283	15418	28560	11.56	1.0E-30	AA664377.1	EST_HUMAN	ac77508.x1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:3688599 3'
2533	16698	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	60202260F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4157991 5'
3120	16286	28310	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST186808 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
7801	20953	34480	1.96	1.0E-30	BF183230.1	EST_HUMAN	601808932F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
8176	21258	34780	0.49	1.0E-30	BE061586.1	EST_HUMAN	MRO-BT0249-091299-101-g01 BT0249 Homo sapiens cDNA
12786	26117		1.57	1.0E-30	AA299211.1	EST_HUMAN	EST11898 Uterus Homo sapiens cDNA 5' end
12937	26025		5.31	1.0E-30	H55583.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3862	17022	30020	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3862	17022	30021	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65e08.r1 Stralagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8519	21600	35135	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88608.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8519	21600	35136	0.88	9.0E-31	R18214.1	EST_HUMAN	Y88608.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8825	21904		1.99	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05F03 3'
8827	21906	35445	0.55	9.0E-31	AF076779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
13183	25776	31934	1.29	9.0E-31	6755441	NT	Mus musculus syndecan 4 (Sdc4), mRNA
1102	14287	27325	2.52	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2484	15611		7.93	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
729	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2733	15850	28982	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2733	15850	28983	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8585	21676	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8585	21676	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9468	22523		1.03	7.0E-31	BE409611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
3769	16930		3.42	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8347	21428		1.39	6.0E-31	AF055086.1	NT	Homo sapiens MHC class 1 region

Page 269 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8528	21607	36146	0.75	8.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element:
10578	24055	37689	1.43	8.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEIMBA1005050 5'
12327	25236	32108	3.7	8.0E-31	AW372863.1	EST_HUMAN	RC5-BT0377-081289-031-D12 BT0377 Homo sapiens cDNA
12459	25947		2.54	8.0E-31	BE694488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	28450	3.39	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	13420	28451	3.39	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	5.0E-31	BF056540.1	EST_HUMAN	7106104.X1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR.Q13637 Q13637
609	13798		3.02	4.0E-31	AJ271735.1	NT	SIMILAR TO POGO ELEMENT, contains L1.L1 repetitive element:
							Homo sapiens Xq pseudautosomal region, segment 1/2
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYL TRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYL TRANSFERASE) (GALNAC-T1)
2849	15007		2.09	4.0E-31	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10764	23787	37402	0.48	4.0E-31	AF084484.1	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
12787	25526		1.55	4.0E-31	11430273	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
12824	26609		2	4.0E-31	AB008881.1	NT	Homo sapiens KIA0569 gene product (KIA0569), mRNA
							Homo sapiens gene for activin receptor type IIB, complete cds
2680	15782	28997	1.75	3.0E-31	6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
7494	20569	34041	8.04	3.0E-31	4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (18kD, ASH1) (NDUFB8) mRNA
7663	20730	34208	1.23	3.0E-31	11420329	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8355	21438		1.51	3.0E-31	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C006
9779	22819	36397	2.59	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10822	23655	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	zu06d04.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731047 5'
10897	23952	37582	2.03	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (R1G PROTEIN)
11421	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	601459531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1997	15110	28211	1.58	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-033 L10051 Homo sapiens cDNA
2288	15420	28552	1.05	2.0E-31	A1393388.1	EST_HUMAN	tg44g06.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2416	15545	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513_r1 791 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:839413 3' similar to contains aa8811.51 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:2733833 3'
2511	15637	28758	4.63	2.0E-31	AA458824.1	EST_HUMAN	THR12 THR repetitive element:
5389	18591	31583	0.78	2.0E-31	AW444486.1	EST_HUMAN	UIH-B13-akb-f-08-0-U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2733833 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER28.b3
9277	22363					EST_HUMAN	MER28 repetitive element.
9408	22482	36046	1.53	2.0E-31	AA877784.1	EST_HUMAN	h08g04.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537
10110	23148	36748	3.46	2.0E-31	7661535	NT	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
10280	23315	36914	2.75	2.0E-31	BE408611.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10280	23315	36915	2.75	2.0E-31	BE408611.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12578	26202		2.59	2.0E-31	AI114527.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
17	13255	28256	9.91	1.0E-31	U93163.1	NT	Homo sapiens hexokinase II gene, promoter region
1696	14848	27932	2.86	1.0E-31	O95371	SWISSPROT	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
1696	14848	27933	2.86	1.0E-31	O95371	SWISSPROT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
1696	14848	27934	2.86	1.0E-31	O95371	SWISSPROT	(MAGE-B1) genes, complete cds
5407	18808	31681	3.97	1.0E-31	AW391679.1	EST_HUMAN	OLFACTORY RECEPTOR 2C1
8261	19435	32781	2.57	1.0E-31	AF048727.1	NT	OLFACTORY RECEPTOR 2C1
7441	20518	33990	0.84	1.0E-31	AF126145.1	NT	MR3-ST0220-151209-028-a08_1 ST0220 Homo sapiens cDNA
8005	21055	34567	1.35	1.0E-31	BE972818.1	EST_HUMAN	Homo sapiens minisatellite ccb1 repeat region
10441	23476	37080	0.5	1.0E-31	U93163.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
11158	24227	37857	2.35	1.0E-31	AI086434.1	EST_HUMAN	601682052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
8776	19631	33327	2.19	9.0E-32	AV723976.1	EST_HUMAN	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
7630	20603	34077	0.66	9.0E-32	L31770.1	NT	(MAGE-B1) genes, complete cds
7766	20825		0.91	9.0E-32	11430822	NT	qf21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595
2139	16275	28397	5.1	8.0E-32	AI056770.1	EST_HUMAN	Q16595 FRAXIN ;
5599	18794	31843	0.77	8.0E-32	AW997214.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
12406	26285		2.36	7.0E-32	X17283.1	NT	Bos taurus vacuolar H+-ATPase subunit mRNA, complete cds
7523	20596		1.32	6.0E-32	BE888016.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

Page 271 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12869	25181		2.5	8.0E-32	AA884653.1	EST_HUMAN	oh37c03.e1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1458972 3' similar to contains L1.13 L1 repetitive element;
1059	14225	27292	10.42	6.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
954	14127		1.64	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7779	20835	34328	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
9594	21635		0.93	4.0E-32	BE094410.1	EST_HUMAN	RC4-BT0311-141198-011-H06 BT0311 Homo sapiens cDNA
468	13683	26899	2.64	3.0E-32	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731600.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK07 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2973	16149	29169	0.76	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9594	22849	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
9594	22849	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
11166	24237	37868	3.43	3.0E-32	AA77621.1	EST_HUMAN	265a07.at Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;
12433	25307		7.95	3.0E-32	BE278086.1	EST_HUMAN	601158285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12843	16149	29169	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
13020	25671		6.47	3.0E-32	BE278086.1	EST_HUMAN	601158285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19651	32907	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6608	19768	33156	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6608	19768	33157	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8473	21654	35085	3.34	2.0E-32	AA114284.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21654	35086	3.34	2.0E-32	AA114284.1	EST_HUMAN	zn66c08.r1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3183	16338		1.26	1.0E-32	BE743289.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20065	33478	6.64	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8795	21874	35413	4.56	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCL_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element;

Page 272 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6550	16712		3.17	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8988	22067	35607	1.81	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158670 5'
11038	24117		4.55	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI590115.1	EST_HUMAN	1012609.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element:
2714	15832		7.95	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE06 5'
3314	16487		15	7.0E-33	AW971307.1	EST_HUMAN	EST383368 MAGE resequences, MAGL Homo sapiens cDNA
9147	22226		0.97	7.0E-33	X54890.1	NT	Human hLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphate) (EC 3.1.3.48)
11087	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158670 5'
11526	24932	38286	1.59	7.0E-33	AW971568.1	EST_HUMAN	EST383667 MAGE resequences, MAGL Homo sapiens cDNA
12413	26292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	1016101.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element:
3830	16890		0.93	8.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6192	19368	32717	0.91	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6192	19368	32718	0.91	8.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8778	21857	35400	1.86	8.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8699	21978	35517	3.12	8.0E-33	11429198	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10214	23250	36839	2.03	8.0E-33	6756609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10214	23250	36840	2.03	8.0E-33	6756609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1818	14967		1.9	5.0E-33	BF373515.1	EST_HUMAN	QV1-F70169-100700-271-g02 F70169 Homo sapiens cDNA
1831	15074		1.32	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1847	15090	28190	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1947	15090	28191	1.63	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4169	17319	30312	0.86	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
10454	23469	37097	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10454	23469	37098	0.82	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

Page 273 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	25165		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1152	14316		2.25	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2194	16329	28454	3.37	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15518		1.16	4.0E-33	AA625621.1	EST_HUMAN	ab51b11.11 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2810	13734	28860	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4808	17743	30722	2.38	4.0E-33	AW293349.1	EST_HUMAN	U1-HB12-ah-c-03-Q-UJ.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5519	18717	31731	24.75	4.0E-33	AA053053.1	EST_HUMAN	z171a08.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:810038 5' similar to gb:X12671_rna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6522	18887	33060	0.79	4.0E-33	8933994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6522	19887	33081	0.79	4.0E-33	5333994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		5.62	3.0E-33	BE360127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element ;
1114	14278		5.83	3.0E-33	BE360127.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element ;
2522	16084		1.16	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLC09C09 3'
10655	23689	37298	0.87	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407647 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE ;
18	13256		1.57	2.0E-33	AI160189.1	EST_HUMAN	q067q03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
107	13256		5.53	2.0E-33	AI160189.1	EST_HUMAN	q067q03.x1 Soares_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.t1 OFR repetitive element ;
4539	17677		4.53	2.0E-33	BE156039.1	EST_HUMAN	MRQ-HT0403-150300-202-c08 HT0405 Homo sapiens cDNA
5100	18228	31199	8.64	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.11 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:X00734_cd81 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31294	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5553	19716	33091	1.39	2.0E-33	AI27492.1	EST_HUMAN	q06d01.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
9301	22377		2.15	2.0E-33	AI052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gb:M26836 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
9	13247		1.61	1.0E-33	AF003628.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7565	20537	34113	0.86	1.0E-33	MT13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10227	26229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24655	38340	1.56	1.0E-33	AW986818.1	EST_HUMAN	QV9-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11962	24947	38662	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AW904461.1	EST_HUMAN	RC5-NN1055-280400-021-G03 NN1055 Homo sapiens cDNA
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12929	13247		5.7	1.0E-33	AF003528.1	NT	AV727809 HTC Homo sapiens cDNA clone HTCNC12.5
12960	25626	31978	2.19	1.0E-33	AV727809.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
13179	25766		4.77	9.0E-34	AJ271735.1	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
2240	15373	28501	0.98	8.0E-34	8922751	NT	QV2-BT0258-071289-019-g07 BT0258 Homo sapiens cDNA
4620	17757	30739	1.93	8.0E-34	BE062570.1	EST_HUMAN	MR4-BT0389-200100-001-h03 BT0389 Homo sapiens cDNA
7874	21024	34537	0.67	8.0E-34	BE069882.1	EST_HUMAN	Yd15605.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5'
1476	14628	27714	2.5	7.0E-34	T70845.1	EST_HUMAN	Yd15605.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5'
10204	14628	27714	0.54	7.0E-34	T70845.1	EST_HUMAN	Yd15605.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108320 5'
12482	26334		3.85	7.0E-34	H12866.1	EST_HUMAN	Yd14c10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	26711	1.74	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
483	13677	26712	1.74	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.88	6.0E-34	AW998811.1	EST_HUMAN	PM0-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
12290	25215	32099	2.22	6.0E-34	U03686.1	NT	Mus musculus DAB/2J hair-specific (hach-1) gene
1829	15072		3.16	5.0E-34	7708600	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5173	18295	31257	5.24	5.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRp-55) mRNA, complete cds
9087	22146	35693	1.17	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10890	23974	37605	2.02	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11532	24588		1.83	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2054	15195	28309	2.09	4.0E-34	A1804667.1	EST_HUMAN	tg94c06.x1 NCJ CGAP Pr28 Homo sapiens cDNA clone IMAGE:2249184 3'
3241	19415	28430	0.9	4.0E-34	5803168	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
5881	19168	32486	0.82	4.0E-34	AA881773.1	EST_HUMAN	ak35c01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407836 3'
9238	22315	35857	0.83	4.0E-34	BF209778.1	EST_HUMAN	601874650F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102213 5'
6361	19531	32890	0.66	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11420	24481		2.96	3.0E-34	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
							wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
9152	22230	35774	0.75	2.0E-34	AI678101.1	EST_HUMAN	MER29.12 MER29 repetitive element ;
9152	22230	35775	0.75	2.0E-34	AI678101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
11431	24492	38156	8.54	2.0E-34	P51805	SWISSPROT	MER29.12 MER29 repetitive element ;
							PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11431	24492	38157	8.54	2.0E-34	P51803	SW/SSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1534	14887	27787	10.13	1.0E-34	P12236	SW/SSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14887		7.18	1.0E-34	AU136024.1	EST_HUMAN	AU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
3764	16025	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY009397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.28	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240400-016-H08 BT0506 Homo sapiens cDNA
6266	19440	32787	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
6266	19440	32788	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886989 5'
9327	22692	36163	0.64	1.0E-34	P23266	SW/SSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
9898	22638	36523	8.07	1.0E-34	AL036635.1	EST_HUMAN	DKFZ558A1563_r1 584 (synonym: hfb2) Homo sapiens cDNA clone DKFZp664A1663 5'
11469	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11469	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.92	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12880	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X88203
12950	26660		5.84	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3735	16936	26600	1.3	9.0E-35	AW663302.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
232	13453		7.21	8.0E-35	6031190	NT	h777b06.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988787 5'
1776	14925	28019	3.63	8.0E-35	BF589937.1	EST_HUMAN	Homo sapiens prohibitin (PHB) mRNA
1776	14925	28019	3.63	8.0E-35	BF589937.1	EST_HUMAN	h833a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1776	14925	28020	3.63	8.0E-35	BF589937.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA ;
4989	18118	31097	2.61	8.0E-35	BF183195.1	EST_HUMAN	h833a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
10929	24011	37645	1.53	8.0E-35	BE378480.1	EST_HUMAN	O76912 DIACYLGLYCEROL KINASE IOTA ;
12404	25283		5.89	8.0E-35	BF669282.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
6813	19773	33164	1.61	7.0E-35	11429417	NT	601238468F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
1415	14598	27675	1.06	6.0E-35	AA757115.1	EST_HUMAN	602184624F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300680 3'
2026	15168	28271	4.63	6.0E-35	6005975	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
4184	17314	30309	0.8	6.0E-35	AW297191.1	EST_HUMAN	h153h03.s1 Soares_teste_NHT Homo sapiens cDNA clone 1308307 3'
8081	21163	34680	4.03	6.0E-35	6005921	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
8908	21886	35624	0.57	6.0E-35	X94232.1	NT	U1-H-BWO-qjd-d-09-Q-U1 s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
							Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
							H. sapiens mRNA for novel T-cell activation protein

Page 276 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8006	21985	35525	0.57	6.0E-35	X94232.1	NT	H.sapiens mRNA for novel T-cell activation protein
8967	22907	36492	0.61	6.0E-35	AB002364.1	NT	Human mRNA for KIAA0368 gene, partial cds
10107	23145	36743	2.87	6.0E-35	AB037786.1	NT	Human sapiens mRNA for KIAA1363 protein, partial cds
148	13373	26406	0.61	5.0E-35	AF154830.1	NT	Human sapiens carboxyl phosphate synthetase 1 mRNA, complete cds
1748	14893	27889	2.25	5.0E-35	X63392.1	NT	H.sapiens immunoglobulin kappa light chain variable region L14
2844	15558	29067	0.99	5.0E-35	AB007866.2	NT	Human sapiens mRNA for KIAA0406 protein, partial cds
3074	16250	29271	2.87	5.0E-35	6912639	NT	Human sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4529	17667	30663	1.72	5.0E-35	AF023268.1	NT	Human sapiens cdk2 kinase (CLK2), protein, coter, coter, glucocorticoidase (GBA), and melanin genes, complete cds; melanin pseudogene and glucocorticoidase pseudogenes; and thrombospondin3 (THBS3) gene, partial cds
8378	21459		4.25	5.0E-35	BE890992.1	EST_HUMAN	601431084F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21486	35015	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	z184f12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:428015 5'
1465	14619	27703	20.46	4.0E-35	BE257807.1	EST_HUMAN	SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249 ;
1862	15008	28114	11.21	4.0E-35	H61183.1	EST_HUMAN	601109710F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
7358	20437		1.87	4.0E-35	BE350127.1	EST_HUMAN	y188a07.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
8715	21795	35332	8.05	4.0E-35	AL046596.1	EST_HUMAN	6010901.x1 NCI_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
12088	25078	38786	2.5	4.0E-35	AF114186.1	NT	DKFZp434L148_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
1610	14763	27843	33.92	3.0E-35	BE268182.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZF) gene, complete cds
2408	15539		2.84	3.0E-35	AF224492.1	NT	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
5456	18656	31694	23.43	3.0E-35	BF433100.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31635	23.43	3.0E-35	BF433100.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
9689	22738		1.45	3.0E-35	AF223391.1	NT	Q9QZH7 F-BOX PROTEIN FBL2 ;
10378	23413	37022	1.5	3.0E-35	AW003063.1	EST_HUMAN	7n25a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
							Q9QZH7 F-BOX PROTEIN FBL2 ;
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							w03a05.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-35	N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1216	14376	27438	1.89	2.0E-35	T11909.1	EST_HUMAN	REPETITIVE ELEMENT
2262	15424	28358	4.56	2.0E-35	AB018413.1	NT	A971F Human Homo sapiens cDNA clone A971
2748	16655	28976	1.13	2.0E-35	AW665005.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
3386	16556	29570	1.08	2.0E-35	6912459	NT	h186a12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979168 3' similar to
3386	16556	29571	1.08	2.0E-35	6912459	NT	SW-TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12 ;
3647	16910		0.77	2.0E-35	AB020702.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4019	17178	30184	0.85	2.0E-35	BE247576.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4019	17178	30185	0.85	2.0E-35	BE247576.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4792	17927		3.01	2.0E-35	H49239.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
5700	18894	32186	1.93	2.0E-35	BF332417.1	EST_HUMAN	q19a12.f1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:274079 5'
7263	20336	33785	0.8	2.0E-35	BE832636.1	EST_HUMAN	QV0-BT0701-210400-169-504 BT0701 Homo sapiens cDNA
7263	20336	33786	0.8	2.0E-35	BE832636.1	EST_HUMAN	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
11036	24116	37749	2.93	2.0E-35	X59417.1	NT	CM2-MT0125-280700-297-G02 MT0125 Homo sapiens cDNA
12157	16556	29570	1.22	2.0E-35	6912459	NT	H. sapiens PROS-27 mRNA
12157	16556	29571	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32111	1.33	2.0E-35	BE904978.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12342	25247	32112	1.33	2.0E-35	BE904978.1	EST_HUMAN	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
12931	25614		7.22	2.0E-35	AL163210.2	NT	601496774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'
13056	16005	26372	1.74	2.0E-35	N88965.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
47	13266	26295	5.76	1.0E-35	AA631949.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
47	13266	26298	5.76	1.0E-35	AA631949.1	EST_HUMAN	REPETITIVE ELEMENT
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27001	35.82	1.0E-35	AW389473.1	EST_HUMAN	frnc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
832	14107		1.28	1.0E-35	T87947.1	EST_HUMAN	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2607	15730	28847	1.89	1.0E-35	7705994	NT	IL2-ST0162-131099-006-d12 ST0162 Homo sapiens cDNA
2826	15940	29050	1.34	1.0E-35	BE350127.1	EST_HUMAN	y83a01.1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115762 5' similar to
							SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
							h109g01.x1 NC1_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
							MER29 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2826	15940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	h00901.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MER28.b3
3212	16366	29397	1.87	1.0E-35	6006030	NT	MER29 repetitive element ;
3232	16406	29418	1.87	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCBE1L) mRNA
3232	16406	29419	1.87	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEP06 3'
4542	17680	30661	4.82	1.0E-35	7656905	NT	AV650422 GLC Homo sapiens cDNA clone GLCCEP06 3'
4542	17680	30662	4.82	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6627	18821	31896	1.48	1.0E-35	11526236	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7135	18561	31476	0.74	1.0E-36	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7135	18561	31476	0.74	1.0E-36	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-d07 ST0111 Homo sapiens cDNA
7652	20720	34198	0.99	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
7819	20874	34373	0.91	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9742	26661	36383	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAC33 Homo sapiens cDNA clone PLAC3300382 3'
9742	26661	36384	2.46	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAC33 Homo sapiens cDNA clone PLAC3300382 3'
10805	23838	37462	0.72	1.0E-35	BF589594.1	EST_HUMAN	naa06d06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10805	23838	37463	0.72	1.0E-35	BF589594.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE ;
12055	25036	38743	1.49	1.0E-35	AB028980.1	NT	naa06d06.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12055	25036	38744	1.49	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE ;
12062	25043		2.04	1.0E-35	AI525119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12405	26284		1.26	1.0E-35	11418110	NT	promma-7.D01.r b1 tumor Homo sapiens cDNA 5'
12806	25539		2.49	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
6131	19310	32650	0.67	8.0E-36	X78478.1	NT	607594833FT NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3638986 5'
9430	22504	36070	0.76	8.0E-36	AA348480.1	EST_HUMAN	B.bovis BBSo mRNA for schlerin
2997	16173	28182	1.53	7.0E-36	AW857579.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
3188	16363		5.25	7.0E-36	4957498	NT	CM1-CT0315-091299-063-d07 CT0315 Homo sapiens cDNA
5273	18392	31360	1.09	7.0E-36	Q27409	SWISSPROT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
5273	18392	31361	1.09	7.0E-36	Q27409	SWISSPROT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
7832	20887	34389	6.31	7.0E-36	U06672.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
7832	20887	34390	6.31	7.0E-36	U06672.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)
7832	20887	34390	6.31	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LIN
12570	25388	32040	27.38	7.0E-36	AF052051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exons L and LIN

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2060	15201	28315	1.92	6.0E-36	7706822	NT	Homo sapiens nirxurin 2 (NINJ2), mRNA
2490	15617		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3729	16850	29884	0.59	6.0E-36	BF516101.1	EST_HUMAN	U1H-BW1+ant-c-12-0-U1.at NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5446	16646	31624	7.17	6.0E-36	AI435169.1	EST_HUMAN	tf93b06.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126196 3' similar to gb:M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7258	20341	33792	3.03	6.0E-36	AW780143.1	EST_HUMAN	tf06h02.x1 NCL CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036827 3' similar to SW:IMA2_HUMAN
8853	21832	35471	4.62	6.0E-36	AF208161.1	NT	PS2292 IMPORTIN ALPHA-2 SUBUNIT;
10430	23465		0.63	6.0E-36	CT6927.1	EST_HUMAN	Homo sapiens synchyrin precursor, mRNA, complete cds
11841	24830	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	CT6927 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN:536C11 5'
140	13366	26399	15.16	5.0E-36	AJ271735.1	NT	tf95c09.x1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER0.b2
2809	15923	29033	21.08	5.0E-36	BE398436.1	EST_HUMAN	MER0 repetitive element;
3700	16861	29863	3.24	5.0E-36	AL163209.2	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
4909	18039	31029	1.31	5.0E-36	5729729	NT	Homo sapiens APIS-like 1 (APIBL1), mRNA
4909	18039	31029	1.31	5.0E-36	5729729	NT	Homo sapiens APIS-like 1 (APIBL1), mRNA
7986	21016	34628	0.59	5.0E-36	11070227	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12165	13366	26399	6.11	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
12458	25322	32095	2.36	5.0E-36		NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1677	14829	27913	1.36	4.0E-36	BE362574.1	EST_HUMAN	Homo sapiens PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
2297	15429	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
3435	16603	29622	1.1	4.0E-36	AW24772.1	EST_HUMAN	601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628386 5'
3435	16603	29622	1.1	4.0E-36	BE398299.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
4877	18008	30992	0.69	4.0E-36	AL163204.2	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604188 5'
5833	19024	32704	0.96	4.0E-36	RE4023.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604188 5'
6180	19356	32704	2.49	4.0E-36	11487041	NT	Homo sapiens chromosome 21 segment HS21C004
7831	20886	34388	1.78	4.0E-36	M33320.1	NT	Y19105.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:139713 6'
8752	21831	35370	1.45	4.0E-36	D87675.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
11235	24304	37941	3.13	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12476	25328		1.91	4.0E-36	11420516	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12520	25961		4.27	4.0E-36	AV763628.1	EST_HUMAN	z669c10.r1 Scores tests_NHT Homo sapiens cDNA clone IMAGE:743260 5'
714	13888	26934	2.93	3.0E-36	AF069810.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							AV763628 TP Homo sapiens cDNA clone TPGBH01 5'
							Homo sapiens neurodin II-alpha gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4624	17761	30743	7.5	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (jp1-pending), mRNA
11368	24429	38088	1.84	3.0E-36	BF036327.1	EST_HUMAN	601488531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW880376.1	EST_HUMAN	QVQ-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5903	18798	31848	2.88	2.0E-36	AF267747.1	NT	Mus musculus p47-phox gene, complete cds
6970	19166	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBB.28 5' end
6706	19864	33254	13.94	2.0E-36	T69629.1	EST_HUMAN	yc44807.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83508 5'
9888	22843	36212	0.94	2.0E-36	BF512784.1	EST_HUMAN	UJ-H-BW1-emu-a-11-0-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22697	36258	0.74	2.0E-36	4607848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9749	22697	36258	0.74	2.0E-36	4607848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
908	14083	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	18346	28474	1.71	1.0E-36	BE148523.1	EST_HUMAN	RC1-HT0217-131199-021-M07 HT0217 Homo sapiens cDNA
2212	18346	28475	1.71	1.0E-36	BE148523.1	EST_HUMAN	RC1-HT0217-131199-021-M07 HT0217 Homo sapiens cDNA
2275	19408	28538	1.83	1.0E-36	BF673761.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3425	18594		3.33	1.0E-36	AF159962.1	NT	Homo sapiens human endogenous retrovirus W proO6-19 protease (pro) gene, partial cds
5847	19037	32344	0.84	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6312	19484		4.27	1.0E-36	AI867714.1	EST_HUMAN	wb37c12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6519	19684	33055	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6519	19684	33056	1.9	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6820	19973	33381	0.72	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A229_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A229 5'
8147	21229	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	z051a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8147	21229	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z051a12.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
8243	21325	34841	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc80e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8243	21325	34842	0.76	1.0E-36	AA420467.1	EST_HUMAN	nc80e08.r1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8373	21454	34978	0.68	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9229	22307	35850	3.33	1.0E-36	AW103658.1	EST_HUMAN	xs82b07.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2814357 3'
10320	23355	36964	3.83	1.0E-36	BF364189.1	EST_HUMAN	QV3-NN1023-010800-189-H01 NN1023 Homo sapiens cDNA
10534	23569	37176	0.64	1.0E-36	AW855868.1	EST_HUMAN	RC3-CT0278-040500-017-a10 C10278 Homo sapiens cDNA

Page 281 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23698	37177	0.94	1.0E-36	AW865893.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
11180	24259	37895	2.55	1.0E-36	AW1897633.1	EST_HUMAN	GM3-NN0081-140400-147-H12 NN0081 Homo sapiens cDNA
11682	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	UIHF-BNO-ale-c-03-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
12048	25029		10.8	1.0E-36	11646801	NT	Homo sapiens P32227 protein (P32227), mRNA
12340	25245		2.93	1.0E-36	11418177	NT	Homo sapiens Ren GTPase activating protein 1 (RANGAP1), mRNA
12835	25556		5.78	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.76	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 urc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80807.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	9.0E-37	AW009277.1	EST_HUMAN	ws80807.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:2504245 3'
12819	25417		3.57	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5081-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	28624	1.4	8.0E-37	4757979	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
5363	18566		1.7	8.0E-37	BE598077.1	EST_HUMAN	CMG-UT0003-050800-503-009 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	ht09d01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5949	19135	32449	3.48	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element;
5998	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element;
8068	21150	34870	6.2	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
1313	14489		4.92	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
6228	18390	31320	3.04	7.0E-37	AW969823.1	EST_HUMAN	EST380899 IMAGE resequences, MAG1 Homo sapiens cDNA
10694	24073	37706	8.66	7.0E-37	A1817700.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
11134	24206	37831	1.89	7.0E-37	A1536702.1	EST_HUMAN	PTR5 repetitive element;
8634	21714	35251	0.59	6.0E-37	AF160689.1	NT	hm87g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2186140 3' similar to contains L1.b3 L1
12864	25575		2.3	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternative isoform (PCDH-alpha10) mRNA, complete cds
12884	25641		4.5	6.0E-37	AF202723.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo-olfr17-01 (OR17-01) pseudogene, complete cds
6218	19393	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Sad1 urc-84 domain protein 2 (SUN2) mRNA, partial cds
9218	18393	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST118035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	EST118035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
11160	24231		4.02	5.0E-37	7667117	NT	AV750211 NPC Homo sapiens cDNA clone NPOBGH09 5'
12335	25242		3.63	5.0E-37	AF149773.1	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2495	15622	28741	2.97	4.0E-37	AA702794.1	EST_HUMAN	z60b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
6416	15585	32947	0.68	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9556	22621	36192	0.56	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares_pancreatic_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1405442 3'
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L2418
2581	15706		1.54	3.0E-37	AW661150.1	EST_HUMAN	EST373222 MAGC resequences, MAGF Homo sapiens cDNA
3030	16206		4.02	3.0E-37	AW661150.1	EST_HUMAN	EST373222 MAGC resequences, MAGF Homo sapiens cDNA
5685	19170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067.1 647 (synonym: hibr1) Homo sapiens cDNA clone IMAGE:2373896 3' similar to TR:Q13537
7728	20790	34279	0.72	3.0E-37	A1749952.1	EST_HUMAN	Q13537 SIMILAR TO POGO ELEMENT. ;
392	13629	26666	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
302	13626	26667	0.89	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
1105	14270	27329	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'
2021	15162	28267	1.32	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3999	17199	30162	6.71	2.0E-37	4803210 NT	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4360	17503	30485	0.6	2.0E-37	4826685 NT	NT	Homo sapiens DEAD/1 (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6504	18703		0.9	2.0E-37	BF035327.1	EST_HUMAN	601485531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
6676	18835	33224	0.6	2.0E-37	11690617 NT	NT	Homo sapiens mouse thiamin pyrophosphokinase homodolog (TPK1), mRNA
6798	19953	33353	3.72	2.0E-37	AA346720.1	EST_HUMAN	EST52831 Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34790	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8185	21267	34791	0.47	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657 5'
8227	21309	34829	2.32	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12787	26770		1.44	2.0E-37	11417972 NT	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
13184	25770		4.19	2.0E-37	11417972 NT	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
2154	15290	28417	6.95	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C031
3267	19441		1.03	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
5055	18163	31158	2.34	1.0E-37	BF371719.1	EST_HUMAN	GVQ-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6127	19306		0.89	1.0E-37	7305360 NT	NT	Mus musculus obgolin (Obg), mRNA
8409	21460	35019	1.12	1.0E-37	BE546032.1	EST_HUMAN	601072416F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308 5'
8933	22012	35551	3.59	1.0E-37	AA171406.1	EST_HUMAN	zp21502.1 Stralagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1.12 L1 repetitive element ;

Page 283 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10837	24019	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (Hc1) processed pseudogene, complete cds
12671	25447		1.84	1.0E-37	BE771814.1	EST_HUMAN	CM3-F10096-140700-243-407 F10096 Homo sapiens cDNA
5898	19088	32398	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC66788), mRNA
1249	14408	27470	1.96	8.0E-38	11436055	NT	Homo sapiens Grb2-associated binder 2 (K1A00571), mRNA
2987	15692	28817	1.21	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NC1_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153992 5'
12735	14408	27470	1.37	8.0E-38	11436853	NT	Homo sapiens Grb2-associated binder 2 (K1A00571), mRNA
13210	26049		1.44	8.0E-38	AB002089.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	15387	28515	1.7	7.0E-38	AW972825.1	EST_HUMAN	EST384920 IMAGE sequences, MAGI Homo sapiens cDNA
3107	16283	28289	1.98	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3856348 5'
5709	18939	32192	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5709	18939	32193	0.98	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20567	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31861	1.78	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13926	26967	0.9	5.0E-38	AW971819.1	EST_HUMAN	EST383908 IMAGE sequences, MAGI Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3766	16957	29961	0.94	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3871	16957	29961	0.77	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
5288	15650	28774	0.98	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
7172	20305	33748	1.83	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3894074 5'
121	13351	26380	4.28	4.0E-38	Z25466.1	NT	B laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14346	27403	1.15	4.0E-38	Z25466.1	NT	B laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2167	15302		4.42	3.0E-38	AF003630.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3787	16948		1.49	3.0E-38	7549807	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3858	17116	30119	2.46	3.0E-38	P53538	SWISSPROT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRP4), mRNA
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6893	25838	33453	6.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7363	20471	33937	0.58	3.0E-38	AW302461.1	EST_HUMAN	W04401.X1 NC1_CGAP_Brn53 Homo sapiens cDNA clone IMAGE:2827009 3'
7763	20822	34313	6.53	3.0E-38	BF373564.1	EST_HUMAN	CM3-F10181-140700-241-r07 F10181 Homo sapiens cDNA
8851	21930	35469	2.11	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'
8881	21930	36470	2.11	3.0E-38	H85494.1	EST_HUMAN	yv88b04.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:249775 5'

Page 284 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24631		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12980	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
51	13280	26303	1.96	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14566	27639	3.66	2.0E-38	5902097	NT	Homo sapiens SIMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	zw00d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:70785 5' similar to SW:MA12 RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1-2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	zw00d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:70785 5' similar to SW:MA12 RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1-2-MANNOSIDASE ;
3622	16796		0.92	2.0E-38	AF070870.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17638	30824	18.99	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA
5252	18338	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	zw61d09.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:768128 5' similar to TR:G817957 G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5838	19026	32331	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
5838	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20849	34457	1.47	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8680	21760		4.47	2.0E-38	BE166980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
9096	22176	36719	0.48	2.0E-38	F06490.1	EST_HUMAN	HSC18F031 normalized infant brain cDNA Homo sapiens cDNA clone c-18f03
9165	22243	35786	1.26	2.0E-38	AF069765.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22406		1.36	2.0E-38	BE222256.1	EST_HUMAN	hu09g02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168130 3' similar to TR:O02710 O02710 GAG POLYPROTEIN ;
10665	23699	37309	1.67	2.0E-38	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11781	24771	38467	4.88	2.0E-38	BE1712790.1	EST_HUMAN	QV2-HT0698-080800-293-a05 HT0698 Homo sapiens cDNA
11939	24925	38826	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11939	24925	38827	2.86	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25186		6.21	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
12246	25187		1.26	2.0E-38	AB012729.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12546	26370		3.36	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
12559	26381	32073	4.81	2.0E-38	H55641.1	EST_HUMAN	CHR220360 Chromosome 22 exon Homo sapiens cDNA clone c22_788 5'
12632	26425		2.87	2.0E-38	S74906.1	NT	E1 beta-pyruvate dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
13174	25762		1.36	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

Page 285 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.98	1.0E-38	AA401570.1	EST_HUMAN	zu62b02.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:742639 5' similar to contains element
2055	15193	28310	2.82	1.0E-38	4885288	NT	MER19 repetitive element;
2077	15217	28336	1.33	1.0E-38	7661869	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2564	15689	28815	1.89	1.0E-38	AF270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4271	17416	30405	0.93	1.0E-38	AB037863.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
							Homo sapiens mRNA for KIAA1442 protein, partial cds
4439	17579	30558	0.6	1.0E-38	4506016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4444	17584	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4444	17584	30564	2.15	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4719	17854	30837	1.08	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5268	18387	31355	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8161	19327	32872	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
8161	19327	32873	4.59	1.0E-38	7305360	NT	Mus musculus otogelin (Otog), mRNA
7663	20635	34110	2.65	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
9354	22429	35987	0.58	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9810	22665	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	h09g01.x1 NC1_CGAP_K1d13 Homo sapiens cDNA clone IMAGE:3148266 3' similar to contains MER29.53
12403	26877		4.79	1.0E-38	AL183284.2	NT	MER29 repetitive element;
12116	25086	38801	1.64	8.0E-39	AA112438.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
55	13284	26309	4.93	8.0E-39	4502812	NT	znt2707.r1 Streptococcus pneumoniae (#937208) Homo sapiens cDNA clone IMAGE:526885 5'
1425	14576	27652	1.3	8.0E-39	4758229	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 18kD (ATP9C) mRNA
							Homo sapiens estrogen receptor-binding fragment-associated gene 9 (ESAG9) mRNA
1876	16020		1.8	8.0E-39	AB23404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (ESAG9) mRNA
2160	16288	28421	7.08	7.0E-39	AL183227.2	NT	wh53710.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to TR:P87890 P87890
11047	24124	37758	2.4	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN ;
13064	25697		2.24	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1032	14201	27259	1.64	6.0E-39	AF003528.1	NT	QY1-BT0631-040800-357-02 BT0631 Homo sapiens cDNA
							7634c03.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R161.6
							CE00828 ;
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3050	16228	29247	9.33	5.0E-39	AI760154.1	EST_HUMAN	at6b04.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q16408
12720	25478		1.53	6.0E-39	11420289	NT	Q16408 NEUTRAL PROTEASE LARGE SUBUNIT : contains LTR7.1 LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

Page 286 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
564	13766	26762	4.39	4.0E-39	AB016610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
3663	16826	20835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5950	19136	32450	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5950	19136	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA682949.1	EST_HUMAN	aa82g04.s1 Stralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9530	22596	36165	0.46	4.0E-39	D84116.1	NT	ORF.b1 ORF repetitive element ;
9530	22596	36166	0.46	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494		6.38	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12884	25598		2.56	4.0E-39	BE836452.1	EST_HUMAN	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
48	13287	26297	11.98	3.0E-39	AA631949.1	EST_HUMAN	QVQ-FN0083-260600-278-c06 FN0063 Homo sapiens cDNA
48	13287	26298	11.98	3.0E-39	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	26299	11.98	3.0E-39	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12238	25180	36348	6.59	3.0E-39	AJ084557.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12238	25180	36349	6.59	3.0E-39	AJ084557.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12284	25212		5.72	3.0E-39	H37903.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTES.TINE ;
920	14095		7.78	2.0E-39	BE409203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTES.TINE ;
935	14110		11.55	2.0E-39	AI525119.1	EST_HUMAN	Y551c06.s1 Soares retina N264HR Homo sapiens cDNA clone IMAGE:190954 3'
1057	14223		3.9	2.0E-39	AF000573.1	NT	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1560	14713		33.59	2.0E-39	AW372318.1	EST_HUMAN	promma-7.D01.7 bvtumor Homo sapiens cDNA 5'
2030	15171	28279	4.48	2.0E-39	AA720574.1	EST_HUMAN	Homo sapiens homocitissate 1,2-dioxygenase gene, complete cds
2692	15812	28928	1.89	2.0E-39	AL163248.2	NT	PMX-BT0340-211269-003-d02 BT0340 Homo sapiens cDNA
4523	17662	30649	1.74	2.0E-39	BF370207.1	EST_HUMAN	THR repetitive element ;
5608	18803	31866	4.45	2.0E-39	AA509880.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
7526	20596	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
7702	20767	34252	0.68	2.0E-39	AL163202.2	NT	ng86f03.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:941653
7702	20767	34252	0.68	2.0E-39	AL163202.2	NT	zr06f02.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
8506	21586	36120	0.63	2.0E-39	AF078776.1	NT	Homo sapiens chromosome 21 segment HS21C002
9826	22666		0.79	2.0E-39	AI686690.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
11716	24756	39452	2.13	2.0E-39	D86964.1	NT	Rattus norvegicus putative four repeat lcn channel mRNA, complete cds
1543	14695	27774	2.83	1.0E-39	AJ006345.1	NT	Human mRNA for KIAA0205 gene, partial cds

Page 287 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1543	14695	27775	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1561	14714	27791	5.96	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
1763	14912	28007	1.14	1.0E-39	H55224.1	EST_HUMAN	CHR220183 Chromosome 22 exon Homo sapiens cDNA clone C22_206 5'
4782	17917	30903	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW951995.1	EST_HUMAN	EST384065 MAGE resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
5474	18973	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5474	18973	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T80876.1	EST_HUMAN	yt26g06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element: contains LTR1 repetitive element:
5781	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
5781	18973	32279	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6965	20193	34069	1.95	1.0E-39	11438736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7521	20594	34069	2.16	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	35382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNAse K6)
11165	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
669	13781	26786	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27488	16.02	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3885	17044	30043	1.18	9.0E-40	4503784	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.99	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4486	17606	30884	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase 1-3) (USP13) mRNA
3108	16282	29298	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43	8.0E-40	BE396541.1	EST_HUMAN	60128958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3819166 5'
7894	20946	34452	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear: gene encoding mitochondrial protein, complete cds
7894	20946	34453	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear: gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

Page 288 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	15904	29011	9.91	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2788	15904	29012	9.91	6.0E-40	AA361276.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6060	19242		1.85	6.0E-40	BE504786.1	EST_HUMAN	h24g01.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3210480 3'
6275	19449		1.38	6.0E-40	7661989	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7075	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7075	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
10182	23219	36812	6.09	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2670	15791	28907	2.75	6.0E-40	AL183285.2	NT	Homo sapiens chromosome 21 segment HS21Q085
1925	15088	28173	3.81	4.0E-40	AI686005.1	EST_HUMAN	tt81b01.x1 NCL_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR-O73505 O73505 POL PROTEIN.;
2178	15310		6.81	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4508	17647	30635	7.2	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	21152	34672	0.84	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	nv34610.1 NCL_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
9255	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
9255	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10935	24036	37671	1.95	4.0E-40	AW841855.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4250	17398	30385	0.9	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4993	18122		0.83	3.0E-40	AA05518.1	EST_HUMAN	z18109.s1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:377163 3'
6592	19752	33137	0.66	3.0E-40	4506736	NT	Homo sapiens ribosomal protein S9 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
6777	19932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8575	21656	35197	3.86	3.0E-40	5484167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
9169	2247	35790	1.27	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9412	22486	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D86954.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24600	38276	9.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI233036.1	EST_HUMAN	gg52h08.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1838847 3'
817	13998		5.58	2.0E-40	AW303868.1	EST_HUMAN	xt24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761088 3' similar to SW-RS5_MOUSE P87461 40S RIBOSOMAL PROTEIN S6.;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1988	15130	28233	2.6	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1988	15130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropath) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	15269	28389	1.39	2.0E-40	AI988562.1	EST_HUMAN	w80a11.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2238	15371	28500	2.21	2.0E-40	5453592	NT	ZINC FINGER PROTEIN.1
2764	15871		1.66	2.0E-40	BE276932.1	EST_HUMAN	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
3186	16371	28378	5.27	2.0E-40	5453592	NT	501121597F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348784 5'
5021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
606	14081		1.2	1.0E-40	AA225989.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2686	15806	28922	1.82	1.0E-40	BF036881.1	EST_HUMAN	nc03609.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2760	15887		3.88	1.0E-40	BE018348.1	EST_HUMAN	601480375F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863803 5'
3370	16542		2.14	1.0E-40	4607142	NT	b679a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92158 Q92158
4733	17868	30851	3.89	1.0E-40	4808012	NT	SYNTAXIN 17.1
6385	19554	32812	0.68	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens sorting nexin 3 (SNX3) mRNA
6385	19554	32913	0.68	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	zh78f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7381	20459	33922	0.82	1.0E-40	P26808	SWISSPROT	rl42f04.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:985187 3'
11157	24228	37858	5.41	1.0E-40	AU148345.1	EST_HUMAN	rl42f04.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:985187 3'
11983	24978	38583	1.49	1.0E-40	AA614255.1	EST_HUMAN	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H 1]
11983	24978	38584	1.49	1.0E-40	AA614255.1	EST_HUMAN	AU148345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
12079	25059		1.86	1.0E-40	AL163249.2	NT	np09h03.s1 NCI CGAP_P3 Homo sapiens cDNA clone IMAGE:1116881 similar to TR:G1136406
12687	26032		5.64	1.0E-40	BF334112.1	EST_HUMAN	G1136406 KIAA0173 PROTEIN.1
3806	17055	30064	0.59	9.0E-41	W01596.1	EST_HUMAN	np09h03.s1 NCI CGAP_P3 Homo sapiens cDNA clone IMAGE:1116881 similar to TR:G1136406
8106	21188	34708	1.6	8.0E-41	AL163203.2	NT	G1136408 KIAA0173 PROTEIN.1
851	16024	27089	2.52	7.0E-41	AI934364.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
851	16024	27090	2.52	7.0E-41	AI934364.1	EST_HUMAN	np04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
							wp04h04.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'

Page 290 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5379	18581	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6132	15311	32651	2.71	7.0E-41	11419208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6483	19630	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
1171B	24758	38453	2.06	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNIG10) mRNA
11931	24917	38620	1.41	7.0E-41	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028		8.58	7.0E-41	11417972	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
291	13508	26543	1.13	6.0E-41	AB037163.1	NT	Homo sapiens DSCR55 mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
615B	21240	34760	1.31	6.0E-41	BF513783.1	EST_HUMAN	UI-HBW1-amp-b-03-q-UI.s1 NCI CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
1315B	25952		1.25	6.0E-41	AW873637.1	EST_HUMAN	hs4408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to containo
1845	14591	28092	1.37	5.0E-41	T62628.1	EST_HUMAN	MER32.b3 MER32 repetitive element;
4223	17371		1.17	5.0E-41	4855636	NT	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:76628 3'
6678	19837		2.34	5.0E-41	BE087042.1	EST_HUMAN	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
402	13559		1.89	4.0E-41	BE156318.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
1122	14287	27342	2.37	4.0E-41	AU119344.1	EST_HUMAN	QV0-HT0367-130200-114-g09 HT0367 Homo sapiens cDNA
1442	14595	27670	14.6	4.0E-41	AI027117.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
1442	14595	27671	14.6	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
1454	14607	27687	3.34	4.0E-41	AB006881.1	NT	TR:Q00597 Q00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
1665	14817	27900	7.72	4.0E-41	AI500406.1	EST_HUMAN	ow45e06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to
2953	16130	29144	5.02	4.0E-41	AJ229041.1	NT	TR:Q00597 Q00597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element;
2953	16130	29145	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
4262	17407	30393	2.13	4.0E-41	X92695.1	EST_HUMAN	tr96e04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1
6638	19797		1.8	4.0E-41	AF758295.1	EST_HUMAN	OFR repetitive element;
9895	22935	36519	5.06	4.0E-41	BF304683.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11958	24064		7.38	4.0E-41	AV710480.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
							AV758295 BM Homo sapiens cDNA clone BMFBHC06 5'
							601880096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
							AV710480 Cu Homo sapiens cDNA clone CUAACC07 5'

Page 291 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12900	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADGARE02 5'
13110	26726	31942	1.61	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
970	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cdo
4455	17595	30575	4.03	3.0E-41	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5609	18804	31869	11.76	3.0E-41	X87889.1	NT	H. sapiens mRNA for putative p64 CLCP protein
6511	19676	33046	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7967	21017	34529	0.71	3.0E-41	RS4765.1	EST_HUMAN	y75d08.r1 Soares breast 2NH8at Homo sapiens cDNA clone IMAGE:154578 5'
12119	25099	38804	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12119	25099	38805	1.36	3.0E-41	AW994941.1	EST_HUMAN	QV0-BN0040-170300-160-H08 BN0040 Homo sapiens cDNA
12198	25153		1.98	3.0E-41	AA6039788.1	EST_HUMAN	af17f10.st Soares testis_NHT Homo sapiens cDNA clone IMAGE:1031847 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	601782340F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026031 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15163	28258	2.17	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2293	15425	28559	1.26	2.0E-41	D88962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28806	5.52	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	29591	0.69	2.0E-41	AA449549.1	EST_HUMAN	z08b04.r1 Soares_tad_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:785839 5'
3641	17100	30087	0.69	2.0E-41	5032106	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17878	30862	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17878	30863	1.23	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5656	18850	32132	0.6	2.0E-41	AA584576.1	EST_HUMAN	nc12a07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb.X52851_ma1
6763	19919	33314	0.88	2.0E-41	4504778	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7850	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8269	21341	34858	1.36	2.0E-41	M86044.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8269	21341	34869	1.36	2.0E-41	M86044.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8268	21340	34891	1.42	2.0E-41	AA328265.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
9176	22263	35768	1.65	2.0E-41	P52742	SWISSPROT	EST31723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9617	22672	36241	0.66	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9617	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11776	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
13149	25747		1.2	2.0E-41	11420518	NT	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3276	16460	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'

Page 292 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3278	16450	29471	1.05	1.0E-41	BE969735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3949803 5'
4689	17824	30811	9.46	1.0E-41	6078468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9618	22673	36243	1.57	1.0E-41	A1217688.1	EST_HUMAN	q75c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
12334	23241		1.87	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	RCO0-H70613-210300-032-g01 HT0613 Homo sapiens cDNA
8975	22450	35011	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9375	22450	35012	2.81	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
475	13670	25702	5.34	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2178	15311	28439	8.53	8.0E-42	AB028898.1	NT	h07c02.st NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304
12375	28035		30.09	8.0E-42	AA493896.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG MRNA ;
12398	25904		2.91	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12
955	14128		2.23	7.0E-42	AL153285.2	NT	OFR repetitive element ;
8666	21746		0.5	7.0E-42	R10983.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9445	22561	36124	1.32	7.0E-42	AI204393.1	EST_HUMAN	yf38g04.r1 Soares_fetal_liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:128174 5'
1903	15046	28155	3.24	6.0E-42	AF012872.1	NT	qf58g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
1903	15046	28156	3.24	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
							Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2363	15494		3.6	6.0E-42	AW238656.1	EST_HUMAN	xp28f03.x1 NCI_CGAP_JH110 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.L1 L1
5584	18779	31824	1.66	6.0E-42	AB028990.1	NT	repetitive element ;
5834	18779	31824	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
138	13384		8.34	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
451	13647	26883	1.96	5.0E-42	BE217913.1	EST_HUMAN	h031e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
488	13694		3.05	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
500	13695		1.14	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6825	19878	33385	0.94	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6825	19878	33386	0.94	5.0E-42	11433083	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6941	20254	33691	2.57	5.0E-42	11417957	NT	Homo sapiens myobulatin related protein 3 (MTMR3), mRNA
7351	20430	33892	1.55	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8978	22057	35589	2.88	5.0E-42	AB037716.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431188	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431188	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24315	37653	1.77	5.0E-42	8823182	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
772	13953	27003	5.6	4.0E-42	AF055066.1	NT	Homo sapiens MHC class 1 region
1091	14256	27312	1.82	4.0E-42	AF189011.1	NT	Homo sapiens ribonuclease III (RN3), mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4343	17486	30489	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4364	17507	30488	4.87	4.0E-42	4506486	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4), mRNA
4706	17941	30825	17.64	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5265	18404	31372	0.93	4.0E-42	7661035	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	CVIC-BT0282-171299-127-503 BT0282 Homo sapiens cDNA
10884	23968	37597	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
10884	23968	37696	2.32	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AI432225.1	EST_HUMAN	U11402.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24695	38387	1.69	4.0E-42	BF036327.1	EST_HUMAN	607466531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1812	14663	27760	3.79	2.0E-42	BF376634.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2466	15593	28718	1.6	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB08 5'
2463	15610		4.24	2.0E-42	AW88344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2466	15623	28742	3.6	2.0E-42	AW25059.1	EST_HUMAN	2879263 3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2818283 3'
5876	10065	32372	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
5876	10065	32373	11.82	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences, MAGC Homo sapiens cDNA
6892	20044	33462	0.9	2.0E-42	AI052566.1	EST_HUMAN	ow83405.x1 Scarsa fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1863417 3'
10046	23084	36685	1.28	2.0E-42	BE538918.1	EST_HUMAN	607081284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23295	36892	0.64	2.0E-42	P81649	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
10260	23295	36893	0.64	2.0E-42	P81646	SWISSPROT	RIBONUCLEASE K3 (RNASE K3)
12037	25019	38723	1.53	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
762	13632	26977	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW265809.1	EST_HUMAN	U114-B1-eth-e-04-0-J1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1128	14280	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14200	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	16033	27498	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1271	18033	27488	11.99	1.0E-42	AF087186.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1735	14884	27977	1.15	1.0E-42	11423219	NT	encoding mitochondrial protein, complete cds
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens rec (LOC51201), mRNA
2009	13733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens PDNP1 gene, exon 17
3029	18205	28228	0.15	1.0E-42	4505524	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
3789	19960	29984	3.31	1.0E-42	7662027	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3895	17054	30054	1.11	1.0E-42	5031810	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4036	17192	30202	0.99	1.0E-42	AL163280.2	NT	Homo sapiens Gdgi vesicular membrane trafficking protein p18 (BET1) mRNA
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C067
4716	17851	30834	0.81	1.0E-42	AW813617.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
4867	18000	30984	2.37	1.0E-42	5803122	NT	RC3-ST0197.161089-012-a03 ST0197 Homo sapiens cDNA
4867	18000	30985	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4801	18031	31020	6.13	1.0E-42	4506758	NT	Homo sapiens proteasome inhibitor (P31), mRNA
11440	24501	38169	1.38	1.0E-42	BE408611.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
10281	23326	36929	8.16	9.0E-43	4757969	NT	607304125F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:368310 5'
669	13855	26893	20.77	8.0E-43	AV736824.1	EST_HUMAN	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
669	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26938	5.12	8.0E-43	8923276	NT	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26939	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
718	13900	26940	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5816	18006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
3731	16892	28896	7.48	7.0E-43	AW246442.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
8968	22047		3.98	7.0E-43	AI936748.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
1374	14529		11.62	6.0E-43	AA491890.1	EST_HUMAN	2822251.5prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2822251 5'
2657	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	wp69b01.x1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
4893	18082	31068	252.27	6.0E-43	AI421540.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element ;
6441	19608	32871	2.53	6.0E-43	9955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA

Page 285 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	20101	33518	1.8	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910881 3' similar to contains MER1.8 MER1 MER1 repetitive element;
10056	23094	36888	1.77	6.0E-43	AA195154.1	EST_HUMAN	z35e03.r1 Soares_NHIMP.L1 S1 Homo sapiens cDNA clone IMAGE:965410 5' similar to TR:G528641
11363	24424		2.45	6.0E-43	AL119158.1	EST_HUMAN	G528641 DB1, COMPLETE CDS: contains element PTR7 repetitive element;
145	13370		1.82	5.0E-43	AL163213.2	NT	DKFZp761L1712_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761L1712 5'
515	13706	26736	3.4	5.0E-43	AA382780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2808	16066	29100	1.59	5.0E-43	AV732578.1	EST_HUMAN	EST96033 Testis 1 Homo sapiens cDNA 5' end
6435	20096	33612	0.9	5.0E-43	AI613509.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANC08 5'
7043	20096	33612	0.89	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260492 3'
8381	21462	34985	0.64	5.0E-43	AA442271.1	EST_HUMAN	tw22e07.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260492 3'
8381	21462	34988	0.64	5.0E-43	AA442271.1	EST_HUMAN	z64a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9080	22160		0.73	5.0E-43	H74277.1	EST_HUMAN	z64a03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9564	22706	36272	4.09	5.0E-43	AA465288.1	EST_HUMAN	y449g12.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:226610 6'
10609	23643	37251	2.6	5.0E-43	AI733244.1	EST_HUMAN	aa33d08.r1 NCI_CGAP_G051 Homo sapiens cDNA clone IMAGE:816055 5'
10651	23685	37266	1.02	5.0E-43	AL049110.1	EST_HUMAN	cc52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568810 3' similar to TR:P00591 P00591
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	PV14 GENE.;
11213	24282	37921	2.24	5.0E-43	W29011.1	EST_HUMAN	DKFZp434D0119_r1 434 (synonym: htae3) Homo sapiens cDNA clone DKFZp434D0119
995	16987	27227	4.4	4.0E-43	AF003628.1	NT	MR2-SN0007-200400-004-c02 SN0007 Homo sapiens cDNA
5373	18576	31444	1.09	4.0E-43	AI058338.1	EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
6469	19665	33028	0.68	4.0E-43	6996009	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7280	20363		1.6	4.0E-43	11416768	NT	cy47h03.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:1666013 3'
8371	21462	34975	5.18	4.0E-43	AI244341.1	EST_HUMAN	Homo sapiens glycyl-IRNA synthetase (GARS), mRNA
8371	21462	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
10521	23556	37164	1.02	4.0E-43	6009587	NT	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868354 3' similar to contains MER10.13
12311	25227		2.7	4.0E-43	R20950.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868354 3' similar to contains MER10.13
13030	25898		1.33	4.0E-43	AI436093.1	EST_HUMAN	q176a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868354 3' similar to contains MER10.13

Page 296 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14080	27971	2.52	3.0E-43	X97869.1	NT	H. sapiens gene encoding La autoantigen
2120	16055	28377	1.1	3.0E-43	R83422.1	EST_HUMAN	yp8201.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:183945 5' similar to contains MSR1 repetitive element;
3682	16825	29834	1.22	3.0E-43	S68002.1	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4405	17548	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	h55608.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6014	19198	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	19654	33016	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6487	19654	33017	1.56	3.0E-43	7305360	NT	Mus musculus otogelin (Otog), mRNA
6867	20019	33428	5.09	3.0E-43	U65487.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa8811.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR.12 THR repetitive element;
9020	22059	35639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10068	23106	36709	0.68	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
12028	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
188	13410		7.24	2.0E-43	AI190764.1	EST_HUMAN	q081c09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13 PTR7 PTR7 repetitive element;
6604	19764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
6604	19764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Bm41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7426	20603	33973	1.29	2.0E-43	AW207390.1	EST_HUMAN	UI-H-B11-af1-a-09-q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
8503	21584		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11478	24535		4.75	2.0E-43	T03007.1	EST_HUMAN	FBTG5 Fetal brain, Stragene Homo sapiens cDNA clone FBTG5 3' end similar to LINE-1
1681	14833	27917	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1681	14833	27918	2.95	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27985	4.12	1.0E-43	AL163284.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2786	15902	20009	4.73	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5526	18723	31740	0.88	1.0E-43	4865544	NT	602022313F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4167668 6'
6744	19900	33291	6.84	1.0E-43	4507168	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19900	33292	6.84	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7106	18553	31488	1.19	1.0E-43	R19751.1	EST_HUMAN	y840e01.r1 Soares infant brain T1B1 Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38 ;
8117	21199	34720	0.6	1.0E-43	AF175265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8256	21338		2.17	1.0E-43	AF189490.1	NT	Homo sapiens 8q22.1 region and MTG8 (OBFA211) gene, partial cds
9037	22116	35659	28.54	1.0E-43	AW963675.1	EST_HUMAN	EST375749 IMAGE resequences, MAGH Homo sapiens cDNA
10498	23533	37143	0.56	1.0E-43	AW953229.1	EST_HUMAN	EST365299 IMAGE resequences, MAGH Homo sapiens cDNA
11209	24275	37812	5.81	1.0E-43	AI984981.1	EST_HUMAN	w87h01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494708 3'
11647	24726	38418	3.05	1.0E-43	11424378	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
12248	25189		2.29	1.0E-43	AL137964.1	EST_HUMAN	DKF26781D1015 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781D1015 5'
12550	25373	32071	3.16	1.0E-43	AI675416.1	EST_HUMAN	w89b04.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
12805	25538	32013	3.21	9.0E-44	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
913	14088	27153	5.32	8.0E-44	AI222985.1	EST_HUMAN	qf23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845562 3'
913	14088	27154	5.32	8.0E-44	AI222985.1	EST_HUMAN	qf23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845562 3'
8736	21615	35350	2.89	8.0E-44	X94354.1	NT	H. sapiens DNA for Cere cGMP-PDE gene
10546	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
10546	23580	37190	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C), mRNA
11436	24497	38164	2.87	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
11887	24972	38877	1.76	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12501	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
12544	25735	31946	2.17	8.0E-44	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
12946	25838	31760	1.85	8.0E-44	11418088	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
13126	25735	31946	2.29	8.0E-44	11418088	NT	Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
676	13862		1.13	7.0E-44	R06035.1	EST_HUMAN	y89e01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124920 5'
2307	15438	28573	1.19	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29228	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3865	17123	30126	2.71	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4356	17499	30479	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4356	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21480	34983	2.39	7.0E-44	AU169839.1	EST_HUMAN	AU169839 Y9AA1 Homo sapiens cDNA clone Y9AA1000486 3'
6228	19404	32754	0.67	6.0E-44	Z20946.1	EST_HUMAN	HSAAADEYU P_Human fetal Brain Whole tissue Homo sapiens cDNA
314	13530		4.25	5.0E-44	AJ289980.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene
342	13563		2.42	5.0E-44	AJ289980.1	NT	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTFL1 gene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34673	4.12	5.0E-44	AI588523.1	EST_HUMAN	ht40d02.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.H
9884	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3501	10668	29678	4.27	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5128	18253		0.89	4.0E-44	AI435225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7639	20708	34187	0.87	4.0E-44	BE893178.1	EST_HUMAN	ht11d02.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8468	21547	35077	0.88	4.0E-44	L21948.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8079	22158		0.71	4.0E-44	BE178618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11513	24570	38247	5.84	4.0E-44	U60878.1	NT	RC3-HT0585-010400-023-008 HT0585 Homo sapiens cDNA
1827	14975		1.5	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3167	18342	29350	5.11	3.0E-44	AA168851.1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
7670	21020	34533	0.65	3.0E-44	BE894820.1	EST_HUMAN	zp18p05.11 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:608777 5'
9719	22784	36355	0.63	3.0E-44	AF003273.1	NT	601510547F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1074	14240	27286	1.43	2.0E-44	4826685	NT	Sus scrofa domestica submandibular apomucin mRNA, complete cds
1074	14240	27287	1.43	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1234	14363	27455	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1340	14496	27568	8.82	2.0E-44	AF133588.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	hw14g06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2219	15353	28484	9.07	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2605	15728		1.26	2.0E-44	4507592	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2642	15785	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2676	15796		2.3	2.0E-44	5901833	NT	Human mRNA for integrin alpha subunit, complete cds
3559	16724	29740	1.34	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4892	17827	30813	1.75	2.0E-44	AW884378.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6220	18395	32744	1.75	2.0E-44	11448901	NT	PM4-SN0016-120500-003-ed04 SN0016 Homo sapiens cDNA
6996	18515	31507	2.18	2.0E-44	AF038986.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7572	20644	34121	3.8	2.0E-44	11419228	NT	Homo sapiens general transcription factor 2i (GTF2i) mRNA, alternatively spliced product, complete cds
7572	20644	34122	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8819	21898	35437	1.8	2.0E-44	BE389058.1	EST_HUMAN	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
							601285914F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813986 5'

Page 299 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12152	26122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Bay/α-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.58	2.0E-44	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
63	13292	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Misschep/NIK-related kinase (MINK), mRNA
63	13292	26307	6.24	1.0E-44	7657334	NT	Homo sapiens Misschep/NIK-related kinase (MINK), mRNA
594	13784	26804	1.63	1.0E-44	AW853132.1	EST_HUMAN	RC1-CT0249-030300-028-H12 CT0249 Homo sapiens cDNA
1224	14384		1.98	1.0E-44	AW894803.1	EST_HUMAN	RC1-EN0039-110300-012-601 BN0039 Homo sapiens cDNA
1605	14758		8.08	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2299	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	z653d02.r1 Soares_t01us_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element
2299	15431	28564	6.17	1.0E-44	AA434554.1	EST_HUMAN	z653d02.r1 Soares_t01us_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR13 THR repetitive element
2818	15932	28043	1.74	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor (IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T84 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel α
3818	16978		3	1.0E-44	AA455688.1	EST_HUMAN	aa01c08.s1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811884 3'
5221	18343	31314	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequences, MAGJ Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequences, MAGJ Homo sapiens cDNA
9648	21927	35466	0.96	1.0E-44	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
9227	22305	35848	0.56	1.0E-44	AJ337183.1	EST_HUMAN	qx88g07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2008628 3'
11284	24333		4.13	1.0E-44	AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBYE03 5'
11820	24809	38505	3.47	1.0E-44	10082064	NT	Homo sapiens Sush domain (SCR repeat) containing (BK65A8.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846987.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4701	17836	30821	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4701	17836	30822	0.98	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6787	18942	33340	1.41	9.0E-45	AB028212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2591	15716	28834	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5193	18315	31283	9.63	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
1583	14735		2.36	8.0E-45	AI075425.1	EST_HUMAN	w889c06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2313802 3' similar to contains L1.1 L1 repetitive element

Page 300 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to
12911	26154		1.89	6.0E-45	11418213	NT	SW:RT3A_HUMAN P40429 60S RIBOSOMAL PROTEIN L19A ;
915	14090		1.71	5.0E-46	AL163203.2	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
2058	15199	28313	4.42	5.0E-45	BF336927.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3281	19455	28477	2.87	5.0E-45	AI523766.1	EST_HUMAN	CMA-CN0044-180200-515-F01 CN0044 Homo sapiens cDNA
5829	19823	31897	8.95	5.0E-45	AA397781.1	EST_HUMAN	tg94f07.x1 NCL CGAP_GL1.1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE
6143	19321	32664	1.09	5.0E-45	Y18933.1	NT	P09084 PAIRED BOX PROTEIN PAX-1 ;
6143	19321	32665	1.09	5.0E-45	Y18933.1	NT	z472d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element
6190	19366	32714	0.92	5.0E-45	AB022318.1	NT	TAR1 repetitive element ;
6190	19366	32715	0.92	5.0E-45	AB022318.1	NT	Homo sapiens MCP-1 gene and enhancer region
6318	19490	32847	0.87	5.0E-45	11496298	NT	Homo sapiens MCP-1 gene and enhancer region
6318	19490	32848	0.87	5.0E-45	11496298	NT	Homo sapiens MCP-1 gene and enhancer region
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens MCP-1 gene and enhancer region
9241	22318	35861	1.45	5.0E-45	4759223	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
11997	24982	36888	2.5	5.0E-45	8923698	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
1167	14330	27385	6.3	4.0E-45	X98826.1	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
2365	15496	28622	2.15	4.0E-46	BE286622.1	EST_HUMAN	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
9157	22235		0.81	4.0E-45	AA226220.1	EST_HUMAN	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
12168	26089	31859	1.36	4.0E-45	T1435947	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
3411	16580		0.93	3.0E-45	T71480.1	EST_HUMAN	60119440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3539425 5'
4199	16580		1.03	3.0E-45	T71480.1	EST_HUMAN	repetitive element ;
6368	19538	32895	1.34	3.0E-45	6753651	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
6366	19536	32896	1.34	3.0E-45	6753651	NT	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
8845	21725	35610	1.76	3.0E-45	AV723976.1	EST_HUMAN	y035f07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110245 5'
8991	22070	37169	4.31	3.0E-45	4758451	NT	Mus musculus dyx1in, axon, heavy chain 11 (Dnahc11), mRNA
10515	23550	37169	7.52	3.0E-45	AL163227.2	NT	Mus musculus dyx1in, axon, heavy chain 11 (Dnahc11), mRNA
10515	23550	37169	7.52	3.0E-45	AL163227.2	NT	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
13040	26078		3.45	3.0E-45	X89211.1	NT	Homo sapiens golgi autoantigen, golgi subfamily a, 2 (GOLGA2) mRNA
2572	15697		3.12	2.0E-46	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C027
3097	18273	29287	0.92	2.0E-45	AJ243213.1	NT	Homo sapiens DNA for endogenous retroviral like element
							Homo sapiens chromosome 21 segment HS21C018
							Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6651	19810	33188	5.45	2.0E-45	LO1665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7786	20842	34334	1.1	2.0E-45	BE782184.1	EST_HUMAN	601467793F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870838 5'
8610	21690	35228	0.91	2.0E-45	AW834834.1	EST_HUMAN	RCQ-L70001-150200-032-311 LT0001 Homo sapiens cDNA
9784	22824	36402	0.51	2.0E-45	AI636786.1	EST_HUMAN	ts66a01.x1 NCI_COAP_K188 Homo sapiens cDNA clone IMAGE:2232552 3'
11042	25867	37754	12.66	2.0E-45	BE934350.1	EST_HUMAN	MFO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa87712.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11784	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	TR-G1144569 G1144569 R-SLY1.
11794	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	xp72803.x1 NCI_COAP_OV40 Homo sapiens cDNA clone IMAGE:2745888 3'
13087	25710		2.73	2.0E-45	11418157	NT	xp72803.x1 NCI_COAP_OV40 Homo sapiens cDNA clone IMAGE:2745888 3'
128	13617		1.22	1.0E-45	BE389855.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
422	13617		1.99	1.0E-45	BE389855.1	EST_HUMAN	601284390F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806183 5'
485	13679	26714	1.02	1.0E-45	4506412	NT	601284390F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3806183 5'
1201	14363	27423	1.68	1.0E-45	7657280	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
3172	16347	29364	10.41	1.0E-45	U32186.1	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3581	16749	29784	0.85	1.0E-45	8659558	NT	Homo pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3684	16827	29836	0.89	1.0E-45	AB046811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C2orf4), mRNA
4599	17736	30718	6.4	1.0E-45	BE396633.1	EST_HUMAN	Homo sapiens mRNA for KIAA1591 protein, partial cds
4848	17861		1.05	1.0E-45	H57443.1	EST_HUMAN	601288116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618803 5'
5081	18209	31181	1.56	1.0E-45	11545798	NT	W05p02.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:204393 5'
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens nban protein (NIBAN), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8808	21886	35425	0.9	1.0E-45	D87875.1	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9321	22397	35950	3.92	1.0E-45	BE887843.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9722	22787	36388	0.99	1.0E-45	AB002297.1	NT	601511228F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912635 5'
12369	25263	32117	3.5	1.0E-45	11418098	NT	Human mRNA for KIAA0298 gene, partial cds
12562	25384		19.43	1.0E-45	11526281	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12668	25387		6.42	1.0E-45	11418171	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
13047	25686	31963	4.02	1.0E-45	11418157	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8423	21504	35037	2.71	9.0E-46	9910293	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8835	21814		6.82	9.0E-46	AL163209.2	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
10897	23730	37335	6.88	9.0E-46	AW246064.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
							2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI433261.1	EST_HUMAN	t332708.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2513	15639	28761	7.67	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
8244	21328		2.72	8.0E-46	BE167244.1	EST_HUMAN	t332708.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:J00314_ma2
4703	17838		4.79	7.0E-40	BE386163.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
4928	18058		1.33	7.0E-46	BE064386.1	EST_HUMAN	RC5-HT0506-280200-012.C12 HT0506 Homo sapiens cDNA
6167	18343	32689	4	7.0E-46	8922708	NT	601277292.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
6623	19783	33171	1.8	7.0E-46	BF105845.1	EST_HUMAN	RC4-BT0310-110300-075-f10 BT0310 Homo sapiens cDNA
12706	25469		2.6	7.0E-46	AL163246.2	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847). mRNA
2812	15926	29037	6.87	6.0E-46	AI884381.1	EST_HUMAN	601822835.F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
2812	15926	29038	6.87	6.0E-46	AI884381.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
6257	19431	32778	11.57	6.0E-46	AI635446.1	EST_HUMAN	wn31f08.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
7366	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	MER19 repetitive element;
7541	20614	34091	0.67	8.0E-46	BF509740.1	EST_HUMAN	wn31f08.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437576 3' similar to contains MER19.12
11673	23901		2.14	6.0E-46	BE784971.1	EST_HUMAN	MER19 repetitive element;
208	13432		5.31	6.0E-46	AL163210.2	NT	ts58h10.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
3617	16781	29786	1.17	5.0E-46	BE677194.1	EST_HUMAN	SA GENE.;
3617	16781	29787	1.17	5.0E-46	BE677194.1	EST_HUMAN	xc42604.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706854 3' similar to gb:L08069 DNAJ
6874	20026	33436	1.52	5.0E-46	BF590442.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
7080	20174	33688	3.69	5.0E-46	BF347229.1	EST_HUMAN	U1H-B14-epg-b-06-0-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
7244	20927	33772	0.75	6.0E-46	AW582253.1	EST_HUMAN	601479409.F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880895 6'
7544	20618	34093	0.59	5.0E-46	BE549744.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	7d81g01.x1 Lupsig_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7d81g01.x1 Lupsig_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							naa38f07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258767 3' similar to TR:O75202
							O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
							602021164.F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
							QV4-S10212-120100-075-f09 S10212 Homo sapiens cDNA
							7638605.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
							nc54e08.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_rna1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1740	14889	27981	2.89	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_rna1
							LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element;

Page 303 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27682	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to db:X14008_mn1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element ;
2798	15913	25021	7.4	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5553	18750	31786	2.1	4.0E-46	M38852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5553	18750	31787	2.1	4.0E-46	M38852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12851	25565	31089	1.36	4.0E-46	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2359	15400	28820	0.84	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4513	17652	30840	1.21	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4898	18028	31015	1.11	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4898	18028	31016	1.11	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8949	22028	35589	12.45	3.0E-46	A1831492.1	EST_HUMAN	w49c04.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element ;
9208	22284	35824	0.81	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
9208	22284	35825	0.81	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11873	24861	38556	1.78	3.0E-46	D31765.1	NT	Human mRNA for KIAA0061 gene, partial cds
860	14037	27099	12.65	2.0E-46	AA468646.1	EST_HUMAN	ne06a09.s1 NCL_CGAP_C63 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element ;
1593	14749		3.78	2.0E-46	AA878246.1	EST_HUMAN	z127a11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431988 3' (L44L) and FTP3 (FTP3) genes, complete cds
1571	14823	27906	5.83	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5089	18217	31188	1.26	2.0E-46	AA399289.1	EST_HUMAN	z159a02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728650 5' similar to SW:RSP1_MOUSE C01730 RSP-1 PROTEIN ;
7653	20721	34197	7.1	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8260	21342		1.29	2.0E-46	BE869161.1	EST_HUMAN	601445137F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3949297 5'
11524	24580		1.82	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
12294	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3987328 5'
12553	25931		1.57	2.0E-46	H48391.1	EST_HUMAN	y32201.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:206977 5'
12996	26401		3.31	2.0E-46	AA001786.1	EST_HUMAN	z184f12.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
12834	28923	31864	4.28	2.0E-46	AW277214.1	EST_HUMAN	xq78103.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2766789 3'
1281	14418	27483	4.31	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2356	15487	28819	4.88	1.0E-46	AW978516.1	EST_HUMAN	EST390625 IMAGE resequences, MAGP Homo sapiens cDNA

Page 304 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	H97330.1	EST_HUMAN	EST48b095 WATM1 Homo sapiens cDNA clone 48b095
3321	10494	29511	2.12	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:U76717 H. sapiens
4895	18124		3.13	1.0E-46	AB023197.1	NT	MT-11 mRNA, (HUMAN);
5817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6098	25818	32609	5.34	1.0E-46	8923762	NT	7c82b01.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	25818	32610	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19602	33295	0.64	1.0E-46	BF196247.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	7n48607.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3667852 3' similar to contains element
11410	24471	38136	1.81	1.0E-46	AJ245621.1	NT	MER22 repetitive element;
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	7c82b01.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	Homo sapiens CTL2 gene
13178	25764		1.99	1.0E-46	AV715377.1	EST_HUMAN	802072284F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
787	13665		3.7	9.0E-47	AJ271735.1	NT	802072284F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
5047	18175	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
6506	19672	33039	0.86	9.0E-47	11425439	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11388	24449	38110	1.4	9.0E-47	11432208	NT	h183e04.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
12874	26027	31675	1.64	9.0E-47	11417968	NT	HYPOTHETICAL 12.4 KD PROTEIN.
1851	14897	28100	32.2	8.0E-47	Y18536.1	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1851	14897	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
2781	15897	29007	1.5	8.0E-47	5453955	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3089	18265	29283	2.04	8.0E-47	AJ229043.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
3715	16876	29881	0.77	8.0E-47	AB041926.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
3715	16876	29882	0.77	8.0E-47	AB041926.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
12962	26922		1.99	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
2613	16737	28851	3.04	6.0E-47	AL163246.2	NT	Homo sapiens 959 kb contig between AVL1 and CBR1 on chromosome 21q22, segment 3/3
8890	21969	35505	0.52	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
9476	22533	36097	0.83	6.0E-47	AI685189.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
9913	22953	36538	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9913	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	19885	33255	5.73	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11035	24114		5.58	5.0E-47	M78590.1	EST_HUMAN	EST100738 Fetal brain, Stragelara (cat#936206) Homo sapiens cDNA clone HFBCF07
1432	14586	27660	7.03	4.0E-47	4557568	NT	Homo sapiens E1A binding protein p300 (EP300), mRNA
6971	20189	33625	0.82	4.0E-47	BE938896.1	EST_HUMAN	MR4-TN0108-280800-201-d04 TN0108 Homo sapiens cDNA
8677	21757	35292	2.22	4.0E-47	BE916483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8677	21757	35293	2.22	4.0E-47	BE916483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8618	21897	35436	0.83	4.0E-47	AW883777.1	EST_HUMAN	RC3-BN0034-220300-015-05 BN0034 Homo sapiens cDNA
11936	24922		1.98	4.0E-47	AW515509.1	EST_HUMAN	xc65b07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW.INT8_MOUSE
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1];
558	13751	26778	2.09	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
841	14019	27075	3.99	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
968	14141	27202	10.04	3.0E-47	AL163284.2	NT	y54b04.s1 Soares_multiple_sclerosis_2kb-HMSP Homo sapiens cDNA clone IMAGE:277327 3'
3376	16548	25562	0.97	3.0E-47	4604116	NT	Homo sapiens chromosome 21 segment HS21C084
4073	17229		6.81	3.0E-47	U63191.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4482	17522	30603	1.14	3.0E-47	M12959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1), mRNA, partial cds
6136	19315	32654	4.88	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19315	32655	4.68	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6694	19952		1.71	3.0E-47	A1222413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7540	20613	34089	0.88	3.0E-47	A1819755.1	EST_HUMAN	q104607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7540	20613	34090	0.88	3.0E-47	A1819755.1	EST_HUMAN	w11h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35654	0.77	3.0E-47	AW963796.1	EST_HUMAN	w11h08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2402559 3'
9033	22112	35655	0.77	3.0E-47	AW963796.1	EST_HUMAN	EST375869 MAGI resequences, MAGH Homo sapiens cDNA
152	13377	26409	1.21	2.0E-47	4505318	NT	EST375869 MAGI resequences, MAGH Homo sapiens cDNA
960	14162	27221	2.45	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
960	14162	27222	2.45	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1998	14751		0.95	2.0E-47	A1969279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1623	14775	27859	1.61	2.0E-47	7682108	NT	Homo sapiens chromosome 21 segment HS21C009
1712	14863	27852	4.49	2.0E-47	AA524514.1	EST_HUMAN	wq98602.x1 NCI_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2478851 3'
4467	17607	30585	1.61	2.0E-47	4504868	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
4503	17643	30628	1.87	2.0E-47	AA569592.1	EST_HUMAN	ng-3h12.s1 NCI_CGAP_O63 Homo sapiens cDNA clone IMAGE:937607 3'
4503	17643	30629	1.87	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4528	17764	30746	2.14	2.0E-47	5174648	NT	nt23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914852
4833	18063	31046	1.25	2.0E-47	AW965168.1	EST_HUMAN	nt23g07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914852
							Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA
							EST377239 MAGI resequences, MAGI Homo sapiens cDNA

Page 306 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18366		0.71	2.0E-47	AI041128.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5004	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signalling 6 variant form (RGS6) mRNA, complete cds
6097	19276	32607	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6097	19276	32608	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7878	25864		1.34	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34763	1.95	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34764	1.96	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8915	21894	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9690	22739	36308	1.27	2.0E-47	11526138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	26073	31653	3.36	2.0E-47	R42423.1	EST_HUMAN	Y82a08.x1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:29986 3' similar to contains OFR repetitive element ;
12394	26078		1.87	2.0E-47	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
1437	14590	27663	5.42	1.0E-47	AI333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1631189 3'
3928	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138693 5'
3928	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138693 5'
5187	18309	31275	2.4	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0187-130400-017-R02 ST0187 Homo sapiens cDNA
7189	20054	33484	10.76	1.0E-47	AI880886.1	EST_HUMAN	at19a06.x1 Barstead aorta HPLR88 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22995
9099	22148		4.24	1.0E-47	AW664648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10564	23589	37205	2.26	1.0E-47	L30115.1	NT	hB4a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2976972 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1643	14795	27879	3.84	9.0E-48	AF223391.1	NT	Paplo hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
3646	16309	29823	0.73	9.0E-48	BF359647.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5797	18987	32291	1.1	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-3:10700-280-105 MT0100 Homo sapiens cDNA
6226	19401	32751	0.57	9.0E-48	AI833168.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
6355	18325	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	601511714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
11378	24439	38088	3.06	9.0E-48	BE303813.1	EST_HUMAN	at75h09.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2377889 3' similar to TR:O60844
1279	14436		1.75	8.0E-48	4501800	NT	O60844 HOMOLOG OF RAT ZYMOGEN GRANULE MEMBRANE PROTEIN. ;
1280	14436		1.85	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
							AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
							601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							Homo sapiens aminocyclase 1 (ACY1), mRNA
							hK61b03.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
3205	16380	26390	5.72	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

Page 307 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW788477.1	EST_HUMAN	h161b03.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb-X64707
4041	17197	30208	0.86	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13598		2.58	7.0E-48	AB033035.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13998		18.89	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1827	14680	27761	1.96	7.0E-48	6912719	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1687	14819	27902	5.39	7.0E-48	6730038	NT	Homo sapiens taurine-like kinase 1 (TLK1) mRNA
6885	18843	33233	24.01	7.0E-48	11416831	NT	Homo sapiens SET domain and methyltransferase fusion gene (SETMAR) mRNA
12125	25105	38809	2.98	7.0E-48	R19823.1	EST_HUMAN	Homo sapiens histidyl-IRNA synthetase (HARS) mRNA
3687	18850	29858	0.88	6.0E-48	A176111.1	EST_HUMAN	y937602.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34747 5'
6183	19359	32707	0.84	6.0E-48	AB008855.1	NT	w691h03.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6924	20239	33674	0.83	6.0E-48	11420995	NT	Homo sapiens mRNA for AIE-75, complete cds
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7028	25849	34179	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1924 protein, partial cds
9323	22399	35953	1.57	6.0E-48	AF028816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9741	22806	36382	1.87	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11008 (FLJ11008) mRNA
9890	22630	36514	2.84	6.0E-48	AA188080.1	EST_HUMAN	z945b06.s1 Striatum hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to
3384	18465	29588	1.48	5.0E-48	4826891	NT	contains Alu repetitive element;
8774	21853	35395	1.04	5.0E-48	BE064410.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
2829	19343	29053	1.02	4.0E-48	R45715.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
11200	24269	37905	3.11	4.0E-48	A1620420.1	EST_HUMAN	Hat140-f Adult heart, Clontech Homo sapiens cDNA clone a140-f
12050	25031	38737	1.76	4.0E-48	BE064410.1	EST_HUMAN	tu47a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2284154 3'
1418	14570	27643	1.81	3.0E-48	AV680984.1	EST_HUMAN	RC4-BT0311-141189-011-h06 BT0311 Homo sapiens cDNA
2032	15173	28283	31.81	3.0E-48	4885170	NT	AV680984 GKC Homo sapiens cDNA clone GKCDRE12 5'
3505	16672	29682	0.93	3.0E-48	AF172453.1	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3721	16882	29888	0.9	3.0E-48	AW664531.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
4362	17505	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	Homo sapiens cplid growth factor receptor mRNA, complete cds
6015	18189	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	h14b12.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972255 3' similar to SW:DCRB_HUMAN
7159	20282	33735	1.07	3.0E-48	AF087913.1	NT	P59658 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
8585	21668		3.73	3.0E-48	AA686830.1	EST_HUMAN	204g03.r1 Soares fetal liver, spleen, 1NF1S_S1 Homo sapiens cDNA clone IMAGE:428844 5'
							MR4-BT0657-080400-201-e10 BT0657 Homo sapiens cDNA
							Human endogenous retrovirus HERV-P-T47D
							mv0305.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1
							PTR5 repetitive element;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11114	24188	37818	8.1	3.0E-48	BF514170.1	EST_HUMAN	UHH-BW1-ant-e-10-0-UJ.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
5	13244	26245	0.66	2.0E-48	AA465007.1	EST_HUMAN	z680c03.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810062 5'
46	13285	26294	1.7	2.0E-48	AA631940.1	EST_HUMAN	fmfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4654	17780	30774	0.99	2.0E-48	BE246085.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5935	19121	32433	0.64	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
5935	19121	32434	0.64	2.0E-48	AA613171.1	EST_HUMAN	no18g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072 3'
7688	20753	34236	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7688	20753	34237	3.99	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7703	20768	34253	3.54	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8550	21831	35168	1.13	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCCGG10 5'
12109	25089	27923	1.36	2.0E-48	AW291799.1	EST_HUMAN	UHH-B12-agl-b-11-0-UJ.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724453 3'
12320	13244	26245	2.98	2.0E-48	AA465007.1	EST_HUMAN	z680c03.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810062 5'
12674	25990	31771	1.25	2.0E-48	BE737154.1	EST_HUMAN	801305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
57	13295	26311	2.33	1.0E-48	7709534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
896	14072	27137	4.67	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1101	14266	27323	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1101	14266	27324	1.52	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1324	14481	27548	4.01	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA
1968	15111	28212	13.8	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3577	16742	29759	0.94	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5240	18362	31330	1.1	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6417	19586	32948	1.24	1.0E-48	A1889077.1	EST_HUMAN	ic17d01.x1 NCI_CGAP_Col16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941
6417	19586	32949	1.24	1.0E-48	A1889077.1	EST_HUMAN	ic17d01.x1 NCI_CGAP_Col16 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14588 SIMILARITY TO U73941
6628	19768	33274	0.87	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
6727	19883	33274	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
6727	19883	33275	0.59	1.0E-48	AB028994.1	NT	Homo sapiens mRNA for KIAA1071 protein, partial cds
7407	20485	33854	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9031	22110	35651	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9031	22110	35652	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	22488	36053	0.89	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9488	22525	36089	6.79	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9781	22821	36399	4.74	1.0E-48	BF304683.1	EST_HUMAN	601888096F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4122116 5'
10581	23616	37221	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP68), mRNA
10681	23616	37222	4.23	1.0E-48	11429808	NT	Homo sapiens B cell linker protein (SLP68), mRNA
12282	28014		1.41	1.0E-48	W28785.1	EST_HUMAN	15d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2054	15204	28320	0.97	8.0E-49	AB026497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
6178	19354	32701	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6178	19354	32702	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8491	21872	35109	3.09	8.0E-49	U23850.1	NT	Human insulin 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10184	23231	36822	0.93	8.0E-48	AB008881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
11096	24169	37804	3.65	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCL_CGAP_U4 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element
12087	25077	38785	2.08	8.0E-49	AA872183.1	EST_HUMAN	cb78a08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337482 3'
142	13602	26637	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
142	13602	26638	1.21	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
405	13602	26637	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
405	13602	26638	1.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
406	13602	26637	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
406	13602	26638	2.25	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA4) mRNA
1248	14407	27469	4.37	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4772	17607	30880	0.9	7.0E-48	O60811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.3
5576	18771	31815	2.33	7.0E-49	AI807191.1	EST_HUMAN	wf26h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356683 3' similar to TR:O54923
5586	18781	31826	1.3	7.0E-49	AL120937.1	EST_HUMAN	O54823 RSEC15.1
5928	18771	31815	0.79	7.0E-49	AI807191.1	EST_HUMAN	DKFZp762C033.s1 702 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762C033 3'
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356683 3' similar to TR:O54923
							O54823 RSEC15.1
202	13425	26456	20.33	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17208.40S
4231	17378	30387	0.84	6.0E-49	AL182091.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE)
5954	19140	32456	0.84	6.0E-48	AW511225.1	EST_HUMAN	DKFZp761A198.s1 761 (synonym: harny2) Homo sapiens cDNA clone DKFZp761A198 3'
6572	18734	33113	1.27	6.0E-49	AU140742.1	EST_HUMAN	hd44a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR:O86638
							O95638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.1
							AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11557	24612	36291	3.39	6.0E-49	AW452218.1	EST_HUMAN	UI-H-B13-alo-a-05-Q-UI.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068048 3'
11961	24946	38650	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
11961	24946	38651	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST77625 Pancreas tumor III Homo sapiens cDNA 5' end
12670	25897		10.54	6.0E-49	AA707667.1	EST_HUMAN	329008.s1 Soares fetal_liver_spleen_INF.LS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
730	13912	26951	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26952	5.84	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1808	14983	28082	10.18	5.0E-49	AA172121.1	EST_HUMAN	zp28c07.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610860 5' similar to
2808	15922	29032	7.1	5.0E-49	U17714.1	NT	TR:G233226 G233226 RTVL-H PROTEIN.; contains LTR7.13 LTR7 LTR7 repetitive element;
3346	16519	29533	7.59	5.0E-49	11436355	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
538	13731	26754	28.39	4.0E-49	AW189533.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC63362), mRNA
7395	20473	33939	0.96	4.0E-49	Z26634.2	NT	X08801.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2676593 3' similar to WP:B0360.2B
7395	20473	33940	0.96	4.0E-49	Z26634.2	NT	CE06703;
7422	20489	33970	0.68	4.0E-49	11525737	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7422	20499	33971	0.68	4.0E-49	11525737	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7992	21042	34554	0.89	4.0E-49	Z662209	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
9065	22144	35690	0.47	4.0E-49	11425374	NT	(GalNAc-T8) (GALNT8), mRNA
9065	22144	35691	0.47	4.0E-49	11425374	NT	(GalNAc-T8) (GALNT8), mRNA
12514	26145		2.74	4.0E-49	AA210798.1	EST_HUMAN	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
12615	25413		2.93	4.0E-49	AF240786.1	NT	(GalNAc-T8) (GALNT8), mRNA
574	13766	26789	0.91	3.0E-49	X68988.1	NT	(GalNAc-T8) (GALNT8), mRNA
2713	15931		2.73	3.0E-49	AA016131.1	EST_HUMAN	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
5068	18226	31108	2.68	3.0E-49	U46999.1	NT	Homo sapiens copine III (CPNE3), mRNA
7577	20949	34127	9.83	3.0E-49	H39479.1	EST_HUMAN	Homo sapiens copine III (CPNE3), mRNA
11582	24638	38316	1.41	3.0E-49	AA337561.1	EST_HUMAN	zr90705.r1 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:682977 5'
678	13954		1.93	2.0E-49	BE165980.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
3294	16468	29487	1.15	2.0E-49	N26446.1	EST_HUMAN	H. sapiens mRNA for acetyl-CoA carboxylase
							z631c05.r1 Soares retina N2b4-R Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
							repetitive element;
							Human type IV collagen (COL4A6) gene, exon 40
							EST25612 WATM1 Homo sapiens cDNA clone 25e12
							EST142572 Endometrial tumor Homo sapiens cDNA 5' end
							MR3-HT0487-150200-113-g01 H10487 Homo sapiens cDNA
							yc23d06.r1 Soares melanocytes 2NBM Homo sapiens cDNA clone IMAGE:262571 5'

Page 311 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	19822	29832	0.86	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6875	20027	33437	1.2	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DGB Homo sapiens cDNA clone DGBALB01 5'
8291	21373		1.87	2.0E-49	M66033.1	EST_HUMAN	EST02558 Fetal brain, Stragene (calf936206) Homo sapiens cDNA clone HFBCY60
12828	26008		2.69	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	14097		9.1	1.0E-49	BF035327.1	EST_HUMAN	601468531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862086 5'
1584	14736	27816	73.58	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KR18) mRNA
1844	14990	28091	2.93	1.0E-49	BE255216.1	EST_HUMAN	601116769F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3359273 5'
5476	18674	31688	4.68	1.0E-49	BF131007.1	EST_HUMAN	601820033F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4052052 5'
6202	19377	32728	0.85	1.0E-49	H18291.1	EST_HUMAN	Yn48h04.r1 Soares adult brain N2b9HB55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to
6208	19383	32733	1.09	1.0E-49	AW964640.1	EST_HUMAN	SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN GT(GAMMA-1 SUBUNIT ;
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	EST376713 MAGE resequences, MAGH Homo sapiens cDNA
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3820863 5'
7453	20530	34003	2.09	1.0E-49	N25884.1	EST_HUMAN	601290330F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3820863 5'
7453	20530	34004	2.09	1.0E-49	N25884.1	EST_HUMAN	Yw78g12.s1 Soares placenta 806weeks_2N6HP869W Homo sapiens cDNA clone IMAGE:258408 3' similar to gb:X69873 KINESIN HEAVY CHAIN (HUMAN);
8874	21853		0.71	1.0E-49	9994184	NT	Yw78g12.s1 Soares placenta 806weeks_2N6HP869W Homo sapiens cDNA clone IMAGE:258408 3' similar to gb:X69873 KINESIN HEAVY CHAIN (HUMAN);
9193	22271	38809	1.48	1.0E-49	BE409340.1	EST_HUMAN	Homo sapiens RNA binding motif protein 7 (LOC51120). mRNA
10331	23366	36975	1.23	1.0E-49	AL043129.2	EST_HUMAN	601300992F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3636398 5'
11304	24359	38010	1.32	1.0E-49	AV751477.1	EST_HUMAN	DKFZp434D2423_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2423 5'
11590	24643	38325	2.91	1.0E-49	11427366	NT	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
12148	25119		1.26	1.0E-49	BE169343.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1). mRNA
12508	25349		1.82	1.0E-49	11418322	NT	MFO-HT0407-010200-008-002 HT0407 Homo sapiens cDNA
5109	18237		0.92	9.0E-50	AF101475.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1). mRNA
6634	28215		0.63	9.0E-50	BE295758.1	EST_HUMAN	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
174	13398	28426	4.18	8.0E-50	AL163202.2	NT	601176250F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:3531588 5'
737	13919	28959	1.92	8.0E-50	X95097.2	NT	Homo sapiens chromosome 21 segment HS21C002
737	13919	28960	1.92	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1803	14952	28046	4.32	8.0E-50	4501860	NT	Homo sapiens mRNA for VIP receptor 2
2552	15677	28800	1.05	8.0E-50	77069394	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2552	15677	28801	1.05	8.0E-50	77069394	NT	Homo sapiens p47 (LOC51674). mRNA
2764	15879	28988	2.42	8.0E-50	4826668	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB). mRNA
2891	15160		2.87	8.0E-50	D90334.1	NT	Homo sapiens hepatocyte growth factor(HGF) gene, exon 18

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
634	13819	26843	1.07	7.0E-50	BE086931.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
6823	20238	33672	0.73	7.0E-50	BF091922.1	EST_HUMAN	RO6-TN0073-190900-011-A12 TN0073 Homo sapiens cDNA
6923	20238	33673	0.73	7.0E-50	BF091922.1	EST_HUMAN	RO6-TN0073-190900-011-A12 TN0073 Homo sapiens cDNA
7457	20533	34008	0.74	7.0E-50	AA627622.1	EST_HUMAN	nc59e12.s1 NCI CGAP_C09 Homo sapiens cDNA clone IMAGE:1148208 3' similar to gb:U669391.60S
10993	24072	37705	23.18	7.0E-50	AI872137.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
4462	17602		0.87	6.0E-50	BE794391.1	EST_HUMAN	hm55g11.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:3943577 5'
8408	21489		3.28	6.0E-50	BE044076.1	EST_HUMAN	hm39h04.x1 NCI CGAP_UK1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
11053	24130	37765	3.32	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element;
11053	24130	37766	3.32	6.0E-50	AA312079.1	EST_HUMAN	EST182776 Jurkat T-cells VI Homo sapiens cDNA 5' end
1835	14982	28080	1.34	5.0E-50	BF332938.1	EST_HUMAN	EST182776 Jurkat T-cells VI Homo sapiens cDNA 5' end
1835	14982	28081	1.34	5.0E-50	BF332938.1	EST_HUMAN	QV0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9294	22370		5.27	5.0E-50	AA557683.1	EST_HUMAN	QV0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
12090	25070	38777	1.78	5.0E-50	AA403053.1	EST_HUMAN	nl45h10.s1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043883 similar to contains PTR5.13 PTR5
940	14114		2.31	4.0E-50	AA601143.1	EST_HUMAN	repetitive element;
3536	16701	29712	2.08	4.0E-50	AL163248.2	NT	xt62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335769
6491	19657	33020	0.92	4.0E-50	11440683	NT	G1335769 GAG-POLYPROTEIN.;
7388	20461	33624	1.02	4.0E-50	BE087836.1	EST_HUMAN	nc54e09.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb:X53741_mae1
1992	15134		9.4	3.0E-50	M18048.1	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3371	16543	29657	0.92	3.0E-50	AA746142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
3846	17009	30008	0.9	3.0E-50	AW755254.1	EST_HUMAN	Homo sapiens cysteinyl-tRNA synthetase (CARS), mRNA
6815	19698	33374	0.99	3.0E-50	11419317	NT	QV1-BT0681-280300-127.f12 BT0681 Homo sapiens cDNA
6815	19698	33375	0.99	3.0E-50	11419317	NT	Human endogenous reovirus RTVL-H2
6904	20219	33648	1.71	3.0E-50		NT	ob03f06.s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
7822	20877	34376	5	3.0E-50	AF233436.2	NT	CMYA5 Human cardiac muscle expression library/Homo sapiens cDNA clone 4151935 similar to CMYA5
7822	20877	34377	5	3.0E-50	AF233436.2	NT	Cardiomyopathy associated gene 5
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
							Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
							Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds

Page 313 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8782	21881	35404	0.66	3.0E-50	6001599	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	23061	36657	1.09	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KIAA1698 protein, partial cds
10032	23070	36670	1.03	3.0E-50	11418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCP10), mRNA
10737	23770	37380	1.04	3.0E-50	AB002297.1	NT	Human mRNA for KIAA0298 gene, partial cds
11384	24425	38080	1.51	3.0E-50	11436955	NT	Homo sapiens Gln2-associated binder 2 (KIAA0571), mRNA
11752	23938	37564	8.19	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
13217	25792	31822	1.35	3.0E-50	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
769	13978		7.94	2.0E-50	AF055086.1	NT	Homo sapiens MHC class 1 region
1104	14269	27327	8.16	2.0E-50	4557752	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1), mRNA
1474	14627	27713	33.77	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
4376	17519	30409	0.75	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
5328	18442	31412	1.37	2.0E-50	AB0118319.1	NT	Homo sapiens mRNA for KIAA0776 protein, partial cds
7007	20143	33562	0.61	2.0E-50	AU124065.1	EST_HUMAN	AU124065 NT2RM2 Homo sapiens cDNA clone NT2RM2001600 5'
8511	21592	35126	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8511	21592	35127	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8650	21730	35268	7.21	2.0E-50	X06993.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8650	21730	35269	7.21	2.0E-50	X06993.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10088	23126	36728	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
10088	23126	36729	1.6	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
11060	24945		1.39	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
474	13689	28701	2.17	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C0209
2438	15556		10.11	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 112
10396	23431	37038	1.65	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6104	16284	32817	1.04	9.0E-51	AW611225.1	EST_HUMAN	hd44e02 x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:085638
6354	19524	32881	0.58	9.0E-51	AA744837.1	EST_HUMAN	Q95638 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
8872	21951	35487	0.7	9.0E-51	A1791154.1	EST_HUMAN	nv67h03.g1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9325	22590	36161	1.29	9.0E-51	AA043738.1	EST_HUMAN	ab23g04.x5 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
9700	22749	36317	0.88	9.0E-51	A1791154.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9700	22749	36318	0.88	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratiogene lung (#837210) Homo sapiens cDNA clone IMAGE:841888 3' similar to
11764	23950	37579	1.97	9.0E-51	H86078.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11764	23950	37580	1.97	9.0E-51	H89078.1	EST_HUMAN	yw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
12059	25050	38768	1.84	9.0E-51	AA885514.1	EST_HUMAN	am10102.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466451 3' similar to SW:CAYP_CANFA_P10463 CALYPTHOSINE:
4559	17697	30677	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4559	17697	30678	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4690	17825	30812	5.38	8.0E-51	AA610842.1	EST_HUMAN	np86e09.s1 NCI_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gbX12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN):
7321	20403	33865	0.71	8.0E-51	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
7830	20885	34387	2.11	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/AY-CO-38), mRNA
8684	22826	29541	1.05	8.0E-51	AU138590.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3354	16526	29541	1.27	7.0E-51	AW889219.1	EST_HUMAN	QV4-NT0028-200400-180-005 NT0028 Homo sapiens cDNA
3447	16915	29633	0.82	7.0E-51	AW274720.1	EST_HUMAN	xn34e03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN:
4282	17427	30416	1.37	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
4282	17427	30417	1.37	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2229 5'
4375	17618	30498	1.18	7.0E-51	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
4471	17611	30589	1.44	7.0E-51	AW285603.1	EST_HUMAN	UHL-BW0- α -b-05- α -U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
11985	24970	38674	1.36	7.0E-51	AF161449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1657	14710	27780	0.94	6.0E-51	6678783	NT	Homo sapiens putative DNA binding protein (M86), mRNA
2036	15177	28287	5.93	6.0E-51	7657268	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
3562	16727	29743	14.65	6.0E-51	7657268	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4426	17598	30547	0.68	6.0E-51	8910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4426	17598	30548	0.66	6.0E-51	8910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6113	19283	32828	1.48	6.0E-51	X01788.1	NT	Human haploglobin related (Hpr) gene exon 3
6124	19303	32842	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6800	20216	33645	0.93	6.0E-51	4506736	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
7032	20168	33660	0.82	6.0E-51	11416751	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7104	18531	31466	2.15	6.0E-51	11428525	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56980), mRNA
9337	22413	35966	0.69	6.0E-51	11428525	NT	Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA
9337	22413	35966	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9885	22928	36508	2.05	6.0E-51	7651635	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA

Page 315 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9994	23003	36598	0.79	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11534	24590	38265	1.84	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
814	13993	27047	6.22	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
828	14004	27081	1.71	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1015	16028	27247	2.39	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1638	14790	27575	1.14	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated pod1 homolog (POH1) mRNA
2658	15781	28694	10.36	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 156
4055	17211	30221	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4055	17211	30222	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5183	18305	31289	1.04	5.0E-51	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11568	24513	38292	3.8	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
137	13363	26397	14.25	3.0E-51	AI597348.1	EST_HUMAN	h81c08.x1 NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1203	14365	27425	48.14	3.0E-51	AI597348.1	EST_HUMAN	h81c08.x1 NCL CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1978	15119	28220	1.38	3.0E-51	AA211296.1	EST_HUMAN	zq87g01.s1 Striatogene INT neuron (#937233) Homo sapiens cDNA clone IMAGE:649008 3'
4448	17588	30587	1.85	3.0E-51	AL169142.1	NT	Novel human gene mapping to chromosome 22
7753	20813	34304	2.3	3.0E-51	R15914.1	EST_HUMAN	y447c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:83233 5' similar to gb:M14123_cds4 RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR5 repetitive element;
9040	22119		3.85	3.0E-51	M29063.1	NT	Human hnRNP C2 protein mRNA
9268	28227		0.61	3.0E-51	AW583777.1	EST_HUMAN	ia04408.y1 Human Pancreatic islets Homo sapiens cDNA 5'
12867	25578		6.56	3.0E-51	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
377	13585	26619	1.98	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
706	13989	26921	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
706	13989	26922	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1723	14873	27965	16.75	2.0E-51	AA233352.1	EST_HUMAN	z330a05.r1 Striatogene INT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTV-L-H PROTEIN; contains LTR7.0 LTR7 repetitive element;
3827	16987	28990	3.05	2.0E-51	AI492415.1	EST_HUMAN	tt27g03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4616	17753	30734	1.21	2.0E-51	AW137828.1	EST_HUMAN	UJ-H-B1-adj-4-02-0-UJ.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5326	18439	31408	0.66	2.0E-51	AI381520.1	EST_HUMAN	ta76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:P93107 P93107 PF20.1;

Page 316 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6139	19317	32658	3.54	2.0E-51	BE782015.1	EST_HUMAN	801470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7462	20537		0.73	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase Iba (DGK1) gene, exon 23
7615	20665	34161	1.29	2.0E-51	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0893), mRNA
8896	21975	35512	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8896	21975	35513	1.61	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9235	22312	35854	1.03	2.0E-51	11037064	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9712	22777	36347	1.76	2.0E-51	AI917078.1	EST_HUMAN	ts74a07.x1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9803	22843	36420	4.86	2.0E-51	BE165680.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
9818	22858	36438	0.69	2.0E-51	AB007926.1	NT	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10648	23682	37283	1.58	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10680	23723	37329	1.07	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11610	18752	31789	5.82	2.0E-51	A1732851.1	EST_HUMAN	EST91296 Synovial sarcoma Homo sapiens cDNA 5' end
11610	18752	31780	5.82	2.0E-51	A1732851.1	EST_HUMAN	cb34f09.x5 NCL_CGAP_Ki45 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12860	25571	31992	1.62	2.0E-51	11419159	NT	P35436 GLUTAMATE [NMIDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
117	13348	26375	10.94	1.0E-51	AV742248.1	EST_HUMAN	cb34f09.x5 NCL_CGAP_Ki45 Homo sapiens cDNA clone IMAGE:1325608 3' similar to SW:NME1_MOUSE
1523	14676	31036	37.16	1.0E-51	AF111168.2	NT	P35436 GLUTAMATE [NMIDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
4918	18048		0.82	1.0E-51	T18662.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4), mRNA
5505	18704	31720	3.7	1.0E-51	T18662.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
7827	20882	34384	1.03	1.0E-51	AI872632.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone GFBGCG12 5'
8087	21169	34884	0.51	1.0E-51	BF434959.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12076	26232		1.97	1.0E-51	AV760590.1	EST_HUMAN	b120568 Testis 1 Homo sapiens cDNA clone b120566
12610	25409		9.43	9.0E-52	AA77621.1	EST_HUMAN	ts39g02.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
156	13381	26412	11.42	8.0E-52	AA720574.1	EST_HUMAN	709b02.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644091 3' similar to TR:P87882 P87882
1526	14678	27760	2.39	8.0E-52	X84900.1	NT	PROTEASE ;
1686	14838	27922	2.85	8.0E-52	11968028	NT	AV760590 MDS Homo sapiens cDNA clone MDS08B02 5'
							z85a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to
							contains THR13 THR repetitive element ;
							hw21g02.s1 NCL_CGAP_GC08 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13
							THR repetitive element ;
							H.sapiens mRNA for laminin-5, alpha3b chain
							Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1686	14838	27923	2.85	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27922	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27923	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7686	20751	34232	0.76	8.0E-52	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7686	20751	34233	0.76	8.0E-52	11416595	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9216	22283	35836	1.86	7.0E-52	W59471.1	EST_HUMAN	zcf58a08.1 Soares, parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1214	14375		0.83	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0637-271299-049-407 BT0537 Homo sapiens cDNA
1729	14879	27970	7.1	6.0E-52	AF109037.1	NT	Homo sapiens S104 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5845	19035	32341	1.05	6.0E-52	A1208794.1	EST_HUMAN	qg4404.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11484	24543	38214	2.36	6.0E-52	BE048172.1	EST_HUMAN	ts46h04.y1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2281671 5' similar to SW:PGBM_MOUSE Q05763 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR:
4562	17700	30682	2.27	6.0E-52	Z78898.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18H7
8902	22647	36218	0.48	5.0E-52	11437365	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1895	14847	27931	1.86	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1829	14677	28072	1.63	4.0E-52	4758943	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4037	17199	30203	0.77	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4862	17995	30980	0.81	4.0E-52	A1766814.1	EST_HUMAN	w89502.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2400469 3'
6401	18603	31574	1.3	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
6401	18603	31575	1.3	4.0E-52	4505132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8228	21310	34830	1.19	4.0E-52	BE822032.1	EST_HUMAN	601440887F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915838 5'
8731	21811	35347	5.5	4.0E-52	11417035	NT	Homo sapiens hydroxyteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12429	26304		3.44	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12687	25642		12.79	4.0E-52	AB002050.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13141	25741		1.3	4.0E-52	ABD11399.1	NT	Homo sapiens gene for AF-6, complete cds
4204	17563		11.41	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
676	13768	26780	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
676	13768	26781	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2071	16211	28328	1.18	2.0E-52	AB033076.1	NT	Homo sapiens mRNA for KIAA1249 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2598	15993	28818	1.5	2.0E-52	BE207375.1	EST_HUMAN	b56607.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16493 M.musculus
2796	15911		11.48	2.0E-52	BF677892.1	EST_HUMAN	mRNA for Zfp1 zinc finger protein (MOUSE);
5092	18220	31160	3.41	2.0E-52	AL137188.3	NT	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5128	18251	31216	1.4	2.0E-52	AI141802.1	EST_HUMAN	Novel human gene mapping to chromosome 20, similar to membrane transporters
5128	18251	31217	1.4	2.0E-52	AI141802.1	EST_HUMAN	q45605.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5821	19011	32317	3.24	2.0E-52	AW848041.1	EST_HUMAN	q45605.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
6497	19683	33026	1.98	2.0E-52	11141868	NT	IL3-CT0214-231289-053-E12 CT0214 Homo sapiens cDNA
6853	20008	33415	0.96	2.0E-52	AB028004.1	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
7081	20175	33597	0.76	2.0E-52	AI762148.1	EST_HUMAN	Homo sapiens mRNA for KIAA1081 protein, partial cds
7896	21046	34558	0.69	2.0E-52	5032158	NT	oa45d12.y5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
7896	21046	34559	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8854	21933		8.71	2.0E-52	AF147880.1	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
9136	22215	35759	0.96	2.0E-52	AA778765.1	EST_HUMAN	Macaca mulatta beta-tubulin mRNA, complete cds
9680	22842		1	2.0E-52	4758789	NT	245905.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
10321	23368	36965	4.6	2.0E-52	5730038	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase)
10321	23359	36968	4.6	2.0E-52	5730038	NT	(NDUFS5) mRNA
11481	24540	38209	3.14	2.0E-52	AI831462.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11481	24540	38210	3.14	2.0E-52	AI831462.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11491	24550	38225	2.52	2.0E-52	AV715377.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11634	24714		1.46	2.0E-52	W70260.1	EST_HUMAN	w49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2
11918	24904		3.25	2.0E-52	11417990	NT	THR repetitive element ;
12234	26194	31541	5.9	2.0E-52	AW236297.1	EST_HUMAN	w49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
12658	25437		5.72	2.0E-52	AI808885.1	EST_HUMAN	THR repetitive element ;
546	13730	26764	1.89	1.0E-52	AA634445.1	EST_HUMAN	Q16859 CARBOXYLESTERASE ;
1402	14556	27630	18.76	1.0E-52	4504026	NT	z175h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
2600	15724		1.86	1.0E-52	4502238	NT	Homo sapiens glutamate-aminoligase (glutamine synthase) (GLUL) mRNA
3126	16302	29315	2.6	1.0E-52	S61070.1	NT	Homo sapiens arylsulfinase D (ARSD), transcript variant 1, mRNA
							poly-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element] RTVL-Hp1, Genomic, 960 nt

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18648	31628	4.43	1.0E-52	M29426.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6523	19688	33082	2.33	1.0E-52	U38864.1	NT	Human PMS2 related (PMSR2) gene, complete cds
7598	20959	34135	2.07	1.0E-52	X07292.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8014	21064	34578	0.59	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
8660	21740		1.18	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9390	22465	36029	0.77	1.0E-52	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10804	23937		0.88	1.0E-52	AW020370.1	EST_HUMAN	d08g05.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10814	23947		1.06	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11004	24083	37720	2.12	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (NPTPCAXX1) mRNA, complete cds
11076	24160		1.72	1.0E-52	11428321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
12135	25115	38819	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exofibronuclease 2 (XRN2), mRNA
12135	25115	38820	1.31	1.0E-52	11421401	NT	Homo sapiens 5'-3' exofibronuclease 2 (XRN2), mRNA
3881	17050	30049	0.89	9.0E-53	AF001448.1	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4611	17650	30638	3.3	9.0E-53	AF001448.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12480	26332		8.85	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR.11
12958	26046		7.06	7.0E-53	AI421782.1	EST_HUMAN	1f44107.x1 NCJ_CGAP_Erm23 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR.11
4214	17363	30351	4.46	5.0E-53	4758643	NT	THR repetitive element
5283	18411	31377	0.92	5.0E-53	AL163282.2	NT	Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
12628	25360		1.93	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
50	13289	26301	2.07	4.0E-53	AL163286.2	NT	RG3-ST0197-161099-011-g10 ST0197 Homo sapiens cDNA
50	13289	26302	2.07	4.0E-53	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
9816	22871		0.67	4.0E-53	AI613037.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C086
8958	22997		0.94	4.0E-53	F13080.1	EST_HUMAN	506h04.x1 NCJ_CGAP_U33 Homo sapiens cDNA clone IMAGE:2278327 3'
11489	24548	38221	2.89	4.0E-53	BF128701.1	EST_HUMAN	H-SC31D041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11489	24548	38222	2.89	4.0E-53	BF128701.1	EST_HUMAN	601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053877 5'
							601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053877 5'
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2726	15944	28066	2.34	3.0E-53	AB025898.1	NT	
3825	16985	29888	1.18	3.0E-53	AW060836.1	EST_HUMAN	wz22cd7.x1 Scores_Dieckgreffe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2558706 3'
4713	17548	30831	0.75	3.0E-53	AW803583.1	EST_HUMAN	IL2-UM0081-240300-056-D03 UM0081 Homo sapiens cDNA
5541	18138	31755	0.97	3.0E-53	AF001212.1	NT	Homo sapiens 26S proteasome subunit 9 mRNA, complete cds
5743	18938	32236	1.01	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6323	19485	32851	1.46	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7247	20330	33776	0.76	3.0E-53	Y10388.3	NT	H.sapiens graf gene
7247	20330	33777	0.76	3.0E-53	Y10388.3	NT	H.sapiens graf gene
8499	21580	35116	10.97	3.0E-53	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
9060	22139	35683	0.85	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9257	22334		9.77	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
12381	25259		1.18	3.0E-53	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
470	13665		11.25	2.0E-53	AA366566.1	EST_HUMAN	EST17525 Pancer tumor III Homo sapiens cDNA 5' end
2068	15209	28325	3.29	2.0E-53	7705394	NT	Homo sapiens hyaluronic acid receptor (HAR), mRNA
2404	15535	28602	6.28	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2601	15725		12.88	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3290	16484	29483	0.79	2.0E-53	7705887	NT	Homo sapiens leucine aminopeptidase (LOC51055), mRNA
3317	16490	29508	1.29	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4170	17320	30313	2.59	2.0E-53	M61873.1	NT	Human Kruppel-related DNA-binding protein (TF34) gene, partial cds
5542	18739	31757	2.46	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8055	21138	34658	1.01	2.0E-53	AW975598.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8198	21278		0.48	2.0E-53	AA095682.1	EST_HUMAN	EST387707 MAGe resequences, MAGN Homo sapiens cDNA
9608	22683		3.47	2.0E-53	AW246676.1	EST_HUMAN	I5429 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
10862	23895	37517	0.89	2.0E-53	BE550195.1	EST_HUMAN	2822865.Sprime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822865 5'
14777	14630	27715	2.2	1.0E-53	AJ271736.1	NT	765002.1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04009 Q04009 MYOSIN HEAVY CHAIN.1
3498	18683	28875	2.99	1.0E-53	AB028898.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5078	18206	31178	1.06	1.0E-53	BE296386.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8831	18884	33392	1.5	1.0E-53	BF364201.1	EST_HUMAN	601178725F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3531919 5'
7397	20475	33942	0.87	1.0E-53	BE012071.1	EST_HUMAN	GM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
8120	21202	34723	0.6	1.0E-53	AA248072.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
9280	22366	35915	4.73	1.0E-53	X79536.1	NT	I8571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12228	26176	38345	1.47	1.0E-53	AW245422.1	EST_HUMAN	H.sapiens mRNA for hnRNP core protein A1
3324	16497	29515	0.61	9.0E-54	4504116	NT	2822943.3prime NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822943 3'
5417	25803	31593	5.86	9.0E-54	4506786	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
212	13435	26485	1.29	8.0E-54	BE386785.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1982	15026	28133	2.08	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6057	19239	32564	23.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
395	13832	26669	1.35	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Scores_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element ;
1877	15021	28128	2.23	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2278	15410	28541	7.63	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Scores_placenta_8to9weeks_2NBHP869W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element ;
10333	23368	36978	2.1	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11365	24426	35081	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11365	24426	35082	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11570	24825		3.42	7.0E-54	AI160169.1	EST_HUMAN	qb67g03.x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.11 ORF repetitive element ;
25	13263	26265	0.84	8.0E-54	AB003618.1	NT	Homo sapiens DNA for MCB, exon 4, 5 and partial cds
398	13633	26670	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
398	13633	26671	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3365	19527	29542	0.72	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4111	17265	30265	22.75	8.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4894	17721	30704	1.09	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TP3AACH10 5'
4868	18087	31073	2.15	8.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4896	18126		2.04	6.0E-54	Y08846.1	NT	H. sapiens ehc pseudogene, p68 isoform
5115	18126		3.31	6.0E-54	Y08846.1	NT	H. sapiens ehc pseudogene, p66 isoform
11741	23927	37552	1.52	6.0E-54	AW813667.1	EST_HUMAN	RC3-ST0187-131089-011-408 ST0197 Homo sapiens cDNA
2218	13352	26483	1.94	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
187	13409		56.19	4.0E-54	AF110103.1	NT	Tupatia belangeri beta-actin mRNA, partial cds
978	14151	27211	14.58	4.0E-54	AA308764.1	EST_HUMAN	EST177698 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1848	14694	28096	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1848	14694	28097	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3274	16448		1.85	4.0E-54	AI935086.1	EST_HUMAN	wid26d11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328269 3' similar to TR:002711
96	13331	26356	8.12	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
1804	14757		0.96	3.0E-54	AW 515742.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2835	15756	28872	1.19	3.0E-54	AL110363.1	EST_HUMAN	hdb7g08.x1 NCI_OGAP_GC8 Homo sapiens cDNA clone IMAGE:2816542 3'
							DKFZp434E0731.1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434E0731 5'

Page 322 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6024	19207	32527	1.36	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7548	20620	34096	1.34	3.0E-54	AA844081.1	EST_HUMAN	ai82c08.s1 Soares_papillary_thyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7548	20620	34097	1.34	3.0E-54	AA844081.1	EST_HUMAN	ai82c08.s1 Soares_papillary_thyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:1388270 3'
11277	24344		1.77	3.0E-54	11434806	NT	Homo sapiens golgi autophagosome, golgi subfamily a, 5 (GOLGA5), mRNA
11341	24404	38053	4.01	3.0E-54	BF345800.1	EST_HUMAN	602019408f1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121 5'
11650	24729	38421	2.86	3.0E-54	AA393382.1	EST_HUMAN	zi70f12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
12338	28249	32110	1.32	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
12379	28149		3.16	3.0E-54	AW748965.1	EST_HUMAN	EST368628 MAGE resequences, MAGEC Homo sapiens cDNA
659	13845	26871	17.67	2.0E-54	5031900	NT	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
1396	14550	27625	1.54	2.0E-54	4507164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
2604	15727	28846	1.25	2.0E-54	AW163176.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2666	15787	28903	2.25	2.0E-54	AL163210.2	NT	ai82g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to SW:GUL1_HUMAN Q13616 CULLIN HOMOLOG 1 ;
2960	16137	29155	1.95	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3392	16662	29677	0.6	2.0E-54	AJ278314.1	NT	wy60b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3638	16802		6.1	2.0E-54	AA532925.1	EST_HUMAN	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
4321	17464		1.74	2.0E-54	4502642	NT	ri45g08.s1 NCI_CGAP_Pf8 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X63777 60S
4563	17701		7.1	2.0E-54	AF208161.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
5591	18786	31833	2.66	2.0E-54	4758069	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
5720	18913	32209	1.21	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens syncytin precursor, mRNA, complete cds
5882	19071	32379	3.99	2.0E-54	11426657	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5982	19167	32488	11.29	2.0E-54	AB046811.1	NT	tz43c11.y1 NCI_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2291348 5'
6786	18951	33351	1.63	2.0E-54	AF008915.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6950	20283	33701	0.68	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6950	20283	33702	0.68	2.0E-54	AB023212.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
7273	20356	33810	8.33	2.0E-54	11426544	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
9828	22899	38451	3.98	2.0E-54	AB001025.1	NT	Homo sapiens neurotrophin 1 (neurotrophin, von Recklinghausen disease, Watson disease) (NF-1), mRNA
10213	23249	38638	1.14	2.0E-54	11429127	NT	Homo sapiens mRNA for brain ryandine receptor, complete cds
10326	23361	38971	0.78	2.0E-54	11418762	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
							Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10328	23361	36972	0.76	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10841	23874	37484	0.46	2.0E-54	AB007031.1	NT	Homo sapiens mRNA for KIAA0482 protein, partial cds
11275	19651	33351	1.46	2.0E-54	AF008916.1	NT	Homo sapiens EVI6 homolog mRNA, complete cds
12027	25011		1.72	2.0E-54	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
12893	25691	31970	4.36	2.0E-54	8667387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
4587	17724		1.55	1.0E-54	BF316418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8927	22006	35545	0.5	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10459	23494	37105	0.52	1.0E-54	AA412408.1	EST_HUMAN	zu10609.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
10469	23494	37106	0.52	1.0E-54	AA412408.1	EST_HUMAN	zu10609.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
13086	25709		2.33	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5' end
10568	23603	37208	1.02	9.0E-55	BE081469.1	EST_HUMAN	QV2-BT0635-160400-143-h12 BT0635 Homo sapiens cDNA
1344	14500		1.59	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1348	14503		2.77	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11471	24530		1.83	8.0E-55	AW409714.1	EST_HUMAN	fh02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2360907 5'
9004	22083		0.48	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2803822 3' similar to TR:O60385
9393	22456	36021	1.28	7.0E-55	AA895681.1	EST_HUMAN	O60386 FOS38654_1_1
9418	22480	36055	1.71	7.0E-55	AU133909.1	EST_HUMAN	ak2ba11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407260 3'
11486	24544	38215	8.08	7.0E-55	AI561056.1	EST_HUMAN	AU136009 PLACE1 Homo sapiens cDNA clone IMAGE:1011576 5'
11483	24544	38216	8.08	7.0E-55	AI561056.1	EST_HUMAN	iq29f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12720	25911	31860	1.18	7.0E-55	BE670608.1	EST_HUMAN	iq29f09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
13050	26063		6.37	7.0E-55	H23306.1	EST_HUMAN	7637c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'
11804	24794	38492	1.96	8.0E-55	AB040934.1	NT	ym57g07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:82444 5'
1810	14959	28051	1.21	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA17601 protein, partial cds
1810	14959	28052	1.21	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
4894	18024	31010	1.51	5.0E-55	AW206021.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6670	19829	33218	1.49	5.0E-55	4502240	NT	UI-H-B11-af*g-09-Q-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6805	25833	33360	1.08	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrocyte/plasma punctata 1) (ARSE), mRNA
6805	25833	33361	1.08	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrocyte/plasma punctata 1) (ARSE), mRNA
7182	20314	33757	1.03	5.0E-55	7382477	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7448	20523	33996	0.72	5.0E-55	11434422	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9244	22321	35865	2.3	6.0E-55	4506902	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9520	22595		0.81	6.0E-55	BE004386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
10243	23278	36872	1.53	6.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10243	23278	36873	1.53	6.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10427	23462	37069	1.13	6.0E-55	5493765	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
11502	24560	38236	1.3	6.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
11502	24560	38237	1.3	6.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
12421	25298		1.73	6.0E-55	11417972	NT	Homo sapiens pascadillo (pascadillo) homolog 1, containing BRCT domain (PES1), mRNA
56	16004	26310	2.24	4.0E-55	AW957994.1	EST_HUMAN	EST370064 MAGe sequences, MAGe Homo sapiens cDNA
689	13873	26906	32.17	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1472	14626	27710	2.16	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1472	14626	27711	2.16	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1544	14696		1.72	4.0E-55	BF061411.1	EST_HUMAN	7552b10.x1 Scores_NSF_F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE3390043 3' similar to contains L1.13 L1 repetitive element
2081	15221	28341	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2081	15221	28342	2.19	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2151	15287	28412	8.39	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2151	15287	28413	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG) mRNA
2384	15516	28844	3.02	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8639	21620		9.85	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11605	24563		2.31	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12937	25244		1.82	4.0E-55	BF303941.1	EST_HUMAN	601885575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
8731	19887	33279	0.88	3.0E-55	AA077156.1	EST_HUMAN	7B09A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B09A09
12273	25205		4.18	3.0E-55	BE176519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
13103	25719		3.53	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C064
388	13594	26830	1.69	2.0E-55	X67147.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
565	13757		1.08	2.0E-55	M10976.1	NT	Human endogenous retrovirus DNA (4-1), complete retroviral segment
666	13852	26860	3.98	2.0E-55	4507296	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
3023	16199	29222	0.89	2.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4897	18027	31014	3.51	2.0E-55	BE719989.1	EST_HUMAN	CM-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7673	25951	34217	0.85	2.0E-55	AW501988.1	EST_HUMAN	UHF-BN0-ake-f-08-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
9265	22342	35892	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76908.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:3134463 3'
9265	22342	35893	0.48	2.0E-55	BF224452.1	EST_HUMAN	h76908.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:3134463 3'

Page 325 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9381	22436		4.33	2.0E-55	AI002836.1	EST_HUMAN	am98h05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
9442	22510		0.67	2.0E-66	BE007069.1	EST_HUMAN	THR.b2 THR repetitive element;
11192	24261	37897	2.39	2.0E-55	AU119344.1	EST_HUMAN	QVQ-BN0147-280400-213-g06 BN0147 Homo sapiens cDNA
13177	16199	29222	1.34	2.0E-55		NT	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
98	13334	26361	1.62	1.0E-55	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
194	13417	26448	40.5	1.0E-66	U09823.1	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
588	13779	26798	1.38	1.0E-55	AI028718.1	EST_HUMAN	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1173	14336	27392	3.92	1.0E-55	AB020710.1	NT	ov65g09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644180 3'
2008	15146	28261	2.33	1.0E-55	BE277861.1	EST_HUMAN	Homo sapiens mRNA for KIAA0903 protein, partial cds
2008	15146	28262	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
2401	15532		4.85	1.0E-55	5803174	NT	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
2415	15697	28873	1.44	1.0E-55	AF000990.1	NT	Homo sapiens SMA3 (SMA3), mRNA
2686	15711	28829	19.88	1.0E-55	X13111.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2620	16743	28857	5.51	1.0E-55	AB007866.2	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2620	16743	28868	5.51	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2677	16767	28914	3.37	1.0E-55	L54067.1	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2850	15904	28073	1.22	1.0E-55	AB033046.1	NT	Homo sapiens CLP mRNA, partial cds
3465	16652	28674	1.16	1.0E-55	W28189.1	EST_HUMAN	Homo sapiens mRNA for KIAA1219 protein, partial cds
4097	17282	30263	4.28	1.0E-55	AL163267.2	NT	43c-5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4409	17551	30536	1.1	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C067
4853	17988		0.94	1.0E-55	N77291.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4949	18078	31054	1.15	1.0E-55	AB037183.1	NT	y44g03.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246620 5'
4949	18078	31055	1.16	1.0E-55	AB037183.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5614	18808	31876	0.65	1.0E-55	AF119856.1	NT	Homo sapiens DSCR5b mRNA, complete cds
6401	19570	32932	7.28	1.0E-55	11433048	NT	Homo sapiens PRO1851 mRNA, complete cds
6401	19570	32933	7.28	1.0E-55	11433048	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8178	21260	34782	1.7	1.0E-55	11432994	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8178	21260	34783	1.7	1.0E-55	11432994	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8266	21348	34863	0.49	1.0E-55	11421649	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8279	21355	34872	0.53	1.0E-55	AF224492.1	NT	Homo sapiens SKAP55 homolog (SKAP-HOM), mRNA
8273	21355	34873	0.53	1.0E-55	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds

Page 326 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11152	24223	37851	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11152	24223	37852	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11733	23919	37544	1.86	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11756	23941	37567	1.34	1.0E-55	T10045.1	EST_HUMAN	seq1576 b4HB3MA Co8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F161 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
11789	24778	38476	2.67	1.0E-55	8922743	NT	Homo sapiens hypothetical protein FLJ10891 (FLJ10891), mRNA
11876	24884	38560	1.78	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
7522	20595	34070	1.85	9.0E-56	BE379074.1	EST_HUMAN	60123702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
11545	24501	38277	1.34	8.0E-56	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2793	15909	29017	7.08	7.0E-56	H19934.1	EST_HUMAN	yn62g03.r1 Soares adult brain N26cHB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element:
7818	20873	34371	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
7818	20873	34372	1.93	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-b07 CT0252 Homo sapiens cDNA
1727	14877	27868	2.7	5.0E-56	AW997712.1	EST_HUMAN	RC3-BND083-170200-011-r01 BN0053 Homo sapiens cDNA
9362	22437	35895	0.71	6.0E-56	AW015507.1	EST_HUMAN	U1-H-B10p-aau-e-05-Q-U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10589	23634	26268	1.35	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12513	26137	31550	2.47	6.0E-56	H55089.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_59 5'
28	13266	26268	8.64	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
28	13266	26269	8.94	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2773	15888	28998	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	15888	28999	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2873	13732	26756	9.22	4.0E-56	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6387	19556	32915	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19556	32916	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10724	23757	37304	1.68	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11163	24234	37863	7.73	4.0E-56	AI498096.1	EST_HUMAN	hm55g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2183046 3'
11163	24234	37864	7.73	4.0E-56	AI498096.1	EST_HUMAN	hm55g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2183046 3'
1372	14527	27601	2.69	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1804	14953	28047	1.84	3.0E-56	6912743	NT	Homo sapiens 5'-3' exoribonuclease 2 (XRN2), mRNA
2217	15351	28482	1.6	3.0E-56	6912697	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3195	16370	29376	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3195	16370	29377	1.67	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3939	17098		2.81	3.0E-56	AF055068.1	NT	Homo sapiens MHC class 1 region

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4507	17646	30634	0.67	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4544	17892	30864	4.42	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4695	17830	30816	2.4	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5801	18991	32263	1.5	3.0E-56	4759163	NT	Homo sapiens spero/osteonecin, cncv and kazal-like domain proteoglycan (testican) (SPOCK) mRNA
5801	18991	32264	1.5	3.0E-56	4759163	NT	Homo sapiens spero/osteonecin, cncv and kazal-like domain proteoglycan (testican) (SPOCK) mRNA
7014	20150	33571	5.5	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7476	20551	34023	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
7476	20551	34024	2.07	3.0E-56	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2) mRNA
8016	22056	35635	6.11	3.0E-56	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10018	23056	36852	0.9	3.0E-56	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10698	23731	37336	1.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10980	24059	37683	2.62	3.0E-56	AB042556.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
11594	24847	38330	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11594	24847	38331	4.64	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
12377	25268	32075	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12377	25268	32076	1.62	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
537	13730	26976	11.95	2.0E-56	AA159818.1	EST_HUMAN	zsf2a08.s1 Stratiogene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:645206 3'
761	16021	26976	1.18	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
751	16021	26976	1.18	2.0E-56	BE084386.1	EST_HUMAN	RC4-BT0310-110300-016-110 BT0310 Homo sapiens cDNA
3053	16228	29249	0.94	2.0E-56	AB037836.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3391	16561	29805	0.84	2.0E-56	AB006981.1	NT	Homo sapiens gene for activin receptor type 1B, complete cds
3624	16788	29805	1.26	2.0E-56	AV703784.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCF310 5'
7239	20323	33767	1.39	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
1003	14174	29928	3.01	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3765	16926	29928	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NC1 CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
3765	16926	29929	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NC1 CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
5145	18268	31238	1.42	1.0E-56	AB06162.1	EST_HUMAN	QV-BT077-130199-079 BT077 Homo sapiens cDNA
10161	23168	36886	0.69	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10254	23269	36886	1.52	1.0E-56	AW545987.1	EST_HUMAN	RC2-OT0163-220985-001-E02 CT0163 Homo sapiens cDNA
642	13927	38227	1.39	9.0E-57	AW580886.1	EST_HUMAN	QV6-OT0033-070300-152-H03 OT0033 Homo sapiens cDNA
11494	24552	38227	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11494	24552	38228	1.72	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11811	24801	38500	2.2	9.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
14	13252	26252	1.02	8.0E-57	8923348	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
308	13524	26558	2.93	8.0E-57	AW816403.1	EST_HUMAN	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
907	14082	27147	7.49	8.0E-57	AW264598.1	EST_HUMAN	xc05d10.x1 NC1_CGAP_Bri53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1859	15005	28112	1.45	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5355	26034	31679	1.92	8.0E-57	11418185	NT	z61b12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5355	19633	33066	0.91	8.0E-57	AB020706.1	NT	Homo sapiens apolipoprotein 2, mitochondrial (APO2), mRNA
5529	19753	33138	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
5593	19753	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
6593	19753	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7607	20977	34152	0.82	8.0E-57	7682283	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7627	20977	34486	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7627	20977	34487	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11768	13252	26252	3.51	8.0E-57	8923348	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12041	25022	38726	1.74	8.0E-57	11433358	NT	Homo sapiens nilein (LOC51199), mRNA
12102	25082	38769	1.53	8.0E-57	11431290	NT	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
12791	25528	32007	1.87	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12808	25528	32007	1.94	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1246	14405	27467	0.88	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
2698	15817	28932	0.97	7.0E-57	7657692	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2698	15817	28933	0.97	7.0E-57	7657692	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3344	15517	29532	0.81	7.0E-57	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3982	17139	30143	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3982	17139	30144	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
13185	26071		3.99	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3949	17009	30010	6.03	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
827	14005	27062	0.64	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1362	14516		12.47	3.0E-57	AA230279.1	EST_HUMAN	nc1307.51 NC1_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2464	15591	28716	1.12	3.0E-57	AA348335.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10 ;
2768	15883	28982	1.03	3.0E-57	BE676622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
							7531610.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
							CE20263 ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2768	15883	28993	1.03	3.0E-57	BE676922.1	EST_HUMAN	733b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H9C.2
3652	19816	28827	1	3.0E-57	AF232708.1	NT	CE20283 ;
3788	16949		51.29	3.0E-57	AW653984.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
8163	18328	32676	1.25	3.0E-57	11225608	NT	RC3-C10254-110300-027-d10 CT0254 Homo sapiens cDNA
8251	19425	32771	3.25	3.0E-57	BE706537.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8338	21418	34945	3.92	3.0E-57	W28130.1	EST_HUMAN	601589896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8363	21444	34968	1.99	3.0E-57	11545798	NT	4216 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8476	21557	35080	0.78	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8624	21704	35240	0.92	3.0E-57	11427757	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9059	22138	35682	5.14	3.0E-57	AU117659.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
9451	22567	36132	0.69	3.0E-57	11545788	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
9451	22567	36133	0.69	3.0E-57	11545788	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
11148	24220	37847	2.34	3.0E-57	AW248374.1	EST_HUMAN	ALU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
12384	25167	31554	6.37	3.0E-57	W23871.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
12882	25640	31984	1.17	3.0E-57	AJ003649.1	EST_HUMAN	2820473.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 6'
1530	14683	27762	2.89	2.0E-57	AF246219.1	NT	2b45d11.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
1530	14683	27763	2.89	2.0E-57	AF246219.1	NT	AJ003649 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp10-1L1
2780	15906	28014	5.5	2.0E-57	AA845419.1	EST_HUMAN	Homo sapiens SNARE protein kinase SNARE mRNA, complete cds
3525	16690		1.4	2.0E-57	AL163204.2	NT	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
3641	16805	28818	0.72	2.0E-57	R07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3641	16806	28819	0.72	2.0E-57	R07702.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:126809 5'
4304	17447	30433	0.71	2.0E-57	AA018299.1	EST_HUMAN	ye98h01.1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:126809 5'
4304	17447	30434	0.71	2.0E-57	AA018299.1	EST_HUMAN	ze94c06.1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:361480 6'
4632	17768	30749	7.42	2.0E-57	AL163283.2	NT	ze94c06.1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:361450 5'
6786	18977		1.48	2.0E-57	AA016131.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
8159	19334		31.41	2.0E-57	BF115266.1	EST_HUMAN	ze93c05.1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:360684 5' similar to contains L1.13 L1 repetitive element ;
8288	19481	32813	6.34	2.0E-57	11431281	NT	Tn80704.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570566 3' similar to contains TAR1.11
8832	21811	35449	1.03	2.0E-57	AF045462.1	NT	MER22 repetitive element ;
10051	23089	36891	1.06	2.0E-57	AF057722.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
							Homo sapiens cell-line KGT transcriptional regulatory protein p64 mRNA, complete cds
							Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4

Page 330 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11548	24604	38281	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11548	24604	38282	1.55	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11592	24845	38327	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX6 related protein
11592	24845	38328	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX6 related protein
13214	26097	31664	2.89	2.0E-57	AF008668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
2305	15437	28569	1.89	1.0E-57	AW503208.1	EST_HUMAN	U1HF-BN0-akt-g-07-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078848 5'
8991	21970		1.87	1.0E-57	BE043031.1	EST_HUMAN	h32408.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3035062 3' similar to TR:O00246 O00246
12545	25368		11.29	1.0E-57	AW470791.1	EST_HUMAN	h33406.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.k3
5794	18985	32298	0.83	9.0E-58	AA297847.1	EST_HUMAN	THR repetitive element;
12854	25507	31990	1.84	9.0E-58	BE395061.1	EST_HUMAN	EST11348 Ulenus Homo sapiens cDNA 5' end
602	13791		1.69	8.0E-58	BE868715.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3650211 5'
671	13857	26896	4.24	8.0E-58	AI798378.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3650211 5'
671	13857	26897	4.24	8.0E-58	AI798378.1	EST_HUMAN	t33407.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
1804	15047	28157	2.4	8.0E-58	11434921	NT	UNNAMED HERV-H PROTEIN;
1904	15047	28158	2.4	8.0E-58	11434921	NT	UNNAMED HERV-H PROTEIN;
3040	16216		2.76	8.0E-58	7706132	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
7387	20465	33930	0.93	7.0E-58	BE561971.1	EST_HUMAN	Homo sapiens DHHC1 protein (LOC51304), mRNA
11095	24168		4.54	7.0E-58	5174542	NT	601348704F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687577 5'
11170	24241	37873	2.61	7.0E-58	AW504109.1	EST_HUMAN	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
11170	24241	37874	2.61	7.0E-58	AW504109.1	EST_HUMAN	(MEF2B) mRNA
2328	15460	28593	1.53	6.0E-58	BE395081.1	EST_HUMAN	U1HF-BN0-ali-g-10-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
2448	15578	28706	5.25	6.0E-58	AU130689.1	EST_HUMAN	U1HF-BN0-ali-g-10-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
2968	16142	29160	1.01	6.0E-58	BE242150.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2968	16142	29161	1.01	6.0E-58	BE242150.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001268 5'
6299	19472	32827	0.98	6.0E-58	AF106911.1	NT	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project= TCAA Homo sapiens cDNA clone TCAAAP1219
10617	23552	37163	1.27	6.0E-58	11434746	NT	TCAAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project= TCAA Homo sapiens cDNA clone TCAAAP1219
12654	25434		1.22	6.0E-58	11526291	NT	sapiens cDNA clone TCAAAP1219
							sapiens cDNA clone TCAAAP1219
							Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
							Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
							Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

Page 331 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	13527	26560	3.06	5.0E-58	4507334	NT	Homo sapiens synaptobin 1 (SYNJ1), mRNA
728	13910	26950	6.96	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160800-016-b05 NT0057 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27442	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1222	14382	27442	2	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3400	16570	26595	4.09	5.0E-58	AA988183.1	EST_HUMAN	α98e07.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4973	17616	30496	0.93	5.0E-58	AI636745.1	EST_HUMAN	ts89e07.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P19994 PROFILIN II;
5748	18938		1.91	5.0E-58	11466282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6307	19479	32834	6.55	5.0E-58	H23072.1	EST_HUMAN	ym51h07.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:52071 5'
6524	19689	33063	0.79	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8600	19760	33148	1.03	5.0E-58	11421330	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
8917	20232	33665	0.6	5.0E-58	AF051334.1	NT	Homo sapiens ribitin (NBS) mRNA, complete cds
8917	20232	33666	0.6	5.0E-58	AF051334.1	NT	Homo sapiens ribitin (NBS) mRNA, complete cds
7255	20338	33788	0.71	5.0E-58	4885400	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA
8156	21238	34759	9.08	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8548	21629	35167	0.68	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
10081	23099	36701	0.96	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10328	23363	36973	1.8	5.0E-58	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10812	23646	37264	0.65	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10612	23646	37265	0.66	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
12362	26065		4.5	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (OECR1), mRNA
12850	26102		1.47	5.0E-58	11428423	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
384	13592	26627	1.71	4.0E-58	4502302	NT	Homo sapiens interleukin 10 receptor, beta (LTORB), mRNA
819	13998	27052	1.87	4.0E-58	4504834	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
1496	14840	27731	1.24	4.0E-58	4503648	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
2696	15916	28930	2.12	4.0E-58	U36251.1	NT	Human mRNA, Xq terminal portion
3402	16372	29587	1.41	4.0E-58	D16470.1	NT	Human mRNA, EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
3834	16994	29966	1	4.0E-58	5031660	NT	Human mRNA, EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
7995	21045	34557	0.68	4.0E-58	BE463857.1	EST_HUMAN	hy18a02.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:3197842 3'
11624	24676	38366	7.44	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 6 (E1B-AP6), mRNA

Page 332 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
346	13556		0.96	3.0E-58	R17878.1	EST_HUMAN	y910a02.r1 Soares infant brain (NIB Homo sapiens cDNA clone IMAGE:31693 5'
1420	14574	27647	2.6	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3246	10420	29435	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3248	10420	29436	3.07	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6390	19559	32918	0.61	3.0E-58	BE089509.1	EST_HUMAN	QV0-BT0702-170400-104-09 B.T0702 Homo sapiens cDNA
6574	19796	33115	1.1	3.0E-58	F07056.1	EST_HUMAN	HSC1TG081 normalized infant brain cDNA Homo sapiens cDNA clone c-1g08
6778	19933	33329	2.49	3.0E-58	AV712977.1	EST_HUMAN	AV712977 DCA Homo sapiens cDNA clone DGAZG04 5'
903	14136	27197	12.47	2.0E-58	AF08624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
							ba08807.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb-X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb-X81987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
1318	14474		7.88	2.0E-58	BE20532.1	EST_HUMAN	xa08a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5451	18661	31630	0.94	2.0E-58	AW074831.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5473	25805	31652	2.63	2.0E-58	BE007186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5473	25805	31655	2.63	2.0E-58	BE007186.1	EST_HUMAN	601499961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6182	19358	32706	1.7	2.0E-58	BF513488.1	EST_HUMAN	U1H-BW1-ams-g-11-0.U1.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
							em57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME1; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN ;
6249	19423	32769	2.16	2.0E-58	A1124874.1	EST_HUMAN	YQ08108.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196378 5'
6283	19456	32806	0.83	2.0E-58	R92587.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7066	20119	33533	0.83	2.0E-58	A1291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33848	2.79	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33849	2.79	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10978	24058	37692	16.01	2.0E-58	BF307745.1	EST_HUMAN	hm25f08.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
11207	24276	37913	1.58	2.0E-58	AW872641.1	EST_HUMAN	Human complement component C3 mRNA, 3'end
740	13922	26982	1.06	1.0E-58	M65134.1	NT	
1093	14258	27314	1.33	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1358	14513	27586	1.12	1.0E-58	AW957182.1	EST_HUMAN	EST369252 IMAGE resequences, MAGD Homo sapiens cDNA
1358	14513	27587	1.12	1.0E-58	AW957182.1	EST_HUMAN	EST369252 IMAGE resequences, MAGD Homo sapiens cDNA
1427	14581	27654	2.8	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1697	14949	27935	1.28	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3196935 3'
2719	15337	28047	1.01	1.0E-58	AF217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2663	15077	29087	1.14	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
2892	15206	28322	1.01	1.0E-58	6174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA

Page 333 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3627	16761	29809	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3627	16761	29810	0.93	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3814	16974	29977	0.66	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
5085	18213	31186	7.13	1.0E-58	A141063.1	EST_HUMAN	ca3h01.x1 Soares_NIH/MPU_S1 Homo sapiens cDNA clone IMAGE:1078129 3'
5964	19160	32466	1.37	1.0E-58	BE061860.1	EST_HUMAN	RC1-BT0254-290100-016-e01 BT0254 Homo sapiens cDNA
7002	20138	33566	0.87	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51260). mRNA
8305	21987		0.49	1.0E-58	AW973537.1	EST_HUMAN	EST385937 MAGC resequences, MAGM Homo sapiens cDNA
9070	22149	35695	0.82	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2). mRNA
9182	22260	35902	0.77	1.0E-58	AV751007.1	EST_HUMAN	AV751007 NPC Homo sapiens cDNA clone NPCACH09 5'
9282	22358	35907	0.84	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9282	22358	35908	0.84	1.0E-58	AA412397.1	EST_HUMAN	z89f05.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10389	23424	37031	0.65	1.0E-58	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chaperon-110) (DLG2). mRNA
12074	25055		2.1	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
12100	25080	38787	2.61	1.0E-58	D61405.1	NT	Human MSH3 gene, exon10
2303	15435	28567	53.38	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6979	20207	33635	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
6978	20207	33636	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST95683 Testis I Homo sapiens cDNA 5' end
8374	21455	34979	1.56	8.0E-59	A1761983.1	EST_HUMAN	wh50406.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
182	16005		1.97	6.0E-59	BF036327.1	EST_HUMAN	f01456531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
8016	21066	34579	0.82	6.0E-59	AA862431.1	EST_HUMAN	cm81 ad4.st NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1553550 3' similar to TR:Q13732 Q13732 SA GENE PRODUCT PRECURSOR.;
8440	21521	35050	0.69	6.0E-59	A1750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
3197	16372	29379	7.75	6.0E-59	A1807484.1	EST_HUMAN	wf48c11.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4780	17915	30901	9.84	6.0E-59	X83497.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7129	18555	31470	8.22	5.0E-59	AW162304.1	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;
8006	22085	35628	1.03	5.0E-59	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39). mRNA
9906	22946	35532	1.44	5.0E-59	AV762869.1	EST_HUMAN	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
11146	24218	37845	4.54	5.0E-59	11434508	NT	Homo sapiens hypothetical protein (LOC57143). mRNA
816	13695	27050	1.9	4.0E-59	D80006.1	NT	Human mRNA for KIAA0784 gene, partial cds
1266	14423	27489	0.61	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products

Page 334 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1266	14423	27490	0.81	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
4912	18042	31032	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4912	18042	31033	1.14	4.0E-59	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5654	18848	32130	0.95	4.0E-59	11034810	NT	Homo sapiens oleanin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12498	25998		3.99	4.0E-59	AF057720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13248		6.74	3.0E-59	AW965624.1	EST_HUMAN	EST377582 MAGE resequences, MAGI1 Homo sapiens cDNA
234	13455	26481	3.88	3.0E-59	7692247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14897	27992	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
1748	14897	27993	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2198	15333	28458	8.54	3.0E-59	AB020035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2198	15333	28480	8.54	3.0E-59	AB020035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3104	16280	29294	0.87	3.0E-59	T18895.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3104	16280	29295	0.87	3.0E-59	T18895.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3199	16374	29383	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3199	16374	29384	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3930	17089	30096	1.19	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4808	17942	30929	2.75	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4865	18094	31071	2.12	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase receptor type, T (PTPRT), mRNA
5182	18284		1.22	3.0E-59	M85961.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 2
6350	19520	32877	2.4	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7516	20589	34064	1.85	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8116	21198	34718	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
8116	21198	34719	1.11	3.0E-59	X12556.1	NT	Human mRNA for dbi proto-oncogene
10250	23285	36860	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
10250	23285	36861	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
12635	25428		11.11	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
6948	20259		0.59	2.0E-59	AA470073.1	EST_HUMAN	298405.51 Soares testis NHT Homo sapiens cDNA clone IMAGE:739377 3'
7216	20081	33494	0.59	2.0E-59	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
9837	22877		4.84	2.0E-59	AA309774.1	EST_HUMAN	EST180833 Jurkat T-cells V Homo sapiens cDNA 5' end
10745	23778		1.34	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT00038-100700-032-07 NT00036 Homo sapiens cDNA
11089	24144	37780	2.19	2.0E-59	AW410698.1	EST_HUMAN	h09704.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11089	24144	37781	2.19	2.0E-59	AW410698.1	EST_HUMAN	ff07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861654 5'
12373	25298	32118	4.28	2.0E-59	AI631809.1	EST_HUMAN	wa36c12.x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12683	26019	31668	3.87	2.0E-59	L11045.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
167	13392		5.65	1.0E-69	BE296411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
1569	14722	27803	1.04	1.0E-69	T92522.1	EST_HUMAN	601178757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531627 5'
2683	15903		2.65	1.0E-59	AA748488.1	EST_HUMAN	y25509.r1 Stratigene lung (#937210) Homo sapiens cDNA clone IMAGE:118768 5' similar to SP:S21348
7735	20798	34285	1.14	1.0E-59	AJ130894.1	NT	S21348 HYPOTHETICAL PROTEIN 4-;
7895	20847	34454	1.3	1.0E-59	BE256814.1	EST_HUMAN	oa58h11.s1 NCLCGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13637
7895	20847	34455	1.3	1.0E-59	BE256814.1	EST_HUMAN	Q13637 MER37 TRANSDUCIBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
9585	22727	36286	0.98	1.0E-59	11419630	NT	Homo sapiens mRNA for transcription factor
9804	22844	36421	0.58	1.0E-59	11428849	NT	Homo sapiens mRNA for transcription factor
9804	22844	36422	0.59	1.0E-59	11428849	NT	Homo sapiens mRNA for transcription factor
11094	20798	34285	10.98	1.0E-59	AJ130894.1	NT	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352892 5'
783	13933	27013	1.45	8.0E-60	AW977845.1	EST_HUMAN	601111951F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352892 5'
1499	14652	27734	3.21	8.0E-60	4759159	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
2241	15374	28502	4.76	8.0E-60	5174656	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
2241	15374	28503	4.76	8.0E-60	5174656	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
6103	16283	32616	1.16	8.0E-60	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6633	19792	33181	0.89	8.0E-60	S83182.1	NT	EST389849 MAGC resequences, MAGO Homo sapiens cDNA
7874	20928	34434	0.89	8.0E-60	11420841	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
8162	21234	34755	3	8.0E-60	X17033.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
9139	22216	35762	2.93	8.0E-60	11428849	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
9671	22633	36202	0.78	8.0E-60	11417118	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
9871	22633	36203	0.78	8.0E-60	11417118	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
10789	23832	37455	0.82	8.0E-60	5453997	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
11071	24146	37783	4.17	8.0E-60	AL163204.2	NT	Human mRNA for integrin alpha-2 subunit
11071	24146	37784	4.17	8.0E-60	AL163204.2	NT	Homo sapiens S-antigen; retina and pineal gland (arrestin) (SAG), mRNA
773	13954	27004	11.11	7.0E-60	AF055086.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
774	13954	27004	25.11	7.0E-60	AF055086.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
838	14016	27071	1.47	7.0E-60	4504634	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2197	15332	28458	1.82	7.0E-60	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2845	15369	29068	0.98	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4295	17438	30425	2.4	7.0E-60	4605488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4698	17853	30818	0.91	7.0E-60	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9607	22662	36235	4.21	7.0E-60	H58041.1	EST_HUMAN	y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains L TRS repetitive element ;
11646	24725	38417	1.73	7.0E-60	H58041.1	EST_HUMAN	y1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains L TRS repetitive element ;
2248	15381	28508	1.16	6.0E-60	BE864974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8632	21712		8.04	6.0E-60	H52486.1	EST_HUMAN	y178h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element ;
86	13321	26348	1.06	5.0E-60	AI807817.1	EST_HUMAN	wf52c07.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2359212 3'
86	13321	26348	1.06	5.0E-60	AI807817.1	EST_HUMAN	wf52c07.x1 Soares NFL_I_GBC S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2308	15440	28574	1.83	4.0E-60	AW503208.1	EST_HUMAN	UIHF-ENO-akt-g-07-Q-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2308	15440	28576	1.83	4.0E-60	AW503208.1	EST_HUMAN	UIHF-ENO-akt-g-07-Q-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
3037	16213		1.45	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7508	20582	34055	0.78	4.0E-60	BF196088.1	EST_HUMAN	tr8105.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE Q61085 GTP-RHO BINDING PROTEIN 1 ;
9326	22402		0.65	4.0E-60	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1907	15050	28181	4.98	3.0E-60	BE662611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1907	15050	28182	4.98	3.0E-60	BE662611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1918	15061		2.81	3.0E-60	6031130	NT	Homo sapiens prohibitin (PHB) mRNA
4579	17716	30689	2.75	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5494	18693	31709	0.69	3.0E-60	BF365143.1	EST_HUMAN	QV4-NIN1149-250800-423-01 NIN1149 Homo sapiens cDNA
5757	18949	32251	2.21	3.0E-60	AW836196.1	EST_HUMAN	RC3-LT0023-200100-012-a01 LT0023 Homo sapiens cDNA
7063	18520	31513	1.07	3.0E-60	AI792814.1	EST_HUMAN	q160111.v5 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE P52624 URIDINE PHOSPHORYLASE ;
8567	21678	35215	4.59	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8567	21678	35216	4.59	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8763	21862	35405	0.6	3.0E-60	AI040235.1	EST_HUMAN	ox56d09.x1 Soares NIH-MFJ S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to
8940	22019	35560	3.84	3.0E-60	5174644	NT	SW:FORM_MOUSE Q05860 FORMIN ;
13053	25058		1.55	3.0E-60	AA485288.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
							ab07h04.r1 Stragene lung (4637210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.L1 LTR10 repetitive element ;

Page 337 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
31	13269	28273	1.7	2.0E-60	AY008285.1	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1455	14608	27698	3.99	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1759	14908	28001	2.2	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3669	18832	28843	0.78	2.0E-60	4757867	NT	Homo sapiens v-ref murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4025	17181	30190	0.73	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6430	19598	32864	0.95	2.0E-60	AI791662.1	EST_HUMAN	mm01112.6 NCL_CGAP_Cc9 Homo sapiens cDNA clone IMAGE:1078495 5' similar to contains THR.t1 THR repetitive element:
6821	19781	33199	1.26	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
8955	20008	33418	1.08	2.0E-60	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6889	18508	31624	2.15	2.0E-60	4503044	NT	Homo sapiens corticotroph releasing hormone receptor 2 (CRHR2) mRNA
6889	18508	31625	2.15	2.0E-60	4503044	NT	Homo sapiens corticotroph releasing hormone receptor 2 (CRHR2) mRNA
7269	20342	33793	8.18	2.0E-60	AA311168.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prolthymocin, alpha
7269	20342	33794	8.18	2.0E-60	AA311169.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prolthymocin, alpha
7810	20866		0.9	2.0E-60	BF512808.1	EST_HUMAN	UI-H-BW1-arnu-c-02-0-UJ.s1 NCL_CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3071210 3'
8194	21276	34799	1.33	2.0E-60	X85597.1	EST_HUMAN	HS15BEST human adult testis Homo sapiens cDNA clone CAM_IEST15
8068	22147	35694	3.12	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
10183	23220	36813	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
10183	23220	36814	1.83	2.0E-60	11991659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA8A), mRNA
11769	23945	37572	1.7	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 80kD, polypeptide 5 (RPS6KA5), mRNA
12972	25448		2.36	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12929	25985		1.47	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12948	25664		1.5	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
535	13728	28762	1.02	1.0E-60	BE176886.1	EST_HUMAN	PM3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA
4011	17169	30176	1.08	1.0E-60	AU143386.1	EST_HUMAN	AUT43389 Y78AA1 Homo sapiens cDNA clone Y78AA1001854 5'
6070	18188	31172	2.57	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8134	21216	34737	1.39	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
8955	22034		2.84	1.0E-60	AA244041.1	EST_HUMAN	nc04e12.1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1 repetitive element:
8982	22081	35601	1.35	1.0E-60	AU754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAE005 5'
12906	26079		1.49	1.0E-60	AJ252313.1	NT	Homo sapiens genomic hybrid Rhesus box
1123	14288	27343	8.4	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'

Page 338 of 550

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8903	21987	35526	0.53	9.0E-61	4885346	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8908	21987	35527	0.53	9.0E-61	4885646	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2735	15852	28965	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2735	15852	28966	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
3018	16192		2.63	8.0E-61	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
8079	21161	34679	1.03	8.0E-61	AA583988.1	EST_HUMAN	m58g06.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
130	13357	26389	0.79	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
130	13357	26390	0.79	7.0E-61	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
276	13484	26524	3.06	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
834	14012	27068	6.49	8.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1352	14507	27579	12.72	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1659	14811	27896	1.04	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1679	14831	27916	2.91	6.0E-61	AA590333.1	EST_HUMAN	m86h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
3381	16553	29667	8.16	6.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2R23 Homo sapiens cDNA clone NT2R23001263 5'
6155	19331	32877	2.96	6.0E-61	S79249.1	NT	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7497	20572	34045	1.49	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7799	20851	34343	1.85	6.0E-61	AF035737.1	NT	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
12564	14012	27068	1.69	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
13157	26752	31925	1.42	6.0E-61	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
226	13448	26476	2.54	5.0E-61	8922880	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
228	13448	26477	2.54	5.0E-61	8922880	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
370	13579	26612	0.7	6.0E-61	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
1713	14884	27953	2.84	5.0E-61	4505008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3101	16277	29291	2.19	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3268	16442	29462	1.82	5.0E-61	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
4090	17245		2.22	5.0E-61	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
5118	13579	26612	0.75	5.0E-61	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
1798	14947	28039	1.94	4.0E-61	AU140307.1	EST_HUMAN	AU140307 PLACE2 Homo sapiens cDNA clone PLACE2000302 5'
5636	19122	32435	0.71	4.0E-61	7661637	NT	Homo sapiens DKFZP566B023 protein (DKFZP566B023), mRNA
12349	25252		9.47	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARB01 5'
8816	21696	35234	0.7	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
511	13705	26733	1.8	2.0E-61	8622829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1239	14398	27460	6.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147.401 HT0513 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1239	14398	27461	6.33	2.0E-61	BE188410.1	EST_HUMAN	QV2-HT0519-060400-147-401 HT0513 Homo sapiens cDNA
1699	14851	27938	1.36	2.0E-61	NE3039.1	EST_HUMAN	y63d11.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:246493 3' similar to gbL29444.60S RIBOSOMAL PROTEIN L39A (HUMAN);
2706	15824		1.72	2.0E-61	N36997.1	EST_HUMAN	y03f11.11 Soares melanocyte 2NDHM Homo sapiens cDNA clone IMAGE:270189 5'
6596	19718	33084	0.88	2.0E-61	11428166	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110116kD) (A TP6N1A), mRNA
9217	22295	35839	1.67	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKG Homo sapiens cDNA clone GKCEL G08 5'
9762	22700		0.98	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
10126	23164	36763	1.34	2.0E-61	AW50256.1	EST_HUMAN	UI-HF-BNO-akd-f12-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10466	23491	37101	2.94	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
11123	24195		4	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
13144	25744	31950	1.45	2.0E-61	AW99528.1	EST_HUMAN	QV0-BN0042-170300-162-f10 BN0042 Homo sapiens cDNA
448	13644		1.37	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
784	13973	27026	1.28	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L), mRNA
1430	14584	27658	1.07	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1809	14958		1.02	1.0E-61	US2657.1	NT	Human polymorphic trinucleotide repeat in X-linked retinitis pigmentosa (RP3) gene region
1906	15049	28160	4.43	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2270	15403	28531	1.54	1.0E-61	AW927281.1	EST_HUMAN	xn11b09.y1 NCL_CGAP_L15 Homo sapiens cDNA clone IMAGE:2603369 5' similar to contains element MSR1 repetitive element;
2896	16075	28093	0.98	1.0E-61	BE386383.1	EST_HUMAN	801273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614867 5'
3463	16630	29550	0.85	1.0E-61	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3828	16986	29989	1.16	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-g06 HT0577 Homo sapiens cDNA
4374	17517	30497	1.05	1.0E-61	M68840.1	NT	Human monamine oxidase A (MAOA) mRNA, complete cds
4561	17699	30680	0.95	1.0E-61	4769249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4561	17699	30681	0.95	1.0E-61	4769249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4981	18110	31086	9.55	1.0E-61	AW288181.1	EST_HUMAN	UI-H-BWO-ajb-b-08-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4981	18110	31087	8.55	1.0E-61	AV238181.1	EST_HUMAN	UI-H-BWO-ajb-b-08-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5075	18203	31175	0.92	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5509	18708	31723	0.71	1.0E-61	MT6423.1	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
5905	18996	32301	1.07	1.0E-61	7662303	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
6004	19189	32508	1.32	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7041	20094	33510	8.92	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds
7240	20324	33768	0.77	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
7341	20421	33883	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA

Page 340 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7341	20421	33884	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8328	21408	34035	2.89	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8508	21588	35123	3.34	1.0E-61	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9482	22539		2.78	1.0E-61	AW869726.1	EST_HUMAN	MR0-BN0070-040400-010-101 BN0070 Homo sapiens cDNA
9557	22622	36103	0.58	1.0E-61	11416280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10235	23270	36861	4.8	1.0E-61	11428892	NT	Homo sapiens KIAA0871 protein (KIAA0871), mRNA
10871	23956	37585	5.81	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11178	24247	37890	1.72	1.0E-61	AB044550.1	NT	Homo sapiens P/OKcl 19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
11325	24388	38033	1.44	1.0E-61	AB007830.1	NT	Homo sapiens mRNA for CSR2, complete cds
12242	26043		21.57	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
12286	26031	31677	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12286	26031	31678	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13028	26676	31859	10.94	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10565	23600	37206	1.08	9.0E-62	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
4673	17808	30798	0.85	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVVK
1131	14298	27361	1.12	7.0E-62	AV714334	EST_HUMAN	P31785 POL POLYPYRROLINE ;
3595	16759	29775	0.84	7.0E-62	P17480	SWISSPROT	AV714334 DOB Homo sapiens cDNA clone DCBAMA08 5'
6038	19221	32544	0.97	7.0E-62	11427865	NT	NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
11632	24712	39403	4.05	7.0E-62	AI208681.1	EST_HUMAN	(AUTOANTIGEN NOR-90)
3063	16239		1.55	6.0E-62	U09410.1	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
3471	16638		5.37	6.0E-62	11418255	NT	cg56a04.x1 Scatres testis NHT Homo sapiens cDNA clone IMAGE:1839160 3' similar to TR:O15103
7803	20859	34351	3.47	6.0E-62	AI762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
7803	20859	34352	3.47	6.0E-62	AI762801.1	EST_HUMAN	Homo sapiens CGI-58 protein (CGI-58), mRNA
8277	21359		0.68	6.0E-62	AW501124.1	EST_HUMAN	wid4d02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2389251 3'
8482	21533	35063	1.52	6.0E-62	11431139	NT	wid4d02.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2389251 3'
9554	22819	36189	3.87	6.0E-62	AW814393.1	EST_HUMAN	UHF-BP0p-ai-d-09-Q-U1r1 NIH_MGC 5T Homo sapiens cDNA clone IMAGE:3072833 5'
428	13624	26864	1.48	5.0E-62	AI950528.1	EST_HUMAN	Homo sapiens CGI-18 protein (LOC61008), mRNA
2478	15605	28729	5.16	5.0E-62	AJ271735.1	NT	MR3-S-T0203-130100-025-e09 ST0203 Homo sapiens cDNA
2478	15605	28730	5.16	5.0E-62	AJ271735.1	NT	wx51e07.x1 NCI_CGAP_Luz2 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
							Q08379 GOLGIN-95, contains element MER22 repetitive element ;
							Homo sapiens Xa pseudautosomal region, segment 1/2
							Homo sapiens Xq pseudautosomal region, segment 1/2

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3608	16673	29883	2.55	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4447	17587	30568	1.75	5.0E-62	AA431093.1	EST_HUMAN	zw78d09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW.NRDC_RAT
8748	21825	35362	0.74	5.0E-62	4506758	NT	P47245 NARDILYSIN
9717	22782	36363	12.91	5.0E-62	AW410887.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11543	24699	38274	2.38	6.0E-62	11425574	NT	h07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2951816 5'
11543	24699	38275	2.38	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
863	14040	27102	2.17	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
863	14040	27103	2.17	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
864	14040	27102	1.32	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
864	14040	27103	1.32	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2529	16554	28778	1.9	4.0E-62	AB27900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2529	16554	28778	9.09	4.0E-62	4557887	NT	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
3488	16654		1.71	4.0E-62	4506978	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6046	19229	32553	1.71	4.0E-62	4506978	NT	w12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
8428	19594	32960	2.81	4.0E-62	11420864	NT	gb:X57138.mn1 HISTONE H2B.2 (HUMAN);
7322	20404	33866	1.75	4.0E-62	11421041	NT	w12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7812	20867	34361	2.21	4.0E-62	7657057	NT	gb:X57138.mn1 HISTONE H2B.2 (HUMAN);
7812	20887	34362	2.21	4.0E-62	7657057	NT	Homo sapiens keratin 18 (KRT18) mRNA
8364	21445	34988	1.12	4.0E-62	11429873	NT	Homo sapiens coltite carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2)
8047	22128	35670	6.42	4.0E-62	AB033098.1	NT	mRNA
11263	24332	37873	2.82	4.0E-62	278766.1	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
11263	24332	37874	2.82	4.0E-62	278766.1	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
11600	24598	38233	63.7	4.0E-62	S70584.1	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
12769	25202	38390	1.18	4.0E-62	11418086	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
12487	26989		1.65	4.0E-62	11418192	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
							Homo sapiens mRNA for KIAA1263 protein, partial cds
							H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
							H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA16D3
							hybrid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]
							Homo sapiens putative nuclear protein (HRIHFB2122), mRNA
							Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

Page 342 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12946	25657	31955	1.66	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13004	25653	31952	6.88	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13004	25653	31953	6.86	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13059	25653	31955	2.16	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13312	26338	0.69	3.0E-62	4557784	NT	Homo sapiens neurofascin 2 (bilateral acoustic neuroma) (NF2), mRNA
3111	16287	29301	1.13	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3111	16287	29302	1.13	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3789	16950	29956	4.19	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8737	21816	35351	3.74	3.0E-62	AI632733.1	EST_HUMAN	wa3304.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2289903 3' similar to contains THR12
1259	14417	27482	2.71	2.0E-62	AL163284.2	NT	THR repetitive element;
8974	22053	35595	5.59	2.0E-62	BF528911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8974	22053	35596	5.59	2.0E-62	BF528911.1	EST_HUMAN	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10376	23411		3.71	2.0E-62	AF224669.1	NT	RC0-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11988	24973		8.83	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1069	14235	27264	1.14	1.0E-62	AF248540.1	NT	(UBE2D3) genes, complete cds
1575	14728	27809	18.41	1.0E-62	L78810.1	NT	QV4-BT0257-081199-017-e03 B T0257 Homo sapiens cDNA
1842	14988	28088	1.64	1.0E-62	AA025207.1	EST_HUMAN	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2081	16157	29176	1.22	1.0E-62	AL039044.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) genes, complete cds
4648	17784	30767	1.84	1.0E-62	8923201	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) genes, complete cds
							ef70e11.r1 Soares_NHHMPV_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
							CE03453 :
							DKFZ566F104_r1 568 (synonym: hRd2) Homo sapiens cDNA clone DKFZ566F104 5'
							Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
							protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR),
							CDM protein (CDM), adrenoleukodystrophy protein >
6418	19587	32950	2.02	1.0E-62	U52111.2	NT	ab05c02.st Siralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839906 3'
7284	20367	33820	1.07	1.0E-62	AA490060.1	EST_HUMAN	zg88f10.st Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7295	20377	33834	2.69	1.0E-62	AA722878.1	EST_HUMAN	zg88f10.st Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7295	20377	33835	2.69	1.0E-62	AA722878.1	EST_HUMAN	zg88f10.st Soares_fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:409771 3'
8897	22036	35577	0.54	1.0E-62	AA280050.1	EST_HUMAN	zs33e07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705060 5'
9258	22335	35865	1.63	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9268	22335	35866	1.65	1.0E-62	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9302	22378	35928	1.92	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9302	22378	35929	1.92	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9757	22595	36263	3.03	1.0E-62	AA465170.1	EST_HUMAN	aa33d08.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11648	24727	38419	2.26	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC8pA14D8
12809	25540		4.83	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13042	25884	31982	3.15	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
348	13558	28587	2.27	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-1B1199-037-105 ST0234 Homo sapiens cDNA
2421	15550		2.17	8.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-558C70 5'
4152	17304	30297	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4152	17304	30298	8.77	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
5388	18484	38824	4.69	9.0E-63	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5582	18777	31822	1.44	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7332	20413	33875	3.78	9.0E-63	11426985	NT	Homo sapiens nucleoporin 88kD (NUP88), mRNA
8009	21059	34571	1.77	8.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
8521	21802	35139	1.18	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
11296	24362	38003	1.3	9.0E-63	BF203406.1	EST_HUMAN	801865828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4088487 5'
2420	15549	28677		8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2446	15574	28703	2.58	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3550	18715	29727	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3550	18715	29728	4.26	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4381	17524	30505	4.36	8.0E-63	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
932	14125		3.38	7.0E-63	AI872137.1	EST_HUMAN	wm56g11.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439808 3'
5455	18655		70.59	6.0E-63	AA420803.1	EST_HUMAN	nc6302.11 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S
6075	22154	35698	0.62	5.0E-63	11526484	NT	RIBOSOMAL PROTEIN (HUMAN):
3398	16588	29584	0.88	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3970	17069	30066	1.06	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3970	17069	30067	1.06	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6576	19737	33116	2.6	4.0E-63	AW760372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6576	19737	33117	2.6	4.0E-63	AW760372.1	EST_HUMAN	CM3-BT0595-190100-072-a09 BT0595 Homo sapiens cDNA
11397	24468	38121	2.02	4.0E-63	AW760372.1	EST_HUMAN	CM3-BT0595-190100-072-a08 BT0595 Homo sapiens cDNA
11397	24468	38122	2.02	4.0E-63	AW134709.1	EST_HUMAN	UI-H-B11-abq-a-02-q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1089	15131	28235	15.19	3.0E-63	AB018266.1	EST_HUMAN	UI-H-B11-abq-a-02-q-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2840	15954	29081	1.49	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2882	14425	27493	11.84	3.0E-63	6005963	NT	Human Met-IRNA-1 gene 1
6803	19783	33181	33.93	3.0E-63	11545810	NT	Homo sapiens zinc finger protein 144 (ZNF144), mRNA
							Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA

Page 344 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9907	22947	36533	0.83	3.0E-63	BE876158.1	EST_HUMAN	60148556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
9907	22947	36534	0.83	3.0E-63	BE876158.1	EST_HUMAN	60148556F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
196	13419	26449	1.69	2.0E-63	U07804.1	NT	Human DNA topoisomerase 1 mRNA, partial cds
203	13426	26457	1.65	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
510	13704		1.19	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
849	14027	27087	3.07	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1597	14760	27834	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1597	14760	27835	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1808	14955	28049	2.02	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638103 5'
2146	15282	28407	1.05	2.0E-63	AB63961.1	EST_HUMAN	wf54602.x1 NCJ CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406603 3' similar to gb:M57609 GLI3 PROTEIN (HUMAN);
3225	16399	29411	1.94	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3357	16528	29544	2.4	2.0E-63	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
4014	17171	30179	3.19	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4988	18117	31096	1.28	2.0E-63	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5379	25802	31447	0.95	2.0E-63	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6005	19190	32509	2.41	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6005	19190	32510	2.41	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6315	19487	32842	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6315	19487	32843	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6841	19994	33403	1.43	2.0E-63	U68059.1	NT	Human gamma T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S3/13S>
6887	20039	33448	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33449	0.72	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7222	20086	33502	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7222	20086	33503	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7957	21007	34517	0.96	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8730	21810	35346	4.29	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9254	22331	35879	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
9254	22331	35880	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10143	23181	36778	1.2	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21 C018
10985	24064	37689	10.73	2.0E-63	N78945.1	EST_HUMAN	zb18b05.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:U7206 40S RIBOSOMAL PROTEIN S4 (HUMAN);
11012	24091	37728	2.89	2.0E-63	AF098810.1	NT	Homo sapiens neuraxin II-alpha gene, partial cds
11012	24091	37729	2.89	2.0E-63	AF098810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
12360	25629	31759	3.84	2.0E-63	11418185	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
13101	25717	31840	1.19	2.0E-63	11418187	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
13172	25760	31930	1.37	2.0E-63	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
786	13963	27016	1.55	1.0E-63	7106448	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
788	13985	27017	1.55	1.0E-63	7106448	NT	Mus musculus wingless-related MMTV integration site 3A (Wnt3a), mRNA
4461	17601	30579	3.31	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4461	17601	30580	3.31	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5468	18668	31647	1.73	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
6880	19078	32388	1.38	1.0E-63	AW562266.1	EST_HUMAN	QV0-ST0216-060100-083-009 ST0215 Homo sapiens cDNA
6821	19886	33058	0.88	1.0E-63	AW451950.1	EST_HUMAN	UJH-B13-alt-h-02-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088763 3'
6821	19888	33056	0.88	1.0E-63	AW451950.1	EST_HUMAN	UJH-B13-alt-h-02-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3088763 3'
8668	21748		2.97	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21 C047
13121	26047		8.88	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21 C007
6089	18270	32598	0.81	9.0E-64	AW401433.1	EST_HUMAN	UJH-BK0-000-b-08-Q-U1.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053153 5'
8051	21134	34854	5.57	9.0E-64	A1478186.1	EST_HUMAN	Im50507.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161625 3'
1071	14237		3.45	8.0E-64	BE280796.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
8268	19442	32791	3.51	8.0E-64	BE885755.1	EST_HUMAN	601508988F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25146		2.79	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12243	25185		3.88	8.0E-64	T80651.1	EST_HUMAN	y988502.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3618	16782		0.74	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4854	17987	30974	6.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4854	17987	30975	6.34	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
10239	23274	30885	2.62	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rp22 and bam22 genes
1780	14909	28002	5.73	6.0E-64	A1651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1780	14909	28003	5.73	6.0E-64	A1651992.1	EST_HUMAN	w651e07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);

Page 346 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3182	16367	20372	3.91	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
3192	16367	28373	3.91	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
5739	18332	32230	2.95	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5739	18332	32231	2.95	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5758	18350	32252	5.32	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5767	18959	32260	0.88	6.0E-64	691248.1	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
5951	19137	32452	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
5951	19137	32453	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7384	20462	33925	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7384	20462	33926	2.54	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9528	22593	36164	7.39	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9708	22755	36328	1.75	6.0E-64	AF274783.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9819	22898	36546	2.16	6.0E-64	S76475.1	NT	tKIC [human, brain, mRNA, 2715 nt]
11008	24087	37724	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11269	16367	37725	4.68	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11269	16367	28372	1.73	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
11269	16367	29373	1.73	6.0E-64	AW028445.1	EST_HUMAN	wv13e03.x1 NCI_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
12400	25280	32081	2.98	6.0E-64	11528198	NT	Homo sapiens Interleukin 10 receptor, beta (IL10RB), mRNA
843	14021	27078	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
843	14021	27079	4.18	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1369	14524	27598	1.02	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1453	14608	27685	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMFRP) gene, complete cds
1453	14608	27686	1.15	5.0E-64	L40933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMFRP) gene, complete cds
1749	14898	27894	1.54	5.0E-64	U89358.1	NT	Human (3)mb1 protein homolog mRNA, complete cds
2887	14663	27746	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2887	14663	27747	4.43	5.0E-64	7662205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4068	17224	30231	7.25	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
8000	21050	34583	0.71	4.0E-64	BE794507.1	EST_HUMAN	601590382F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944397 5'
11051	24128	37763	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-075-e03 ST0197 Homo sapiens cDNA
11051	24128	37764	2.34	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-075-e03 ST0197 Homo sapiens cDNA
2271	15404	28632	8.77	3.0E-64	C18855.1	EST_HUMAN	C18895 Human placenta cDNA (Tfujlura) Homo sapiens cDNA
3327	16500	29618	0.82	3.0E-64	BE794381.1	EST_HUMAN	601598565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3529	16694	29704	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3529	16694	29705	1.83	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6206	18381	32731	1.31	3.0E-64	Z26273.1	NT	H sapiens isoform 1 gene for L-type calcium channel, exon 28
6471	19638	32987	0.68	3.0E-64	AW500861.1	EST_HUMAN	UJHF-BPQp-akc-05-0-UJL1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3073161 5'
6622	19782	33170	3.2	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0018-280600-011-G11 FN0018 Homo sapiens cDNA
8661	21741	35281	1.86	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8661	21741	35282	1.86	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8662	21772	35303	1.48	3.0E-64	BE206821.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8662	21772	35304	1.48	3.0E-64	BE206821.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047875 5' similar to gb:L08069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9627	22682	36251	1.12	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9627	22682	36252	1.12	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9714	22779	36349	0.66	3.0E-64	AW977384.1	EST_HUMAN	EST1389493 MAGe resequences, MAGO Homo sapiens cDNA
0714	22779	36360	0.66	3.0E-64	AW977384.1	EST_HUMAN	EST1389493 MAGe resequences, MAGO Homo sapiens cDNA
11614	24571	38248	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11614	24571	38249	1.54	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11690	24976	38679	2.16	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1112	14277	27334	1.1	2.0E-64	AA609940.1	EST_HUMAN	af09d09.s1 Soares Testis, NIH Homo sapiens cDNA clone IMAGE:1031151 3'
1428	14582	27655	3.2	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA
2592	15717		1.28	2.0E-64	AI927030.1	EST_HUMAN	wo87b01.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2597	15721	28840	2.4	2.0E-64	AL163245.2	NT	Homo sapiens chromosome 21 segment HS21C046
2597	15721	28841	2.4	2.0E-64	AL163245.2	NT	Homo sapiens chromosome 21 segment HS21C046
3887	17046	30045	0.88	2.0E-64	AW688145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
3887	17046	30046	0.88	2.0E-64	AW688145.1	EST_HUMAN	EST370215 MAGe resequences, MAGO Homo sapiens cDNA
6129	19308	32649	2.28	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM202113 5'
6372	19541	32900	1.23	2.0E-64	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
6614	19774	33165	5.04	2.0E-64	BF686337.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280385 5'
6724	19881	33272	1.3	2.0E-64	A078387.1	EST_HUMAN	alpha28003.x1 Soares fetal_Nb2HFB Sw Homo sapiens cDNA clone IMAGE:1676717 3'
6840	19903	33402	2.98	2.0E-64	M77185.1	NT	H sapiens dopamine receptor D6 pseudogene 1, partial cds
7980	21040	34562	0.67	2.0E-64	11431054	NT	Homo sapiens ataxin 2-binding protein 1 (A2BP1), mRNA
8868	21947	35480	1.08	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin), mRNA
8868	21947	35481	1.08	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin), mRNA
9431	22505	36071	1.09	2.0E-64	AU132570.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP400109 5'

Page 348 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10184	23221	36815	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratiogene (cat#836206) Homo sapiens cDNA clone HFBDS88
10184	23221	36816	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratiogene (cat#836206) Homo sapiens cDNA clone HFBDS88
11000	24079	37714	2.21	2.0E-64	BF528114.1	EST_HUMAN	602042862 F1 NCI CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4180556 5'
11308	24371	38012	4.28	2.0E-64	A1922911.1	EST_HUMAN	wn81b06.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
11308	24371	38013	4.28	2.0E-64	A1922911.1	EST_HUMAN	wn81b06.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
11609	24567	38244	1.46	2.0E-64	AW894773.1	EST_HUMAN	PM2-SN0018-220300-002-er12 SN0018 Homo sapiens cDNA
12804	25537		3.59	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
268	13487	26517	1.39	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1820	14969	28061	24.22	1.0E-64	A1929419.1	EST_HUMAN	au60c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gbl:21696 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3076	16252	29274	0.8	1.0E-64	4507334	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
3601	16765	29761	5.47	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel a2
3676	16838	29848	1.14	1.0E-64	AF228527.1	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
3676	16838	29849	1.14	1.0E-64	AF228527.1	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
4008	17165	30173	0.98	1.0E-64	8922829	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
10269	23304	36901	1.17	1.0E-64	AA042875.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
12291	25216		4.56	1.0E-64	AL163246.2	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
2350	15481	28613	1.87	9.0E-65	X89211.1	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
2350	15481	28614	1.87	9.0E-65	X89211.1	NT	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
11826	24815		19.08	9.0E-65	BF330676.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
11799	24789	38486	7.24	8.0E-65	A1929244.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
10358	23393	37004	2.16	7.0E-65	BE081653.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
12095	26075	38782	2.88	7.0E-65	Z21378.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
1081	14247	27304	0.81	6.0E-65	AV721898.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
1974	15117		20.04	6.0E-65	AA550929.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
6899	19657	33247	0.8	6.0E-65	AA550929.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
8945	22024	35564	2.45	6.0E-65	AW089282.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA
9213	22281	35833	4.63	6.0E-65	AA427878.1	EST_HUMAN	Homo sapiens synapobjanin 1 (SYNJ1), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9213	22291	35834	4.63	6.0E-65	AA427678.1	EST_HUMAN	zw53b08.s1 Soares_tata_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:173747 3'
9276	22351	35902	0.82	6.0E-65	A085314.1	EST_HUMAN	q118h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750428 3'
9276	22351	35903	0.82	6.0E-65	A085314.1	EST_HUMAN	q118h05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750428 3'
11113	24185	37817	3.58	6.0E-65	BE567816.1	EST_HUMAN	601340485F1 NIH_MGC.33 Homo sapiens cDNA clone IMAGE:3682677 6'
11294	24360	38001	4.18	6.0E-65	BF340823.1	EST_HUMAN	602037721F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4189677 5'
11788	24778	38476	1.86	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
648	13833	28859	1.99	5.0E-65	AF084604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1384	14539	27613	1.82	5.0E-65	7661851	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1384	14539	27614	1.92	5.0E-65	7661851	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2223	15357	28487	1.07	5.0E-65	AB033788.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3326	16501	29519	1.79	6.0E-65	4507648	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3328	16501	29520	1.79	5.0E-65	4507648	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7008	20144	33583	1.38	5.0E-65	4504608	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10684	23718	37324	1.36	5.0E-65	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pc) mRNA, partial cds
198	13421	26452	1.3	4.0E-65	AL120419.1	EST_HUMAN	DKFZp781G108.t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G108 5'
764	13945	26991	1.23	4.0E-65	A1269468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbrIP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
764	13945	26992	1.23	4.0E-65	A1269468.1	EST_HUMAN	qm46e01.x1 Soares_placenta_8to9weeks_2NbrIP8to9W Homo sapiens cDNA clone IMAGE:1891800 3'
1103	14268	27326	1.44	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1515	14668	27761	24.91	4.0E-65	4306636	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2413	15543	28670	1.02	4.0E-65	BE221468.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
2413	15543	28671	1.02	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171102 3'
6284	18457	32807	4.96	4.0E-65	AB033063.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6284	18457	32808	4.96	4.0E-65	AB033063.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7233	20317	33760	0.66	4.0E-65	AY008372.1	NT	Homo sapiens oxysterol binding protein-related protein 3 (ORP3) mRNA, complete cds
7266	20349	33801	5.04	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7368	20447	33910	2.3	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7721	20785	34273	0.65	4.0E-65	U40372.1	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7721	20785	34274	0.65	4.0E-65	U40372.1	NT	Human 3' 5' cyclic nucleotide phosphodiesterase (HSPDE1C3A) mRNA, partial cds
7693	21043	34555	0.67	4.0E-65	U39866.1	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
8025	21108	34624	0.83	4.0E-65	5453765	NT	Homo sapiens nef (chicken)-like 2 (NELL2), mRNA
8025	21108	34625	0.83	4.0E-65	5453765	NT	Homo sapiens nef (chicken)-like 2 (NELL2), mRNA
9346	22422	35975	0.88	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA

Page 350 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23841		2.12	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11360	24422	38078	1.92	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12828	14268	27526	2.03	4.0E-65	4828735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13201	13421	26452	1.26	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108.5
100	13358	28364	0.65	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1260	15980		18.37	3.0E-65	X78932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1589	14741	27822	4.52	3.0E-65	4504826	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1868	15014	28122	1.31	3.0E-65	AI000692.1	EST_HUMAN	MSR1 repetitive element
3350	16522	29538	1.24	3.0E-65	4504850	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3815	16975	29978	1.08	3.0E-65	AI000692.1	EST_HUMAN	ov23f03.a1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
4773	17908	30391	1.38	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
10274	23309	36905	1.61	3.0E-65	BE787366.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
11872	23900	37523	8.41	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3490	16657	29670	7.53	2.0E-65	BF680294.1	EST_HUMAN	602156062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295966 5'
6606	19825		3.73	2.0E-65	BE263373.1	EST_HUMAN	601180883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3334741 5'
7282	20355	33818	20.62	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
9046	22125	35668	1.2	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
9048	22125	35669	1.2	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10892	23976	37608	1.46	2.0E-65	11419247	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
12241	25184		6.27	2.0E-65	AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12748	28906		3.99	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
93	13328		0.69	1.0E-65	BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
552	13745	26770	1.43	1.0E-65	7657405	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologous (RABEX5), mRNA
1889	15033	28141	3.31	1.0E-65	AB026698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2098	15238	28360	1.48	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3458	16825	29645	0.8	1.0E-65	BE466881.1	EST_HUMAN	h224e09.x1 NCL_GGAP_G06 Homo sapiens cDNA clone IMAGE:3208888 3'
4105	17259	30259	2.07	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4103	17259	30260	2.07	1.0E-65	4504082	NT	Homo sapiens glypican 4 (GPC4) mRNA
4323	17466	30451	2.53	1.0E-65	AW029340.1	EST_HUMAN	wx08c09.x1 NCL CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2543162 3'
4323	17466	30452	2.53	1.0E-65	AW029340.1	EST_HUMAN	wx08c09.x1 NCL CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2543162 3'
5143	19266	31235	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740886 3'
5143	18266	31236	1.57	1.0E-65	AW238282.1	EST_HUMAN	xp20c01.x1 NCL CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740886 3'
5400	18602	31572	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-184-f09 BT0702 Homo sapiens cDNA
5400	18602	31573	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-184-f09 BT0702 Homo sapiens cDNA
5594	18769	31837	0.58	1.0E-65	AI243738.1	EST_HUMAN	qh88h07.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:1854108 3' similar to TR:Q07823
8448	21628	35057	1.5	1.0E-65	AW820481.1	EST_HUMAN	Q07823 MAC30 PROTEIN;
8448	21628	35058	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0288-140200-042-f12 ST0288 Homo sapiens cDNA
8475	21556	35088	0.66	1.0E-65	BE732118.1	EST_HUMAN	QV2-ST0288-140200-042-f12 ST0288 Homo sapiens cDNA
8475	21556	35089	0.66	1.0E-65	BE732118.1	EST_HUMAN	801566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8514	21556	35129	2.04	1.0E-65	AU141285.1	EST_HUMAN	801566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8514	21556	35130	2.04	1.0E-65	AU141285.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
9041	22120	35682	1.01	1.0E-65	BF688707.1	EST_HUMAN	AU141285 THYRO1 Homo sapiens cDNA clone THYRO1000356 5'
9222	22300	35843	1.33	1.0E-65	AU128040.1	EST_HUMAN	802126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
9222	22300	35844	1.33	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9231	22309	35937	2.79	1.0E-65	11431894	NT	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
9308	22395	35937	0.55	1.0E-65	7682227	NT	Homo sapiens insulin 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9308	22395	35937	0.55	1.0E-65	7682227	NT	Homo sapiens KIAA0656 gene product (KIAA0656), mRNA
9678	22640	36210	5.5	1.0E-65	AI191716.1	EST_HUMAN	qds6a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M28581 ZINC
10089	23127	36730	1.32	1.0E-65	AU153783.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element;
10509	23544	37165	0.85	1.0E-65	AA066569.1	EST_HUMAN	AU153783 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10786	23829	37453	1.23	1.0E-65	AB037832.1	NT	z75a04.1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10886	23969	37599	1.91	1.0E-65	M26187.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11016	24095	37734	9.39	1.0E-65	4506960	NT	Homo sapiens platelet factor 4 variation 1 (PF4var1) gene, complete cds
11395	24456	38118	1.8	1.0E-65	BF688707.1	EST_HUMAN	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11486	24545	38217	2.58	1.0E-65	AB21017.1	EST_HUMAN	802126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
12282	25217	32078	3.77	1.0E-65	11418041	NT	ts76a06.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L16633_mat
12391	25276	32078	3.77	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
73	13310	26334	0.9	9.0E-66	AL160311.1	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
73	13310	26334	0.9	9.0E-66	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
73	13310	26335	0.9	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
73	13310	26335	0.9	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22

Page 352 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1385	14540	27615	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1385	14540	27616	1.53	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1513	14666		5.93	9.0E-66	M87289.1	NT	Human transposon-like element, partial
4007	17164	30171	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4007	17164	30172	0.66	9.0E-66	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
11628	24708		1.9	7.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141188-Q11-106 BT0311 Homo sapiens cDNA
4485	17625	30605	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449587 3' similar to WP.F15G8.4A CE18595.
4485	17625	30606	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449587 3' similar to WP.F15G8.4A CE18595.
4485	17625	30607	1.16	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449587 3' similar to WP.F15G8.4A CE18595.
8620	21709		0.46	6.0E-66	BE178663.1	EST_HUMAN	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
11427	24488	38152	3.22	6.0E-66	X89181.1	NT	H. sapiens mRNA for ribosomal protein L31
1398	14552	27627	2.45	5.0E-66	BE064410.1	EST_HUMAN	RC4-BT0311-141188-Q11-106 BT0311 Homo sapiens cDNA
9494	22551	36113	8.4	5.0E-66	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA
813	13992	27046	1.8	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1775	14924	28018	0.97	4.0E-66	AW897798.1	EST_HUMAN	RC1-NN0063-100500-022-402 NN0063 Homo sapiens cDNA
2355	15486	28618	5.3	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2543	15668		3.15	4.0E-66	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4805	18035		5.02	4.0E-66	8635487	NT	Human endogenous retrovirus, complete genome
5698	18862	32147	3.57	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6861	18051	32358	0.87	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-067-g10 DT0069 Homo sapiens cDNA
6895	18614	31508	4.91	4.0E-66	AW965473.1	EST_HUMAN	EST377548 IMAGE resequences, MAGI Homo sapiens cDNA
7281	20364	33617	7.88	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, complete cds
7807	18862	32147	0.83	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8269	21351	34967	6.14	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8327	21409	34936	0.7	4.0E-66	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
10896	23980	37612	1.49	4.0E-66	BF507493.1	EST_HUMAN	UI-H-BW1-ami-a-10-Q-UI.s1 NCI_CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070747 3'
11660	24739	38430	1.63	4.0E-66	AB023215.1	NT	Homo sapiens mRNA for KIAA0988 protein, partial cds

Page 353 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1458	14611	27692	14.93	3.0E-68	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1459	14611	27693	14.93	3.0E-68	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2039	15180	28280	1.04	3.0E-68	N55323.1	EST_HUMAN	Y27612.1 Scores multiple sclerosis 2N6HMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2 [2] PIR:B56612;
2039	15180	28281	1.04	3.0E-68	N55323.1	EST_HUMAN	Y27612.1 Scores multiple sclerosis 2N6HMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2 [2] PIR:B56612;
2039	15180	28282	1.04	3.0E-68	N55323.1	EST_HUMAN	Y27612.1 Scores multiple sclerosis 2N6HMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1_TIGCA P35068 HISTONE H2B.1H2B.2 [2] PIR:B56612;
2772	15887	28987	3.44	3.0E-68	11141850	NT	Homo sapiens TGF-beta-induced transcription factor 2 (TGIF2), mRNA
3186	16361	29387	7.29	3.0E-68	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5693	18778	31823	0.85	3.0E-68	AB020880.1	NT	Homo sapiens mRNA for KIAA0692 protein, partial cds
5695	18889	32180	0.86	3.0E-68	M13976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1), mRNA, complete cds
5893	18081	32391	1.72	3.0E-68	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5893	18081	32392	1.72	3.0E-68	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
7585	20657	34134	1.74	3.0E-68	X92211.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (18-1)
8725	22790	36361	0.59	3.0E-68	AK024453.1	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8920	22950	36547	0.52	3.0E-68	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10278	23313	36911	0.86	3.0E-68	7019480	NT	Homo sapiens protodactylin beta 1 (PCDH-beta1), mRNA
10741	23774	37399	0.93	3.0E-68	AF155659.1	NT	Homo sapiens polydactylin cofactor biosynthesis protein E (MCPPE), mRNA, complete cds
11800	24780	39487	4.55	3.0E-68	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B59), alpha isoform (PPP2R6A), mRNA
62	13291	26304	1.48	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
52	13291	26305	1.48	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
435	13235	26235	0.87	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
435	13235	26236	0.87	2.0E-68	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L), mRNA, and translated products
1873	15017	28128	2.02	2.0E-68	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3039	16216	28236	1.07	2.0E-68	X66959.1	NT	H. sapiens pseudogene for the low affinity L-8 receptor
3009	16773	29788	0.85	2.0E-68	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3861	17021	30019	0.78	2.0E-68	AL117233.1	NT	Novel human gene mapping to chromosome 1
4176	17326	30317	0.69	2.0E-68	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1), mRNA, complete cds

Page 354 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4778	17913	30898	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
4778	17913	30899	13.88	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leucocyte antigen B
5937	19123	32436	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
5937	19123	32437	0.82	2.0E-66	AW968854.1	EST_HUMAN	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
9048	22127	35671	3.57	2.0E-66	N45480.1	EST_HUMAN	y59022.f1 Soares_multiple_sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:277826 5'
12637	26147		2.84	2.0E-66	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1717	14867		1.14	1.0E-66	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3006931 5'
2959	16136	29153	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2959	16136	29154	1.47	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29153	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4504	16136	29154	4.18	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
5497	18696	31712	5.97	1.0E-66	BF673088.1	EST_HUMAN	602152996F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5900	19089	32402	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04-NT0101 Homo sapiens cDNA
5900	19089	32403	0.67	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04-NT0101 Homo sapiens cDNA
7078	20131	33548	1.53	1.0E-66	BF328623.1	EST_HUMAN	RC5-BN0193-010900-034-G08-BN0193 Homo sapiens cDNA
8662	21732	35271	1.2	1.0E-66	AA608958.1	EST_HUMAN	aa60894.s1 NCJ_CGAP_GC81 Homo sapiens cDNA clone IMAGE:827262 3'
9626	22681	36250	0.64	1.0E-66	AA018828.1	EST_HUMAN	ze57612.f1 Soares_telina_N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10682	23617	37223	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10582	23617	37224	0.93	1.0E-66	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
11185	24254	37889	2.24	1.0E-66	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
12398	25278		1.92	6.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
6034	18162		0.91	8.0E-67	M78158.1	EST_HUMAN	similar to L1 repetitive element
391	13628	26665	1.63	7.0E-67	AW162232.1	EST_HUMAN	EST01750 Subtracted Hippocampus, Striatum (cat. #336205) Homo sapiens cDNA clone HHCPN31
1413	14567	27641	2.66	7.0E-67	AA383416.1	EST_HUMAN	au75602.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1585	14737	27817	1.39	7.0E-67	W85947.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1585	14737	27818	1.39	7.0E-67	W85947.1	EST_HUMAN	EST06812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid
2089	15229	28350	1.94	7.0E-67	7657243	NT	ZK353
2089	15229	28351	1.84	7.0E-67	7657243	NT	zh5605.t1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2871	13628	26665	1.36	7.0E-67	AW162232.1	EST_HUMAN	zh5605.t1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
							Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
							Homo sapiens inositol 1,3,4-triphosphate 5/6 kinase (ITPK1), mRNA
							au75602.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
							ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);

Page 355 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6205	19380	32730	0.88	7.0E-67	10190695	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6400	19569	32830	1.97	7.0E-67	11425672	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6400	19569	32831	1.67	7.0E-67	11425672	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6863	20015	33425	1.12	7.0E-67	4885084	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP6A1A), mRNA
7809	20864	34358	0.69	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
7809	20864	34359	0.69	7.0E-67	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8268	21340	34857	0.52	7.0E-67	4828895	NT	Homo sapiens phosphodiesterase 11 nucleotide pyrophosphatase 3 (PDNRP3), mRNA
8518	21598	35134	0.7	7.0E-67	4857732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9132	22211	35768	0.68	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11685	24820		2.42	7.0E-67	11434679	NT	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA
11973	24958	38660	2.02	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
12168	25131	38829	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12168	25131	38830	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12664	26441	32053	1.92	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
13108	26721		1.74	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
673	13765	26788	1.09	6.0E-67	X88968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
818	13997	27051	2.4	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1302	14458	27524	1.07	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3, 4, 5, 6 & 7
3237	16411	29426	1.39	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA
3824	16889	29698	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
3524	16889	29699	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
4243	17389	30375	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4243	17389	30376	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4827	17860	30947	2.22	6.0E-67	7667020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4827	17860	30948	2.22	6.0E-67	7667020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13224	17665	29788	2.74	6.0E-67	X88968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
3263	18467	29486	2.26	5.0E-67	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11230	24298		2.17	5.0E-67	BE010038.1	EST_HUMAN	PM3-BN0178-100400-001-g04 BN0178 Homo sapiens cDNA
1369	14514	27598	1.13	4.0E-67	R80818.1	EST_HUMAN	Y02411.1 Soares adult brain N264HB557 Homo sapiens cDNA clone IMAGE:167253 5'
8211	21293	34813	0.8	4.0E-67	AF733032.1	EST_HUMAN	Q26c05.x5 NC1 CGAP_K13 Homo sapiens cDNA clone IMAGE:1493286 3' similar to SW:Z33A_HUMAN
8576	21657		1.48	4.0E-67	BF357321.1	EST_HUMAN	Q08730 ZINC FINGER PROTEIN 33A ;
							RCO-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11318	24381		1.78	4.0E-67	AA714284.1	EST_HUMAN	hw06a01.s1 NCL CGAP_S51 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
2874	13835	26862	2.03	3.0E-67	AA333788.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
3542	16707	29718	2.05	3.0E-67	BE064410.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
4816	17949	30934	2.96	3.0E-67	AW869159.1	EST_HUMAN	RC4-BT0311-141189-011-106 BT0311 Homo sapiens cDNA
4845	17978		1.38	3.0E-67	AL183279.2	NT	MR3-SN0068-040300-008-f01 SN0068 Homo sapiens cDNA
8375	21456	34980	1.37	3.0E-67	BF196088.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11537	24593		15.42	3.0E-67	AA927874.1	EST_HUMAN	hw1f05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
193	13416	26445	0.59	2.0E-67	BE348354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1 ;
888	14044	27109	5.29	2.0E-67	AW816405.1	EST_HUMAN	hw1f05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1129	14294		2.48	2.0E-67	AF167460.1	NT	Q61807.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1933	15076	28179	1.23	2.0E-67	BE303037.1	EST_HUMAN	hw1f05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WP:F23H11.9
1933	15076	28180	1.23	2.0E-67	BE303037.1	EST_HUMAN	CE08617 ;
2468	16685	28713	1.18	2.0E-67	AF309561.1	NT	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cDNA
2502	16629	28749	1.37	2.0E-67	4758785	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
3557	16722	29737	3.78	2.0E-67	AA625755.1	EST_HUMAN	hw1f05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:O94892 O94892
4109	17263	30263	3.13	2.0E-67	AL163300.2	NT	KIAA0798 PROTEIN ;
6197	16372	32723	0.83	2.0E-67	AL049784.1	NT	hw1f05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:O94892 O94892
6262	19426	32772	4.95	2.0E-67	BF240758.1	EST_HUMAN	hw1f05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:O94892 O94892
6425	19593	32958	1.74	2.0E-67	AB051763.1	NT	KIAA0798 PROTEIN ;
6425	19593	32959	1.74	2.0E-67	AB051763.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
6779	19934	33330	0.64	2.0E-67	AL120542.1	EST_HUMAN	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
8755	21834	35374	1.09	2.0E-67	AA334609.1	EST_HUMAN	zhu1g01.s1 Soares_Tesit_NHT Homo sapiens cDNA clone IMAGE:745392 3'
8755	21834	35375	1.09	2.0E-67	AA334609.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
9197	22275	35812	1.31	2.0E-67	AW602635.1	EST_HUMAN	Novel human gene mapping to chromosome 13
9197	22275	35813	1.31	2.0E-67	AW602635.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
9768	22763	36332	0.55	2.0E-67	AV731333.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
9910	22960	36536	0.99	2.0E-67	AW263624.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
10848	23881	37501	0.53	2.0E-67	AA928089.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
11141	24213	37940	1.75	2.0E-67	BF685788.1	EST_HUMAN	Homo sapiens cDNA clone DKFZp761A229 5'
							EST38860 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
							EST38860 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
							RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
							RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
							RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
							AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
							U1H-B12-ahh-a-10-Q.U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'
							on86b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541 3'
							602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11310	28230		2.55	2.0E-67	11436448	NT	Homo sapiens KIA00885 protein (KIA00885), mRNA
11504	24592	38240	2.06	2.0E-67	BE265714.1	EST_HUMAN	601175782F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11743	23929	37555	2.44	2.0E-67	BF377189.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12527	25888	31770	2.47	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70KD (Ku antigen) (G22P1), mRNA
283	13482	28514	2.37	1.0E-67	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
726	13908	26948	0.95	1.0E-67	AA702794.1	EST_HUMAN	z180b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4480163'
4833	17988	30954	0.73	1.0E-67	BF439247.1	EST_HUMAN	ndb0108.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'
11288	24337		1.47	1.0E-67	BE010038.1	EST_HUMAN	PM3-BN0178-100400-001-g04 BN0178 Homo sapiens cDNA
12105	25085		3.44	9.0E-68	4606090	NT	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA
2245	15378	28506	8.3	8.0E-68	BE870732.1	EST_HUMAN	60144858F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3862284 5'
3973	17130	30133	5.75	8.0E-68	AA208458.1	EST_HUMAN	z182h10.r1 Stratiene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC C07590 SAV PROTEIN.;
3973	17130	30134	5.75	8.0E-68	AA208458.1	EST_HUMAN	z182h10.r1 Stratiene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC C07590 SAV PROTEIN.;
8293	21375	34895	0.56	7.0E-68	A1810505.1	EST_HUMAN	Wb89e03.X1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:2312860 3'
10666	23700	37310	6.43	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
11417	24478	38143	1.31	6.0E-68	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
12868	25579		2.84	6.0E-68	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855781 6'
13165	25756	31927	1.45	6.0E-68	BF310675.1	EST_HUMAN	601894935F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124144 5'
825	15988	27050	2	5.0E-68	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27076	4.93	5.0E-68	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27077	4.93	5.0E-68	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
3216	16390	29401	2.99	5.0E-68	AB037852.1	NT	Homo sapiens chromosome 21 unknown mRNA
4297	17440		0.84	5.0E-68	4828967	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2594	15719	28836	1	4.0E-68	11421388	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
2594	15719	28837	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5090	18218		7.11	4.0E-68	P04403	SWISSPROT	Homo sapiens transcription factor NRF (NRF), mRNA
6085	19287	32596	0.69	4.0E-68	AF157083.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6912	20227	33659	6.03	4.0E-68	11055991	NT	Homo sapiens sodin (SEDL) gene, exon 4
6912	20227	33660	6.03	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7869	20913	34418	0.84	4.0E-68	7981683	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
							Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9240	22317	35859	5.58	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9240	22317	35860	5.58	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9380	22455	36018	3.17	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
11251	24320	37960	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11251	24320	37961	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11434	24495	38161	1.72	4.0E-68	AB040948.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
12728	25495	32026	1.17	4.0E-68	11417966	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
3751	16912	28915	3.54	3.0E-68	AF236092.1	NT	q38h02.x1 Soares_fetal_Jung_NHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR12 THR repetitive element;
8656	21099		3.5	3.0E-68	AI342323.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
10720	23753	37359	1.35	3.0E-68	F28784.1	EST_HUMAN	QV1-DT0072-010200-056-i06 DT0072 Homo sapiens cDNA
13111	25602		2.83	3.0E-68	AW839485.1	EST_HUMAN	Griectulus longicaudatus mRNA for EF-1 alpha, complete cds
2925	18474		29.7	2.0E-68	D00522.1	NT	711502.x1 NCL_CGAP_QLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:080828 O80828
4135	17288	30283	0.79	2.0E-68	BE675766.1	EST_HUMAN	HYPOTHETICAL 88.8 KD PROTEIN.;
4803	17938	30928	2.33	2.0E-68	AB006881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
7015	20151		9.21	2.0E-68	R49088.1	EST_HUMAN	y938g04.s1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:34868 3'
7209	20074	33486	3.81	2.0E-68	BF036316.1	EST_HUMAN	601458614F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882034 5'
7527	20600	34074	0.68	2.0E-68	BF338745.1	EST_HUMAN	IL3-CT0534-180900-273-A01 CT0534 Homo sapiens cDNA
9150	22228	35772	0.58	2.0E-68	O03859	SWISSPROT	FORMIN 4 (LIMB DEFORMITY PROTEIN)
11521	24577	38255	1.49	2.0E-68	BF330594.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
12285	26170		1.59	2.0E-68	BE8097376.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
13192	25775		1.32	2.0E-68	AW016803.1	EST_HUMAN	U1-H-B10-aam-b-05-O.UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
81	13316	26344	0.53	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
307	13523	26567	16.49	1.0E-68	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2328	15458	28590	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2328	16468	28591	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
4117	17271	30270	0.9	1.0E-68	BE266032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5140	18263	31231	0.71	1.0E-68	AA897343.1	EST_HUMAN	ta47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5437	18637	31616	1.92	1.0E-68	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
7853	20908	34412	0.76	1.0E-68	11436716	NT	Homo sapiens sentrin/SUMO-specific protease (SENP1), mRNA
10385	23420	37027	0.45	1.0E-68	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC633214), mRNA
11058	24163	37789	2.16	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11089	24163	37800	2.18	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11142	24214	37841	2.81	1.0E-69	L78418.1	NT	Homo sapiens MIF2 suppressor (HSMIT3) mRNA, complete cds
11468	24527	38200	1.7	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
11580	24634	38313	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11580	24634	38314	2.83	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11863	24948	38653	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11863	24948	38654	1.81	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12849	13316	26944	2.53	1.0E-68	4503222	NT	Homo sapiens methionine (disrupted in balanced translocation) 1 (MN1), mRNA
13100	26092	31681	3.05	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13164	25755		1.88	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
22	13260	26280	2.42	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
22	13260	26261	2.42	9.0E-69	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1063	14219	27275	0.99	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1063	14219	27276	0.99	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4246	17392	30380	0.8	9.0E-69	4757887	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAP) mRNA
4268	17411	30397	0.89	9.0E-69	4504010	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8KD) (GLCLR) mRNA
11128	24200		7.89	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3473	16840		1.26	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
6482	19649	33011	4.44	7.0E-68	9966912	NT	Homo sapiens actin-related protein 3-beta (ARPBETA), mRNA
8047	21130	34649	1.85	6.0E-69	AI192764.1	EST_HUMAN	q62h01.x1 Soares fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gbl:11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8047	21130	34650	1.85	6.0E-69	AI192764.1	EST_HUMAN	q62h01.x1 Soares fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to gbl:11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
9174	22282	35795	1.05	6.0E-69	AA826039.1	EST_HUMAN	q66a03.s1 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:1372300 3'
533	13726		1.18	4.0E-69	AI873630.1	EST_HUMAN	wm26h11.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2437125 3'
5881	28812	32378	1.53	4.0E-69	BE561063.1	EST_HUMAN	601344705F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3677641 5'
5966	19152	32467	4.62	4.0E-69	AI764973.1	EST_HUMAN	wh57006.x1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O56137
6764	19920	33315	3.17	4.0E-69	4557732	NT	O56137 ACYL-COA THIOESTERASE. ;
6764	19920	33316	3.17	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9116	22194	35739	0.55	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
397	13634	26072	5.24	3.0E-69	BE268012.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1009283 5'
627	13812	26834	2.78	3.0E-69	AF221712.1	NT	80110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1586	14738		1.12	3.0E-69	T80514.1	EST_HUMAN	y408a02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48836
2449	15577		2.18	3.0E-69	6729910	NT	A48836 SPEG III=EGF REPEAT-CONTAINING FIBROPELLE-LIKE PROTEIN - SEA URCHIN ;
5057	18483	38823	1.37	3.0E-69	11418185	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
							Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
							Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene
							encoding mitochondrial protein, complete cds
7529	20602	34076	0.76	3.0E-69	AF095703.1	NT	Homo sapiens arm-repeat protein NPRAP/neurogranin (CTNND2) mRNA, partial cds
7578	20650	34128	1.74	3.0E-69	U52351.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
7724	20768	34277	8.4	3.0E-69	AF268075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8967	21648	35190	1.33	3.0E-69	AW138846.1	EST_HUMAN	UIH-B11-acow-g-01-0-UI.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8967	22046		0.74	3.0E-69	AA376399.1	EST_HUMAN	EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
9813	22686	36238	1.74	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide (beta 1-4)-galactosyltransferase
							Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor
							(MIF)-related protein
9733	22798	36372	3.15	3.0E-69	X06233.1	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10034	23072	36672	0.56	3.0E-69	5730036	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10877	23862	37590	2.74	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
11080	24155		7.68	3.0E-69	AA376399.1	EST_HUMAN	EST8807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
12112	25082	38795	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
12112	25092	38796	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
12305	25223		3.1	3.0E-69	11419157	NT	Homo sapiens HGO6.2 protein (HGO6.2), mRNA
131	13612	26651	1.09	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
131	13612	26652	1.09	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
417	13612	26651	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
417	13612	26652	4.42	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1834	15077	28181	1.79	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33560074 5'
2906	16084		4.14	2.0E-69	AA431157.1	EST_HUMAN	zw7192.1 Soares testis NIH_MGC_21 Homo sapiens cDNA clone IMAGE:781682 5'
8761	21830	35368	0.95	2.0E-69	AA114270.1	EST_HUMAN	zm28901.1 Stratagene pancreas (8937208) Homo sapiens cDNA clone IMAGE:527088 5'
1080	14832		1	1.0E-69	BF330124.1	EST_HUMAN	RCQ-BN0305-200600-031-405 BN0305 Homo sapiens cDNA
1739	14886	27980	2.4	1.0E-69	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
5137	18280		0.63	1.0E-69	BE403094.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:335781 5'
6175	19351	32697	0.83	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3358332 5'
6175	19351	32698	0.83	1.0E-69	BE902501.1	EST_HUMAN	601875788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3358332 5'
6738	19894	33285	4.36	1.0E-69	AW393969.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6958	20271	33709	1.22	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6968	20271	33710	1.22	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6978	20204	33631	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6978	20204	33632	2.91	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7021	20187	33578	0.81	1.0E-69	BE531007.1	EST_HUMAN	601278632F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
7021	20157	33579	0.81	1.0E-69	BE531007.1	EST_HUMAN	601278632F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610614 5'
10377	23412	37020	5.01	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10377	23412	37021	5.01	1.0E-69	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10625	23659	37268	0.9	1.0E-69	BF528429.1	EST_HUMAN	602043762F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181325 6'
11112	24184		35.41	1.0E-69	4504918	NT	Homo sapiens keratin 8 (KR18) mRNA
12237	25181	36352	1.86	1.0E-69	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12673	25449		3.4	1.0E-69	AI808984.1	EST_HUMAN	wf64e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1008023
2409	16051	28687	1.56	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.r1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:1008023
4493	17633	30615	1.84	8.0E-70	L77596.1	NT	Homo sapiens DGS-1 mRNA, 3' and
1856	15002	28108	2.42	7.0E-70	AI497807.1	EST_HUMAN	tm89101.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1856	15002	28109	2.42	7.0E-70	AI497807.1	EST_HUMAN	tm89101.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1984	15127	28229	1.87	7.0E-70	AA262955.1	EST_HUMAN	215h04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2125	15261		5.13	7.0E-70	5031688	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4340	17483	30465	4.29	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5600	18795	31844	5.4	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5600	18795	31845	5.4	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7084	20117	33531	1.9	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7945	20995	34508	0.64	7.0E-70	11417309	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8626	21708	35242	2.55	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8626	21708	35243	2.55	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8919	21998	35538	3.8	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
8919	21998	35538	3.8	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9358	22433	35981	5.59	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9358	22433	35982	5.59	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9635	21078	34590	2.88	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9660	21102	34617	1.7	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9660	21102	34618	1.7	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA

Page 362 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9857	22897	36480	0.53	7.0E-70	4557824	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GL-CLC) mRNA
10505	23540	37149	0.85	7.0E-70	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10505	23540	37150	0.85	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11329	24392	38039	1.77	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spasin) (SPG4), mRNA
11329	24392	38040	1.77	7.0E-70	11428685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant spasin) (SPG4), mRNA
11897	24885	38583	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11897	24885	38584	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
894	14070	27135	2.51	8.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-II, Alzheimer disease) (APP), mRNA
2205	15339	28486	2.29	6.0E-70	M30938.1	NT	Human KU (p70/p80) subunit mRNA, complete cds
4629	17765	30747	0.7	6.0E-70	AF164121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
2618	15066	28854	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2618	15066	28855	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12247	25188	33454	5	5.0E-70	BE160034.1	EST_HUMAN	MR3-HT0487-150200-115-a06 HT0487 Homo sapiens cDNA
6894	20045	33454	1.03	4.0E-70	TO6037.1	EST_HUMAN	EST03928 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HIFBDN25
6833	20248	33682	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6833	20248	33683	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1619	14771	27853	1.71	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
1619	14771	27854	1.71	3.0E-70	BE071798.1	EST_HUMAN	RC0-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
5270	18389	31367	1.11	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 122
5737	18930	32227	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
5737	18930	32228	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6066	19248	32675	1	3.0E-70	A1831975.1	EST_HUMAN	wh90d3.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389005 3'
6503	19689	33033	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6503	19689	33034	1.69	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10314	23349	36955	0.62	3.0E-70	BE502973.1	EST_HUMAN	h281h02.x1 NCL CGAP_L124 Homo sapiens cDNA clone IMAGE:3214419 3'
39	13277	26263	1.03	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
707	13890	26923	15.24	2.0E-70	N42161.1	EST_HUMAN	y07a10.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;

Page 363 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
707	13890	26924	15.24	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
723	13905	26947	1.85	2.0E-70	A1246889.1	EST_HUMAN	SW:D3HL RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
1046	14212	27269	1.36	2.0E-70	8923669	NT	qx51h01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1211	14372	27432	2.16	2.0E-70	7661983	NT	Homo sapiens hypothetical protein FLJ20768 (FLJ20768), mRNA
1211	14372	27433	2.16	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1441	14534	27669	1.23	2.0E-70	BE487311.1	EST_HUMAN	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1688	14840	27924	1.07	2.0E-70	AA180093.1	EST_HUMAN	h264c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212768 3'
1688	14840	27925	1.07	2.0E-70	AA180093.1	EST_HUMAN	h264c12.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212768 3'
1781	14930	28023	4.82	2.0E-70	AL163202.2	NT	4p45h05.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
2394	15525		9.42	2.0E-70	AA054010.1	EST_HUMAN	4p45h05.r1 Stratagene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
3923	17082	30076	0.71	2.0E-70	AL133207.2	NT	TR:G1041293 G1041293 D2085.5 ;
4160	17311	30307	5.88	2.0E-70	M69181.1	NT	Homo sapiens chromosome 21 segment HS21C002
5632	18826	31901	8.42	2.0E-70	X72662.1	NT	Z48g04.r1 Soares retina N254HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
5632	18826	31902	8.42	2.0E-70	X72662.1	NT	P03345 GAG POLYPROTEIN ;
6333	19504	32662	1.23	2.0E-70	AF130105.1	NT	Novel human gene mapping to chromosome X
6771	19826	33321	2.69	2.0E-70	D12625.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
6806	19960	33362	10.35	2.0E-70	AF123074.1	NT	H. sapiens gene for schwannomin (CS6)
6806	19960	33363	10.35	2.0E-70	AF123074.1	NT	H. sapiens gene for schwannomin (CS6)
7136	19592	31477	1.5	2.0E-70		NT	Homo sapiens NALP1 mRNA, complete cds
8103	21185	34704	2.81	2.0E-70	M21741.1	NT	Human mRNA for NF-1 protein isoform (neurofibromin isoform), complete cds
8417	21498	35030	0.66	2.0E-70	H47869.1	EST_HUMAN	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
8860	21939	36007	1.34	2.0E-70	H47869.1	EST_HUMAN	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
9370	22445	36089	1.14	2.0E-70	AF123303.1	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIAT6), mRNA
10342	23377	36031	1.26	2.0E-70	AF123303.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-alpha), exons 4 and 5
11324	24387	38031	3.39	2.0E-70	8923420	NT	Human sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen)
11324	24387	38032	3.39	2.0E-70	8923420	NT	storage disease type III (AGL), mRNA
11940	24928	38628	7.78	2.0E-70		NT	Homo sapiens dynactin p82 subunit (LOC51184), mRNA
12662	26439	32050	2.42	2.0E-70	11430460	NT	Homo sapiens dynactin p82 subunit (LOC51184), mRNA

Page 364 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12662	25439	32051	2.42	2.0E-70	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3480	16647		3.72	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3), mRNA
9480	22637		0.64	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416024 5'
10003	23041		0.88	1.0E-70	AA442292.1	EST_HUMAN	z634c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
11176	24244	37877	7.61	1.0E-70	AV738538.1	EST_HUMAN	AV738538 CB Homo sapiens cDNA clone CBLB810 5'
6086	19247	32573	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6085	19247	32574	6.03	9.0E-71	AI143870.1	EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
7175	20308	33751	2.05	9.0E-71	AI654903.1	EST_HUMAN	ws52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
11813	20308	33751	3.47	9.0E-71	AI654903.1	EST_HUMAN	ws52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
9270	22346		2.88	8.0E-71	AA171451.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
10828	23881	37484	0.63	8.0E-71	AW273820.1	EST_HUMAN	ws52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
7633	20608	34081	7.86	7.0E-71	AA442230.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
8877	21956	35491	1.34	7.0E-71	AA705457.1	EST_HUMAN	ws52c05.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213
11614	24635	38353	2.2	7.0E-71	AL163210.2	NT	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
2284	15416	28548	7.11	5.0E-71	AF056322.1	NT	z627d11.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to
4235	17382	30371	1.18	5.0E-71	AF056322.1	EST_HUMAN	TR:G1143061 G1143061 STRAIN XA34 POL ;
6002	19187	32506	1.59	5.0E-71	AW816405.1	EST_HUMAN	KV24d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O64730
8801	18986	33356	1.4	5.0E-71	11641408	NT	O64730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
7060	20113	33528	0.94	5.0E-71	7662209	NT	z60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:768075 5'
7298	20378	33836	0.82	5.0E-71	M38108.1	NT	z61a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
7679	20744	34225	1.79	5.0E-71	11431590	NT	Homo sapiens chromosome 21 segment HS21C010
7884	20636	34471	0.8	5.0E-71	11528445	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
7912	20063	34471	20.85	5.0E-71	AF072810.1	NT	QV4-ST0234-181189-037-05 ST0234 Homo sapiens cDNA
8720	21800	35335	0.56	5.0E-71	5453777	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
8720	21800	35336	0.56	5.0E-71	5453777	NT	Homo sapiens keratin, hair, acidic, 7 (KRT7A7), mRNA
10115	23153		2.06	5.0E-71	X13467.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
10476	23511	37124	0.49	5.0E-71	U70988.1	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
							Homo sapiens neurofibrominosis protein type 1 mRNA, 3' end of cds
							Homo sapiens MAGUK protein p55T; Protein Associated with Lins 2 (LOC51678), mRNA
							Homo sapiens transcription factor WSTF mRNA, complete cds
							Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
							Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
							Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
							Human arreslin (SAG) gene exon 8

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10870	23955	37584	1.45	5.0E-71	5729000	NT	Homo sapiens (GF-1) mRNA-binding protein 3 (KOC1), mRNA
10843	24026	37660	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA160 (H. sapiens) (LOC883170), mRNA
10843	24025	37661	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA160 (H. sapiens) (LOC883170), mRNA
11226	24295	37936	3.85	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11487	24526	38189	2.1	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20183 (H. sapiens) (LOC883325), mRNA
12558	25380		1.75	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 8 (RBM8), mRNA
106	13342	26370	1.84	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
360	13571	26801	31.91	4.0E-71	AF167828.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
360	13571	26802	31.91	4.0E-71	AF167828.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2951	16128	29141	1.67	4.0E-71	4506880	NT	Homo sapiens plasminogen (PLG) mRNA
4548	17886	30867	1.67	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5101	18229	31200	4.58	4.0E-71	7687602	NT	Homo sapiens putative heme-binding protein (SQU), mRNA
9223	21305		1.13	3.0E-71	AL135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone PLACE1002775 5'
10631	24013	37646	3.32	3.0E-71	AA557683.1	EST_HUMAN	HL60.H10.81 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR3.13 PTR5 repetitive element
1288	14418	27481	4.54	2.0E-71	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
5435	18635	31614	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5435	18635	31615	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7107	18534	31489	0.71	2.0E-71	AL042439.1	EST_HUMAN	DKFZ434D1721.1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZ434D1721 5'
9207	22285	35826	0.5	2.0E-71	BF195585.1	EST_HUMAN	7n85c11.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TRQ9Z165
10813	23946	37467	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10813	23946	37468	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10933	24015	37647	4.37	2.0E-71	BE018477.1	EST_HUMAN	b681a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW:R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B
11860	24848	38545	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11860	24848	38546	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598881
11882	24870	38567	2.05	2.0E-71	R55628.1	EST_HUMAN	y77c11.r1 Soares breast 2NBH8at Homo sapiens cDNA clone IMAGE:154772 5'
12318	25231		4.89	2.0E-71	T05489.1	EST_HUMAN	y643c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'

Page 366 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
655	13841	26868	1.55	1.0E-71	AI077927.1	EST_HUMAN	oy15603.s1 Soares_sarcomatous_fibrosarcoma_NbHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element
964	14137	27198	1.38	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51816), mRNA
1124	14286	27344	13.07	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 16 and complete cds
1371	14529	27600	11.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2147	15283	28408	1.82	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2147	15283	28409	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2757	18754	28992	6.06	1.0E-71	7657153	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3590	18754	29769	1.56	1.0E-71	AF119895.1	NT	Homo sapiens SNARE protein kinase SNARK mRNA, complete cds
3685	18848	29855	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARK mRNA, complete cds
3685	18848	29856	6.57	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNARK mRNA, complete cds
3738	16899	29902	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3738	16899	29903	0.9	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3835	16998	29987	2.2	1.0E-71	AF218904.1	NT	Homo sapiens atracilin precursor (ATRNL) gene, exon 19
4593	17730	30712	2.13	1.0E-71	D28476.1	NT	Homo sapiens atracilin precursor (ATRNL) gene, complete cds
6881	20033	33443	1.48	1.0E-71	11426182	NT	Homo sapiens GON5 (general control of amino-acid synthesis, yeast, homodog)-like 2 (GON5L2), mRNA
7235	20319	33762	1.49	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7484	20539	34013	12.52	1.0E-71	U07593.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8340	21421	34948	0.82	1.0E-71	AF105267.1	NT	Homo sapiens glycyl-6 (GPC6) mRNA, complete cds
8302	21443	34965	2.21	1.0E-71	AF105267.1	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
8641	21721	35257	4.23	1.0E-71	8922811	NT	Homo sapiens hypohidrotic protein FLJ10998 (FLJ10998), mRNA
8641	21721	35258	4.23	1.0E-71	8922811	NT	Homo sapiens hypohidrotic protein FLJ10998 (FLJ10998), mRNA
8641	21721	35259	4.23	1.0E-71	8922811	NT	Homo sapiens hypohidrotic protein FLJ10998 (FLJ10998), mRNA
9429	22503	36069	0.88	1.0E-71	S72393.1	NT	CSNK2A1-isoform kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
10211	23247	36837	6.22	1.0E-71	AV761217.1	EST_HUMAN	Homo sapiens cyclochroma c oxidase subunit VII-related protein gene, complete cds
10273	23308	36837	6.22	1.0E-71	AV761217.1	EST_HUMAN	Homo sapiens cyclochroma c oxidase subunit VII-related protein gene, complete cds
10759	23702	37411	2.74	1.0E-71	11433142	NT	AV761217 MDS Homo sapiens cDNA clone MDSEA03 5'
11024	24103	37824	2.49	1.0E-71	AV761217.1	EST_HUMAN	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
11121	24193	38138	3.31	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11413	24474	38138	3.2	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11473	24474	38139	3.2	1.0E-71	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12708	25471	40171	10.17	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
420	13815	28854	0.77	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCL_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element;
420	13816	28855	0.77	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.x1 NCL_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element;
6237	19412	32760	0.86	8.0E-72	BF035752.1	EST_HUMAN	901468747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862451 5'
4228	17375	30361	1.75	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4228	17375	30362	1.75	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4228	17375	30363	1.75	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7274	20367	33811	3	7.0E-72	S41694.1	NT	(pseudogene) PTMAP2-prothymosin alpha [human, Genomic, 1182 nt, segment 2 of 3]
12867	25569		1.53	7.0E-72	F28266.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051 G02
8578	21669		6.7	8.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
64	13302	26324	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150800-398-e11 CS0010 Homo sapiens cDNA
64	13302	26325	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150800-398-e11 CS0010 Homo sapiens cDNA
65	13302	26324	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150800-398-e11 CS0010 Homo sapiens cDNA
65	13302	26325	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150800-398-e11 CS0010 Homo sapiens cDNA
1182	14326		2.31	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7089	20183	33607	1.82	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8978	22055	35598	4.18	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782584 5' similar to TR:Q88785 Q88785 HYPOTHETICAL 32.4 KD PROTEIN, contains element MSR1 repetitive element ;
10186	23203	36797	0.71	5.0E-72	AV724632.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5'
11519	24575	38252	2.95	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11519	24576	38253	2.85	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11945	24931	38833	1.65	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
11945	24931	38834	1.55	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823806 5'
12380	28136		2.46	5.0E-72	BE926845.1	EST_HUMAN	QV1-BT0632-280800-342-e10 BT0632 Homo sapiens cDNA
4943	18073		0.91	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (DJ1057B20.2), mRNA
5581	18776	31821	0.68	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
6687	19845	33236	0.85	4.0E-72	T87947.1	EST_HUMAN	yd83a01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115762 5' similar to SP:A44282 A44282 RETROVIRUS-RELATED POL POLYPYRROLINE - HUMAN ;
7587	20639	34115	3.26	4.0E-72	6729887	NT	Homo sapiens heat domain and RLD 2 (HERC2), mRNA

Page 368 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9887	23028	36618	0.87	4.0E-72	8923689	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10312	23347	36953	0.57	4.0E-72	11434344	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10604	23638	37245	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
10604	23638	37246	0.54	4.0E-72	AW836230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens cDNA
							gb87c02.xt Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to TR:Q14498 Q14498 SPLICING FACTOR, [1] contains Alu repetitive element; contains element L1 repetitive element
10634	23668	37278	1.04	4.0E-72	A1248796.1	EST_HUMAN	aa23f09.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR
11563	24618	38298	1.57	4.0E-72	AA465388.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
11563	24618	38299	1.57	4.0E-72	AA465388.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
11818	24907	38503	6.28	4.0E-72	H79421.1	EST_HUMAN	aa23f09.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814121 3' similar to SW:CPTR_FLAPR
11838	24924	38624	2.19	4.0E-72	7657057	NT	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR
11938	24924	38625	2.19	4.0E-72	7657057	NT	yt28ad03.r1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
11978	24951	38663	1.67	4.0E-72	T81910.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							yt28ad09.s1 Soares fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:109949 3'
12779	25521	32003	11.86	4.0E-72	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13269	26269	0.7	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
926	14101		1.48	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1310280 3'
1180	14343	27398	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1180	14343	27399	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1220	14381	27440	3.98	3.0E-72	U80228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1220	14381	27441	3.98	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1548	14700	27779	1.16	3.0E-72	BE242161.1	EST_HUMAN	TCAAPE1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAPE1252
3143	16319	29331	12.72	3.0E-72	AJ229043.1	NT	Homo sapiens 969 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3362	16524	29539	2.7	3.0E-72	8923648	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3927	17086	30082	2.51	3.0E-72	S77599.1	NT	TOR V delta 2-C alpha =1 -cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4667	17802	30789	3.17	3.0E-72	11416196	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4889	18019	31003	1.25	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4889	18019	31004	1.26	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds

Page 369 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5637	18831		1.12	3.0E-72	4759093	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6101	18281	32613	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 6
6101	18281	32614	1.94	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 6
6295	19468	32822	4.53	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6295	19468	32823	4.53	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6747	19903	33268	4.1	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7768	20817	34307	2.01	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8399	21450	34973	5.42	3.0E-72	5031892	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3) mRNA
10846	23690	37280	1.09	3.0E-72	X98289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
12678	26453	32018	2.18	3.0E-72	AB011399.1	NT	Homo sapiens gene for AIF-6, complete cds
6079	19281	32690	1.38	2.0E-72	11428671	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9297	22373	35923	0.64	2.0E-72	BF308960.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131481 5'
9297	22373	35924	0.64	2.0E-72	BF308960.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131481 5'
10978	24057	37691	5.46	2.0E-72	AA789277.1	EST_HUMAN	6128509 s1 Soares_testis_NHT Homo sapiens cDNA clone 1391609 3' similar to gb:X02087 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN):
12772	25515	31999	3.39	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylphosphorylurate translocator mRNA, complete cds
2137	15273	28394	8.14	1.0E-72	AA84625.1	EST_HUMAN	618302.s1 Soares_parathyroid_tumor_NGHPA Homo sapiens cDNA clone IMAGE:1387385 3'
5887	18075	32384	3.84	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homologue) (VPS41), mRNA
6689	19847	33237	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6769	25832	33319	1.29	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
7815	20870	34369	3.5	1.0E-72	AV751818.1	EST_HUMAN	AV751818 NPD Homo sapiens cDNA clone NPDAE11 5'
7815	20870	34387	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9790	22830	36408	7.37	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9790	22830	36409	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
1488	14641	27723	1.17	9.0E-73	AW374968.1	EST_HUMAN	Homo sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds
6164	10340	32887	0.92	9.0E-73	11525883	NT	MRO-CT0083-071099-002-h11 CT0083 Homo sapiens cDNA
11183	24262		24.49	9.0E-73	11424099	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
1063	14228	27286	0.73	8.0E-73	AW071755.1	EST_HUMAN	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
5698	18892	32184	0.98	8.0E-73	4506798	NT	was55c06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2801088 3' similar to TR:Q69050 Q59050 HYPOTHETICAL PROTEIN MJ1696 ;
							Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	19860	33250	6.29	8.0E-73	11426469	NT	Homo sapiens lysozyme homolog (LOC57151), mRNA
8287	21369	34890	2.1	8.0E-73	AF13129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9553	22618	36188	4.35	8.0E-73	BE019900.1	EST_HUMAN	b62a08.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9841	22980	36570	1.78	8.0E-73	11626037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9841	22980	36571	1.76	8.0E-73	11626037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10134	23172	36770	0.91	8.0E-73	X91940.1	NT	H. sapiens mRNA for WNT-88 protein
10834	23897	37490	0.47	8.0E-73	4607828	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPT1) mRNA
12001	24988	38690	1.48	8.0E-73	AF084520.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12988	25403	32044	1.2	8.0E-73	AB002059.1	NT	Homo sapiens DNA for Human P2X4, complete cds
12842	25580	31988	4.96	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1157	14321	27376	1.61	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3373	16545	29558	0.7	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5059	18187		1.29	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
162	13387		3.04	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7323	20405	33867	3.42	6.0E-73	BE166574.1	EST_HUMAN	QV0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5386	18571	31439	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
1911	15054	28165	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1911	15054	28166	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
8637	19990	33398	0.73	3.0E-73	AA196403.1	EST_HUMAN	zn05604.e1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:585950 3' similar to gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8958	22037	35578	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA0771 5'
8958	22037	35579	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA0771 5'
10927	24010	37970	1.45	3.0E-73	X99660.1	NT	H. sapiens SH3GLP2 pseudogene, 5' end
11261	24330	37970	1.41	3.0E-73	BE711238.1	EST_HUMAN	RC8-HT0678-290600-013-H10 HT0678 Homo sapiens cDNA
11261	24330	37971	1.41	3.0E-73	BE711238.1	EST_HUMAN	RC8-HT0678-290600-013-H10 HT0678 Homo sapiens cDNA
11910	24897		1.82	3.0E-73	AI004040.1	EST_HUMAN	cu11d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625055 3'
13118	25730		3.04	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13122	25732		2.05	3.0E-73	AW69081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
874	14050	27115	1.57	2.0E-73	AF139897.1	NT	Homo sapiens BASS1 (BASS1) mRNA, partial cds
2000	15141		9.67	2.0E-73	AW69081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
2371	15502		1.49	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3249	16423	29440	2.03	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA

Page 371 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3640	16804	28816	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3640	16804	28817	0.68	2.0E-73	7669539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4655	17693		1.31	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6667	19729	33106	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6567	19729	33107	0.59	2.0E-73	AF086824.1	NT	Mus musculus rho/rao-interacting citron kinase (Crik) mRNA, complete cds
6610	19770	33160	5.46	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6839	19962	33400	1.87	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6839	19962	33401	1.87	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7694	21033	34546	1.01	2.0E-73	M94048.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
9732	22797	36370	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9732	22797	36371	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10637	23671	37281	1.31	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10716	23748	37355	1.38	2.0E-73	11496990	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
10716	23748	37356	1.38	2.0E-73	11496990	NT	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA
11309	24374	38017	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11309	24374	38018	2.91	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11339	24402	38051	1.44	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12599	15141		4.32	2.0E-73	AW88081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
1824	14973	28068	3.52	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
8490	19656	33019	1.19	1.0E-73	BE151283.1	EST_HUMAN	CM1-HT0282-11189-042-h10 HT0282 Homo sapiens cDNA
							qg61b07.r1 Sceres, tests_NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contig element
9689	22748	36316	1.22	1.0E-73	AI147427.1	EST_HUMAN	MER22 repetitive element ;
11738	23922	37547	3.74	1.0E-73	BE385477.1	EST_HUMAN	601276071FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617105 5'
12045	25028	38731	1.34	9.0E-74	X77225.1	NT	H. sapiens mRNA for TFIIA
12045	25028	38732	1.34	9.0E-74	X77225.1	NT	H. sapiens mRNA for TFIIA
769	13640	26885	4.83	8.0E-74	4557426	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6036	19219	32541	1.73	8.0E-74	S83104.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
6036	19219	32542	1.73	8.0E-74	S83104.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
2004	15144	28249	4.96	7.0E-74	AJ001689.1	NT	Homo sapiens NKG2D gene, exon 10
3407	16577	29592	1.83	7.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9444	22560	36123	1.48	7.0E-74	BE967432.1	EST_HUMAN	601649284FT NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932897 5'
12841	25559	31985	4.73	7.0E-74	BE266305.1	EST_HUMAN	601191827F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3638855 5'

Page 372 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Describer
1146	14311	27368	3.65	6.0E-74	AF109007.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1656	14809	27893	1.03	6.0E-74	AW263177.1	EST_HUMAN	h78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700638 3'
2390	15521	28649	15.52	6.0E-74	BE388280.1	EST_HUMAN	601283321F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2390	15521	28650	15.52	6.0E-74	BE388280.1	EST_HUMAN	601283321F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2927	16104	29119	0.97	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-aah-h-03-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2927	16104	29120	0.97	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-aah-h-03-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3805	16965	29968	1.22	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3805	16965	29969	1.22	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5481	18680	31695	3.49	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
828	14103	27166	1.63	6.0E-74	AW020986.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2767	15882	31736	4.98	5.0E-74	AW362756.1	EST_HUMAN	PM0-CT0289-271099-001-407 CT0289 Homo sapiens cDNA
5523	18720	31736	1.62	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (P13L), mRNA
5910	19099	32413	12.5	5.0E-74	X69870.1	NT	H. sapiens mRNA for TPCR18 protein
5961	19147	32462	8.1	5.0E-74	4607865	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6030	19213	32533	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6030	19213	32534	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7035	20171	33593	3.69	6.0E-74	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8226	21308	34828	2.33	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10973	24053	37686	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10973	24053	37687	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
11090	24164	37801	1.38	5.0E-74	5729768	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
280	13507	26542	3.31	4.0E-74	D67875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
875	14051	27116	10.3	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2018	15158	28262	3.07	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2018	15158	28263	3.07	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2134	15270	28390	9.66	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2134	15270	28391	9.98	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2201	15336	28463	1.32	4.0E-74	AB032984.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2499	15925	28745	1.18	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	16335	26346	6.22	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3616	16780	26795	1.1	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4174	17324	30315	1.29	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4679	17514	30802	1.86	4.0E-74	7662183	NT	Homo sapiens KIAA0669 gene product (KIAA0669), mRNA
4735	17870	30854	1.07	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5133	18266	31224	1.03	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
5185	18307	31271	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
5185	18307	31272	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
8747	21826		3.53	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 6' end similar to similar to ribosomal protein L37
8773	21852	36394	0.62	3.0E-74	5906912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9572	22714	36282	2.32	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #836206) Homo sapiens cDNA clone HHCP591
10546	23591	37191	2.16	3.0E-74	AA601493.1	EST_HUMAN	nc17g05.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:100984 3'
980	14163	27213	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
980	14163	27214	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1202	14384	27424	1.63	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-147D
1273	14430	27501	1.44	2.0E-74	AI950528.1	EST_HUMAN	w51e07.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG96_HUMAN Q08379 GOLGIN-96; contains element MER22 repetitive element;
1625	14777	27861	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1625	14777	27862	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
2668	15789	28005	2.18	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.r.tumor2 Homo sapiens cDNA 3'
5119	18245	31210	2.62	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5119	18245	31211	2.52	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5919	25813	32419	1.88	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0078-226500-011.C03 HT0078 Homo sapiens cDNA
6017	25816	32518	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6017	25816	32519	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6037	25816	32518	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6037	25816	32519	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7252	20335	33784	2.9	2.0E-74	BF030788.1	EST_HUMAN	601857524F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827549 5'
8126	21208	34728	1.8	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds

Page 374 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9582	22724	36294	6.27	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12526	25359		2.87	2.0E-74	AA196181.1	EST_HUMAN	z996a06.s1 Stragogene muscle 037209 Homo sapiens cDNA clone IMAGE:628018 3'
13169	26176		1.16	2.0E-74	BF002855.1	EST_HUMAN	7a50a08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309878 3'
54	13283	26308	1.5	1.0E-74		NT	Homo sapiens Mismatch/NIK-related kinase (MINK). mRNA
347	13558	26586	3.71	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-Q37-f05 ST0234 Homo sapiens cDNA
512	13708	26734	1.8	1.0E-74	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026). mRNA
519	13712	26739	2.59	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
614	13803	26823	1.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259). mRNA
804	13984	27036	0.86	1.0E-74	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
1024	14195	27253	2.26	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2301	15433	28566	6.03	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3209	16383	29394	2.82	1.0E-74	4758697	NT	Homo sapiens memosidase, alpha, class 2A, member 1 (MAN2A1). mRNA
3460	16627	29646	1.29	1.0E-74	AA258549.1	EST_HUMAN	z60c01.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
3480	16627	29647	1.29	1.0E-74	AA258549.1	EST_HUMAN	z60c01.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:667776 5'
4031	17187	30197	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4031	17187	30198	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4075	17231	30237	5.41	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4175	17325	30316	0.85	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270800-019-f06 BT0642 Homo sapiens cDNA
4382	17525	30508	0.87	1.0E-74	BE467769.1	EST_HUMAN	hz3h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP:80611.12
6844	19897	33404	1.29	1.0E-74	M89814.1	NT	CE-17351
7804	20860	34353	1.05	1.0E-74	11417877	NT	Human neurofilament (NF1) gene, complete cds
8246	21328	34844	1.27	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens KIAA0852 protein (KIAA0852). mRNA
8246	21328	34845	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9005	22084	35627	7.81	1.0E-74	AF214562.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
9034	22113	35656	0.67	1.0E-74	BF351951.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (PLLUNC) gene, complete cds
10445	23480	37086	0.65	1.0E-74	AJ251550.1	NT	MFO-HT0559-230500-021-e03 HT0559 Homo sapiens cDNA
10445	23480	37087	0.65	1.0E-74	AJ251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10689	23732	37337	1.77	1.0E-74	11420549	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
12154	25124	38826	1.94	1.0E-74	11417856	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783). mRNA
12238	25182		4.97	1.0E-74	11417856	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783). mRNA
12386	15433	28566	1.61	1.0E-74	AB002059.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2). mRNA
12925	25810		1.38	1.0E-74	AF240786.1	NT	Homo sapiens DNA for Human P2XM, complete cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2709	15827		5.1	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12652	28375		3.07	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2395	15526	28654	1.25	6.0E-75	AI817415.1	EST_HUMAN	wk38a03.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
11780	24770	38466	1.39	6.0E-75	BE791831.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
9109	22188	36731	1.09	5.0E-75	BE272325.1	EST_HUMAN	601126068F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940130 5'
9317	22353	35944	0.77	5.0E-75	AA132811.1	EST_HUMAN	601126068F1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2989895 5'
9395	22470	36034	0.47	5.0E-75	BE561655.1	EST_HUMAN	zot17e08.t1 Straglene colon (#937204) Homo sapiens cDNA clone IMAGE:387174 5'
9395	22470	36035	0.47	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3887458 5'
9573	22715	36283	1.1	5.0E-75	BF600254.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3887458 5'
10439	23474	37078	2.64	5.0E-75	AI639623.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
115	13346	26373	2.1	4.0E-75	BE081333.1	EST_HUMAN	h31e12.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P87361 P87361
471	13668		1.68	4.0E-75	N39757.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN ;
1805	14954	28043	1.08	4.0E-75	AV1897230.1	EST_HUMAN	QY1-BT0632-210200-078-e02 BT0632 Homo sapiens cDNA
2910	16088	29101	5.64	4.0E-75	BE408464.1	EST_HUMAN	X490108.t1 Scores melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:266055 5'
5646	18840	32120	0.68	4.0E-75		NT	CMD-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
6399	19598	32929	5.18	4.0E-75	11417846	NT	601303666F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6898	20048	33459	1.4	4.0E-75	11417846	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10224	24007	37642	10.52	4.0E-75	7666505	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1027	14188	27266	3.8	3.0E-75	AF157623.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1028	14198	27256	3.59	3.0E-75	AF157623.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
1883	15027	28134	2.23	3.0E-75	AB011153.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
2180	16315	28444	1.44	3.0E-75	4507334	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
2484	16521	28740	4.39	3.0E-75	4759153	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
3086	16522	28279	0.95	3.0E-75	AL163201.2	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
3258	16432	28449	1.09	3.0E-75	AB011153.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
3431	16599	28616	0.93	3.0E-75	M72393.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
3431	16599	28617	0.93	3.0E-75	M72393.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
3833	16593	28695	0.6	3.0E-75	M72393.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
4283	17428	30418	2.92	3.0E-75	D87873.1	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5385	18598	31434	1.15	3.0E-75	11420556	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA

Page 376 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5365	18598	31435	1.15	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6637	19798	33185	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6637	19798	33186	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6909	20224	33654	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6909	20224	33655	1.57	3.0E-75	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7285	20368	33821	4.12	3.0E-75	7682209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7285	20368	33822	4.12	3.0E-75	7682209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7800	20896	34346	2.65	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7800	20896	34347	2.65	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9185	22263	35805	1.33	3.0E-75	11420804	NT	Homo sapiens snail 1 (Drosophila homolog), zinc finger protein (SNA1), mRNA
9880	22920	36504	0.83	3.0E-75	11420222	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
5790	18882		1.34	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cDNA Homo sapiens cDNA clone cABED02 5'
8950	22029	35570	1.36	2.0E-75	AI311783.1	EST_HUMAN	9e91e02.x1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1918898 3' similar to TR:Q69386 Q69386
2377	15508	28635	10.98	1.0E-75	AW168135.1	EST_HUMAN	POL1ENV GENE ;
3012	16188	29213	2.95	1.0E-75	X52221.1	EST_HUMAN	PG60d02.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.11
7762	20821	34312	0.64	1.0E-75	BE082528.1	EST_HUMAN	PT77 repetitive element ;
7762	20821	34312	0.64	1.0E-75	BE082528.1	EST_HUMAN	H sapiens ERCC2 gene, exons 1 & 2 (partial)
8609	21889		3.12	1.0E-75	AA399270.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
9628	22883	36253	3.95	1.0E-75	BF313845.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
9628	22883	36254	3.95	1.0E-75	BF313845.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
11122	24194		6.88	1.0E-75	AA694377.1	EST_HUMAN	z157h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13932 40S
11351	24413	38067	2.22	1.0E-75	AF223391.1	NT	z157h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:M13932 40S
12440	18502	31838	1.97	1.0E-75	BE884192.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN);
45	13284	26292	0.89	9.0E-76	AI652648.1	EST_HUMAN	601800294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
45	13284	26293	0.89	9.0E-76	AI652648.1	EST_HUMAN	601800294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
2486	15613		0.94	9.0E-76	AA702415.1	EST_HUMAN	601800294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
							ac77608.s1 Stratagene lung (#637210) Homo sapiens cDNA clone IMAGE:368599 3'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							applied
							601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
							WB30010.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1;
							WB30010.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235
							TRAP1;
							z88507.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:447541 3'

Page 377 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10105	23143	38741	5.44	9.0E-76	M12837.1	NT	Human ferritin Heavy subunit mRNA, complete cds
981	14134	27184	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
981	14134	27185	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2976	16152	29173	0.95	8.0E-76	7706724	NT	Homo sapiens mediator (Sur2), mRNA
6300	19473	32828	5.84	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7668	20725	34200	1.17	8.0E-76	11435215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7738	20900	34289	1.05	8.0E-76	11419212	NT	Homo sapiens mitochondrial carrier family protein (LOC656972), mRNA
8482	21873	35110	0.69	8.0E-76	11418861	NT	Homo sapiens AIM-1 protein (LOC51181), mRNA
10588	23624	37231	1.28	8.0E-76	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds
10903	23987	37619	4.29	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 8 (BIRC8), mRNA
12824	25550		2.51	8.0E-76	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
797	13976	27029	1.89	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3366	16638	29551	3.84	7.0E-76	AF056480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3372	10544	29558	9.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4491	17631	30612	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4491	17631	30613	5.52	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1282	14419		37.29	6.0E-76	BE396283.1	EST_HUMAN	601312018F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3656797 5'
11753	20939	37565	2.52	6.0E-76	BE273201.1	EST_HUMAN	601142253F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506029 5'
1997	15138	28243	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28244	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28245	9.61	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3278	16452	28473	0.64	4.0E-76	BE814096.1	EST_HUMAN	QV3-BN0047-270700-283-g06 BN0047 Homo sapiens cDNA
5384	18598	31455	1.13	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10230	23295	36884	5.48	4.0E-76	D81626.1	EST_HUMAN	HUM178G01B Human fetal brain (T Fujivara) Homo sapiens cDNA clone GEN-178G01 5'
10230	23295	36885	5.48	4.0E-76	D81626.1	EST_HUMAN	HUM178G01B Human fetal brain (T Fujivara) Homo sapiens cDNA clone GEN-178G01 5'
648	13831	26856	2.01	3.0E-76	BF516282.1	EST_HUMAN	U1H-BW1-ans-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
648	13831	26857	2.01	3.0E-76	BF516282.1	EST_HUMAN	U1H-BW1-ans-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1029	14781	27866	8.04	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1629	14781	27867	8.04	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3515	16681	28691	6.75	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3515	16681	28692	5.78	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5352	18480	38822	1.82	3.0E-76	Z41314.1	EST_HUMAN	HSCZQD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5851	19041	32347	0.92	3.0E-76	AA160611.1	EST_HUMAN	z073c07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to
6110	18290	32675	0.61	3.0E-76	AW027705.1	EST_HUMAN	gb:1.32976 MIXED LINEAGE KINASE 1 (HUMAN);
6498	19694	33027	8.19	3.0E-76	AF286598.1	NT	ww75c03.x1 Soares_thymus_NHT_Homo sapiens cDNA clone IMAGE:25353588 3'
8344	21425	34951	1.27	3.0E-76	NA2671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
9917	22957	36544	3.03	3.0E-76	AW299353.1	EST_HUMAN	y20g10.r1 Soares_melanocyte 2NtHM Homo sapiens cDNA clone IMAGE:271842 5'
9842	22981	36572	1.08	3.0E-76	AA442309.1	EST_HUMAN	xe48h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:767461 5'
9842	22981	36573	1.08	3.0E-76	AA442306.1	EST_HUMAN	zv54d11.r1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:767461 5'
12144	26943	31763	2.1	3.0E-76	AW967984.1	EST_HUMAN	EST368525 MAGC resequences, MAGD Homo sapiens cDNA
12251	28184	31542	6.95	3.0E-76	AW956455.1	EST_HUMAN	Human mRNA for possible protein TPRDII, complete cds
292	13509	26544	1.11	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26590	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26591	3.21	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
473	13668	26812	0.96	2.0E-76	4657662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
603	13792	26812	1.07	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1058	14222	27281	1.66	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1568	14719	27799	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1568	14719	27800	11.31	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1882	15125	28227	0.89	2.0E-76	AA253954.1	EST_HUMAN	zs60h11.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2804	18082	28097	2.13	2.0E-76	P23266	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3369	16541	28555	2.21	2.0E-76	AA445992.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3369	16541	28556	2.21	2.0E-76	AA445992.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3565	16730	28746	0.93	2.0E-76	A1821149.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT_Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
4284	13509	26544	1.01	2.0E-76	D84295.1	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
4653	17789	30773	0.91	2.0E-76	A1163283.2	NT	ac83b02.y6 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
5062	18190	31165	11.15	2.0E-76	AW879618.1	EST_HUMAN	O14591 SIMILARITY TO P22059 ;
5163	18285	31249	3.13	2.0E-76	5174586	NT	Human mRNA for possible protein TPRDII, complete cds
5424	18625	32226	2.99	2.0E-76	AF127845.1	NT	Homo sapiens chromosome 21 segment HS21C083
5736	18929	34119	4.83	2.0E-76	AB029004.1	NT	QV3-OT0028-220300-132-bt1 OT0028 Homo sapiens cDNA
7570	20642	34119	0.66	2.0E-76	11421326	NT	Homo sapiens murine retrovirus integration site 1 homolog (MRV1) mRNA
7592	20663	34139	0.69	2.0E-76	11426808	NT	Homo sapiens olfactory receptor (GGO18) gene, partial cds
							Gordia gorilla olfactory receptor (GGO18) protein, partial cds
							Homo sapiens KIAA1081 protein, partial cds
							Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
							Homo sapiens A kinase (PRKA) anchor protein 10 (AKAP10), mRNA

Page 379 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7840	20695	34397	1.92	2.0E-76	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10489	23524	37134	1.42	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63160), mRNA
11161	24232	37892	2.44	2.0E-76	7349807	NT	Homo sapiens HIRA interacting protein 4 (dhaJ-like) (HIRIP4), mRNA
4412	17564	30539	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4412	17564	30540	2.49	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5564	18761	31801	5.93	1.0E-76	BE789537.1	EST_HUMAN	601569896F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6374	19543		0.7	1.0E-76	AA333207.1	EST_HUMAN	ES157301 Embryo, 8 week 1 Homo sapiens cDNA 5' end
7063	20116	33530	4.56	9.0E-77	BE889526.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
13003	25662		1.98	9.0E-77	BE410364.1	EST_HUMAN	601502333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
192	13414	26443	0.77	8.0E-77	R83144.1	EST_HUMAN	ypt1h02.r1 Soares breast 3NBHb1 Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1:
4844	17780	30762	1.41	8.0E-77	BF205181.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mox34 homolog) (PSMD7) mRNA
5569	18766	31807	1.37	8.0E-77	4508230	NT	z662802.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11660	24746	38438	1.78	8.0E-77	AA019770.1	EST_HUMAN	z662802.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11669	24746	38439	1.78	8.0E-77	AA019770.1	EST_HUMAN	y669704.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element:
12979	25637	31982	32.5	8.0E-77	R00245.1	EST_HUMAN	z662802.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:748392 3'
1983	15126	28228	2.2	7.0E-77	AA625765.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28733	2.78	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28734	2.78	7.0E-77	4505944	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
273	13491	28522	4	6.0E-77	4504600	NT	EST369823 IMAGE resequences, IMAGE Homo sapiens cDNA
1165	14329	27384	1.05	6.0E-77	AW067753.1	EST_HUMAN	q677h12.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
1674	14727	27808	3.28	6.0E-77	A1204068.1	EST_HUMAN	7 Homo sapiens glucokinase (GCK) gene, exon 2
1264	14421	27488	2.89	5.0E-77	AF041015.1	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
1391	14546	27621	3.46	6.0E-77	4557250	NT	Homo sapiens tauoel-like kinase 1 (TLK1) mRNA, complete cds
2749	15966	28977	1.75	5.0E-77	AF162666.1	NT	Homo sapiens cullin 1 (CUL1) mRNA
2822	15936	28046	1.98	5.0E-77	4503160	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
3611	16775	28791	0.65	5.0E-77	6394518	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
4825	17958	30944	0.97	5.0E-77	5031600	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
4825	17958	30945	0.97	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
5052	18180	31158	3.57	5.0E-77	AL043963.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G1728 5'
6922	20237	33671	0.65	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7480	20555	34027	0.59	5.0E-77	X98286.1	NT	H. sapiens mRNA for ubiquitin hydrolase

Page 380 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7767	20555	34027	0.72	5.0E-77	X98286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8563	21644	35183	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8563	21644	35184	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9769	22765	36335	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9769	22765	36336	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10708	23741	37346	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0298 gene, partial cds
10708	23741	37347	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0298 gene, partial cds
2028	15170	28277	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
2028	15170	28278	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
10496	23531	37139	0.9	3.0E-77	H65167.1	EST_HUMAN	Homo sapiens PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10496	23531	37140	0.9	3.0E-77	H65167.1	EST_HUMAN	Homo sapiens PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
11115	24187	37819	2.83	3.0E-77	BF359917.1	EST_HUMAN	PM3-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1383	14538	27612	1.74	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1484	14618	27702	9.74	2.0E-77	AW987742.1	EST_HUMAN	RC3-BN0053-170200-011-H01 BN0053 Homo sapiens cDNA
2157	15283	28419	1.1	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2170	13305	28432	2.78	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2659	16087	28895	1.69	2.0E-77	AB037839.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2659	16087	28896	1.69	2.0E-77	AB037839.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4143	17295	30287	1.98	2.0E-77	BE044316.1	EST_HUMAN	h043b05.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2 HUMAN P10294 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4534	17672	30656	0.67	2.0E-77	A1613519.1	EST_HUMAN	hw22g02.x1 NCJ_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4534	17672	30657	0.67	2.0E-77	A1613519.1	EST_HUMAN	hw22g02.x1 NCJ_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4891	18021	31006	2.34	2.0E-77	AA653025.1	EST_HUMAN	ns68g12.s1 NCJ_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN
6075	19257	32586	2.08	2.0E-77	BE288940.1	EST_HUMAN	P47914 60S RIBOSOMAL PROTEIN L29 [1], contains element MSR1 repetitive element ;
6301	19474	32829	1.86	2.0E-77	BE787143.1	EST_HUMAN	60111952F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028436 5'
7325	20407	33869	15.02	2.0E-77	A1833003.1	EST_HUMAN	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
							at74e09.x1 Barstead cdon HPURB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
							Q13311 TAX1-BINDING PROTEIN TXBP151 [1];

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8726	21806	35343	0.88	2.0E-77	A1962707.1	EST_HUMAN	qy70c09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017380 3' similar to WP:F20D11.1
9728	22793	35366	5.68	2.0E-77	U50321.1	NT	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN;
9728	22793	35367	5.68	2.0E-77	U50321.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10199	23236	36825	0.47	2.0E-77	BF310349.1	EST_HUMAN	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10199	23236	36826	0.47	2.0E-77	BF310349.1	EST_HUMAN	601885183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
44	13282	28288	2.52	1.0E-77	AB033102.1	NT	601885183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
44	13282	28289	2.82	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
283	13501	28593	1.68	1.0E-77	4502166	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
283	13501	28594	1.68	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27140	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27141	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1989	15112	28213	1.36	1.0E-77	AW058119.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2515	15641	28763	1.17	1.0E-77	AB029024.1	NT	w63a05.x1 Soares thymus NIH-FtH Homo sapiens cDNA clone IMAGE:2536160 3'
3110	16288	29300	2.28	1.0E-77	4503300	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
4473	17613	30592	4.24	1.0E-77	7708288	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEOR1), mRNA
4648	17782	30764	22.17	1.0E-77	AJ220041.1	NT	Homo sapiens CGI-58 protein (LOC51628), mRNA
4774	17809	30892	2.05	1.0E-77	6552322	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4816	17948	30933	0.61	1.0E-77	A1273014.1	EST_HUMAN	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
6051	19233	32557	1.48	1.0E-77	AF086944.1	NT	qy09g04.x1 NCI_CGAP_K168 Homo sapiens cDNA clone IMAGE:1981110 3'
6051	19233	32558	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dyxactin 1 (DCTN1) gene, exons 27 and 28
8172	19348	32694	1.72	1.0E-77	M25844.1	NT	Homo sapiens dyxactin 1 (DCTN1) gene, exons 27 and 28
6577	19739	33120	1.1	1.0E-77	4885182	NT	Human von Willebrand factor gene, exon 20
7168	20063	33473	15.97	1.0E-77	5881412	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7844	20899	34402	0.92	1.0E-77	11420159	NT	Homo sapiens diaphanous (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7940	20990	34500	0.71	1.0E-77	X04571.1	NT	Homo sapiens cullin 1 (CUL1), mRNA
9495	22522	35085	0.83	1.0E-77	X04354.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9465	22522	35086	0.83	1.0E-77	X04354.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10742	23775	37387	1.05	1.0E-77	AB029396.1	NT	H. sapiens DNA for Cone cGMP-PDE gene
10742	23775	37388	1.05	1.0E-77	AB029396.1	NT	Homo sapiens hu-GlcAT-P mRNA for glucuronyltransferase, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10773	23808	37429	2.76	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
6576	19738	33118	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-a05 ET0023 Homo sapiens cDNA
6576	19738	33119	2.29	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-a05 ET0023 Homo sapiens cDNA
88	13323	26351	1.66	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
88	13323	26352	1.66	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3389	16559	29574	0.9	6.0E-78	BF344101.1	EST_HUMAN	602016928F1 NCI_CGAP_Bri64 Homo sapiens cDNA clone IMAGE:4152511 5'
6690	19848		2.54	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
224	13448	26474	6.13	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2629	15752	28887	5.71	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP.Y48B6A.6
3472	16639	29659	5.09	5.0E-78	M55586.1	NT	CE22121
5528	18725	31741	2.73	5.0E-78	AF038536.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5603	18887	32177	18.13	6.0E-78	11416585	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
7304	20388	33846	2.18	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9284	22360	35910	7.02	5.0E-78	U60889.1	NT	EST305180 MAGE resequences, MAGE Homo sapiens cDNA
9285	22361	35911	2.94	6.0E-78	BE960838.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manb) gene, exon 7
1160	14324	27379	1.29	4.0E-78	AL043314.2	EST_HUMAN	601848061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1547	14899	27778	1.81	4.0E-78	AL365841.1	NT	DKFZp434N0323_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
2392	15523	28652	5.1	4.0E-78	AF107403.1	NT	Novel human gene mapping to chromosome 22
4442	17582	30580	6.17	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4896	18026	31012	1.2	4.0E-78	4505806	NT	Homo sapiens syncytin (LOC30816), mRNA
4896	18028	31013	1.2	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5898	19078	32385	1.25	4.0E-78	11420732	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
6302	19475	32830	0.71	4.0E-78	7662109	NT	Homo sapiens SFRS3 protein kinase 2 (SRPK2), mRNA
6302	19476	32831	0.71	4.0E-78	7662109	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
6703	19861	33251	0.74	4.0E-78	4506736	NT	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
7660	20727	34203	0.69	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35677	1.15	4.0E-78	AF012872.1	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35678	1.15	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9568	22710	36278	0.61	4.0E-78	11417251	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
10660	23694	37303	1.95	4.0E-78	11560151	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10660	23694	37304	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11705	24702	38394	1.84	4.0E-78	AF169148.1	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11854	24842	38538	6.72	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12855	25568	31981	3.93	4.0E-78	AB011398.1	NT	Homo sapiens gene for AF-5, complete cds
165	13390	26417	1.69	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
165	13390	26418	1.69	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
2488	15815	28738	1.01	3.0E-78	7706705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3860	17020		0.81	3.0E-78	AU140804.1	EST_HUMAN	AU140804 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3918	17077	30074	0.78	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4221	17077	30074	0.82	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
10493	23828		5.44	3.0E-78	BE144758.1	EST_HUMAN	CMO-HT0180-041099-065-c07 HT0180 Homo sapiens cDNA
11227	24286	37837	2.5	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0367-180200-114-q09 HT0367 Homo sapiens cDNA
3181	16368		2.49	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4122	17276		1.99	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells V1 Homo sapiens cDNA 5' end
7631	20700	34177	1.09	2.0E-78	AW402306.1	EST_HUMAN	UHF-BK0-aej-g-10-q-UJr1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7031	20700	34178	1.09	2.0E-78	AW402306.1	EST_HUMAN	UHF-BK0-aej-g-10-q-UJr1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3054139 5'
7908	20860	34486	3.36	2.0E-78	BF689800.1	EST_HUMAN	602186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4288599 5'
8230	21312	34832	2.49	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF08 5'
8646	21726	35282	1.72	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8646	21726	35283	1.72	2.0E-78	AI557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
11336	24399	38048	9.58	2.0E-78	AI197837.1	EST_HUMAN	q60h05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1869961 3' similar to WP.R80.1
11358	24420		1.47	2.0E-78	BE439409.1	EST_HUMAN	CE08325 PROTEIN KINASE ;
11366	24447	38108	3.01	2.0E-78	N69851.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
5420	18621	31597	3.16	1.0E-78	11417304	NT	2a48112 s1 Soares fetal liver spleen (NFILS) Homo sapiens cDNA clone IMAGE:295823 3'
7094	18521	31514	0.82	1.0E-78	AV648689.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC61306), mRNA
8363	21434		1.81	1.0E-78	U52373.1	NT	AV648689 GLC Homo sapiens cDNA clone GLCBM001 3'
12324	28234	32107	1.83	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12422	25269	32086	2.44	1.0E-78	11435903	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4820	17653	30638	4.04	9.0E-79	11526801	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4956	18115	31093	1.6	9.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5549	18746	31781	16.98	9.0E-79	AB028070.1	NT	RC2-BN0074-000300-014-q12 BN0074 Homo sapiens cDNA
6470	19637	32996	2.52	9.0E-79	6454145	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6752	19908	33301	0.98	9.0E-79	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
							Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7506	26846		0.99	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7748	20808	34208	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS166L18.1), mRNA
7748	20808	34209	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS166L15.1), mRNA
8541	21622	35158	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8541	21622	35159	0.52	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
9263	22340	35890	4.78	9.0E-79	J02863.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9263	22340	35891	4.78	9.0E-79	J02863.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9680	22722	38292	0.66	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10574	23609	37214	0.82	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10632	23666	37274	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216), mRNA, complete cds
10632	23666	37275	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216), mRNA, complete cds
11322	24385	38029	1.61	9.0E-79	AY008273.1	NT	Homo sapiens TRAF8-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11802	24792	38489	2.84	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicoot homolog 2 (SWAP2), mRNA
11802	24792	38490	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicoot homolog 2 (SWAP2), mRNA
13088	25711	31987	1.4	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3836	16996	29998	1.18	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3325	16498	29518	6.38	7.0E-79	BE619648.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
8844	21923		0.62	6.0E-79	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
12169	25132		5.44	6.0E-79	AA698829.1	EST_HUMAN	294e04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462558 3' similar to TR:Q15408 Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;
11786	24776	38473	3.63	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
323	13537	26569	1.74	3.0E-79	AF114488.1	NT	Homo sapiens interocotin short isoform (ITSN) mRNA, complete cds
1001	14172	27233	1.22	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Chn) gene, complete cds
3188	16343	29351	1.74	3.0E-79	U09410.1	NT	Human Zinc finger protein ZNF131 mRNA, partial cds
5477	18876	31689	7.05	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5841	19031	32337	1.69	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5866	19056	32363	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5866	19056	32364	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5889	19077	32386	3.87	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5889	19077	32387	3.87	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6884	20036	33445	0.84	3.0E-79	BE256893.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7206	20071	33481	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
7206	20071	33482	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8012	21082	34574	0.87	3.0E-79	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA

Page 385 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8358	21439	34961	0.78	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
9003	22588	36230	0.59	3.0E-79	10835036	NT	Homo sapiens tetrahydropteridine repeat domain 3 (TTC3), mRNA
10555	23580		0.62	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GK Homo sapiens cDNA clone GKCAHE11 5'
288	13515		1.4	2.0E-79	H63129.1	EST_HUMAN	y4803.31 Soares fetal liver spleen 7N1LS Homo sapiens cDNA clone IMAGE:208541 3'
651	13837	26964	1.05	2.0E-79	BE370926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 6'
957	14124	27188	1.14	2.0E-79	4767841	NT	Homo sapiens BCL2-like 2 (BCL2L2), mRNA
1007	14178	27239	4.97	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1007	14178	27240	4.97	2.0E-79	4886234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1060	14226		2.15	2.0E-79	AI623747.1	EST_HUMAN	fh18107.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685 3'
2216	15349	28478	6.17	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2216	15349	28478	6.17	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2268	15399	28527	1.35	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2387	15516	28648	1.1	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2780	15896	29005	1.2	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0637 protein, partial cds
4023	17179	30188	0.89	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLCA4 (CLCA4) mRNA, complete cds
4280	17425	30414	1.25	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4813	17946	30831	0.83	2.0E-79	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
6788	18980		1.06	2.0E-79	AA312223.1	EST_HUMAN	EST182026 Jurkat T-cells VI Homo sapiens cDNA 5' and similar to C. elegans hypothetical protein, ccsmid B0303.15
5844	19034	32340	0.9	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6373	19542	32801	1.19	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7100	18527	31519	0.89	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7317	20398	33861	2.09	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7317	20398	33862	2.09	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8282	21374	34894	1.1	2.0E-79	4506442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8714	21784	35331	2.13	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8965	22044	35587	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8965	22044	35588	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9205	22283	35823	0.69	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein Mb-9 (H. sapiens) (LOC63961), mRNA
10297	23332	36935	1.88	2.0E-79	S72869.1	NT	H4(D10S170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10297	23332	36936	1.88	2.0E-79	S72869.1	NT	H4(D10S170) putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
11284	24360	37887	2.84	2.0E-79	BE084366.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11284	24350	37988	2.94	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
12208	18498	31534	4.27	2.0E-79	7652357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12208	25219	32100	2.3	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12531	25362	32067	3.08	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6718	26830		3.28	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-B10 NN0087 Homo sapiens cDNA
							IG37e08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
							TEKTN C1.1
6633	19966	33394	0.95	1.0E-79	AI613480.1	EST_HUMAN	IG37e08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
							TEKTN C1.1
6833	19886	33395	0.95	1.0E-79	AI613480.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
8439	21520	35049	0.9	1.0E-79	BE394211.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
11922	24808	38609	1.9	1.0E-79	BF087403.1	EST_HUMAN	ar7a04.x1 Barstaden colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
12326	26107		1.44	1.0E-79	AI460115.1	EST_HUMAN	ai23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3215	16389	29309	6.95	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3215	16389	29400	6.95	9.0E-80	AA725848.1	EST_HUMAN	ai23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
10217	23263	36842	1.3	9.0E-80	BE798803.1	EST_HUMAN	601161652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935061 5'
							Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11554	24609	38288	7.63	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11554	24609	38289	7.63	9.0E-80	11433924	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
3691	16853		1.01	8.0E-80	U94387.1	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7780	20836	34328	2.92	8.0E-80	11422847	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7780	20836	34329	2.82	8.0E-80	11422847	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9602	22357	36228	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9602	22357	36229	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7114	18540	31497	0.81	7.0E-80	AF127882.1	NT	Caillitrix jacobus olfactory receptor (CJA80) gene, partial cds
							tf53a02.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
923	14098	27162	0.74	6.0E-80	AJ422197.1	EST_HUMAN	Q16795 NADH-BIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
1875	14827	27910	2.41	6.0E-80	U64898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2372	15603	28628	1.14	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2372	15603	28629	1.14	6.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
5922	19109	32422	1.46	6.0E-80	11421462	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6200	19375	32726	3.35	6.0E-80	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9) gene

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6388	19528	32886	4.07	6.0E-80	11430736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6402	19571		1.08	6.0E-80	7662393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6452	19619	32982	0.82	6.0E-80	M18633.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
9024	22103	35643	3.4	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9024	22103	35644	3.4	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9221	22269	35842	1.57	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9559	22824	36198	0.86	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
10065	23103	36706	1.83	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exon 21
11183	24252	37887	2	6.0E-80	11427366	NT	Homo sapiens braefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11498	24566	38231	20.86	6.0E-80	AF226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
12053	25034	38740	1.48	6.0E-80	AF10265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
12176	14098	27162	1.75	6.0E-80	A1422197.1	EST_HUMAN	tt58d02.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q19795 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
12309	25972		2	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12512	25351		3.32	6.0E-80	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13081	26115		2.69	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2) gene
601	13790	26811	1.7	5.0E-80	4506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
858	14035	27097	1.89	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
858	14035	27098	1.89	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1218	14377		1.49	5.0E-80	X91847.1	NT	H. sapient nox1 gene (exon 12)
1485	14638		2.69	5.0E-80	AF163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2501	15628	28748	3.51	6.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2855	15999	29078	1.78	6.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4150	17302	30285	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4150	17302	30286	0.9	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
5068	18106	31170	1.23	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C088
8552	21633	35170	1.28	6.0E-80	F26915.1	EST_HUMAN	Mus musculus keratin complex 2, gene 6p (Krt2-6g), mRNA
8458	22574	36140	5.03	4.0E-80	F26915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone s4000045F03
223	13445		6.03	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5028	18157		2.3	3.0E-80	BE817465.1	EST_HUMAN	QV4-BND283-040600-241-g10 BND283 Homo sapiens cDNA
5941	18127	32440	1.78	3.0E-80	A1091875.1	EST_HUMAN	0023612.x1 Soares NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1667084 3' similar to TR:035790 O35790 P10-L ;

Page 388 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1841	14987	28087	4.85	2.0E-80	R35321.1	EST_HUMAN	yg65a08.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
1908	15051	28163	1.57	2.0E-80	A1444821.1	EST_HUMAN	RET487 subtracted retina cDNA library Homo sapiens cDNA clone RET487
2116	16293	28372	7.03	2.0E-80	AL043116.2	EST_HUMAN	DKFZp434D1323_11 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434D1323 5'
6844	20257	33696	0.95	2.0E-80	AA58282.1	EST_HUMAN	nm80401.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1080177 3'
7053	20106	33522	1.88	2.0E-80	11421930	NT	Homo sapiens Gdgl transport complex protein (90 kDa) (GTC09), mRNA
7401	20479	33947	0.89	2.0E-80	T75215.1	EST_HUMAN	yg66f12.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to SP-K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B :
9360	22435	35894	1.21	2.0E-80	AW684270.1	EST_HUMAN	EST376343 IMAGE resequences, MAGH Homo sapiens cDNA
9970	23069	36603	0.99	2.0E-80	AJ007379.1	NT	Homo sapiens GGT gene, exon 6
11109	24181	37815	6.84	2.0E-80	AA393362.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
350	13561		1.52	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
822	14001	27055	1.3	1.0E-80	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
2008	19149		2.42	1.0E-80	A1732656.1	EST_HUMAN	nm01f12.x5 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.11 OFR
4583	17720	30703	0.95	1.0E-80	AF077188.1	NT	repetitive element ;
5343	18466		3.32	1.0E-80	Y13932.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5442	18642		6.25	1.0E-80	BE386819.1	EST_HUMAN	Homo sapiens PRKY exon 7
6093	19274	32603	6.12	1.0E-80	L10347.1	NT	601274306F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6627	19787	33176	1.17	1.0E-80	5174540	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7356	20435	33897	1.18	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7747	20807	34296	8.03	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
7747	20807	34297	8.03	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8426	21507	35039	0.67	1.0E-80	11421211	NT	wq25c05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8897	21978	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8897	21978	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
8897	21978	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), mRNA
9485	22542	36105	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9485	22542	36105	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10640	23674	37284	0.7	1.0E-80	D63478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10887	23971	37601	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
10887	23971	37602	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
12593	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNI1), mRNA
12593	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNI1), mRNA
12593	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens gene for AI-6, complete cds
12593	25398	32042	1.32	1.0E-80	AB011399.1	NT	Homo sapiens gene for AI-6, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
10923	24006	37840	1.93	8.0E-81	AI251752.1	EST_HUMAN	q90g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
10923	24006	37841	1.93	8.0E-81	AI251752.1	EST_HUMAN	q90g05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854286 3'
11422	24483	38147	5.09	8.0E-81	BE394525.1	EST_HUMAN	601310331F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							z21d10.71 Scores_fetal_haer_L_NbHH19W Homo sapiens cDNA clone IMAGE:350835 5' similar to SW:KRHA_RABIT Q02857 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1] :contains element MER22 repetitive element:
2280	16412	28543	0.94	7.0E-81	AA011080.1	EST_HUMAN	z901c08.x5 Scores_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:298818 3'
7402	20480	33948	3.69	7.0E-81	AI822115.1	EST_HUMAN	z901c08.x5 Scores_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:3352840 5'
4508	17645	30632	3.73	6.0E-81	BE256828.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4508	17645	30633	3.73	6.0E-81	BE256828.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5397	18598	31659	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5397	18598	31570	2.28	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9437	22511	36076	1.24	6.0E-81	AA360017.1	EST_HUMAN	EST169129 Fetal lung II Homo sapiens cDNA 5' end
12747	25495	32030	3.38	6.0E-81	BF678022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284901 5'
12747	25495	32031	3.38	6.0E-81	BF678022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284901 5'
2281	15423	28557	2.88	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3346480 5'
8607	21688	35228	3.06	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8607	21688	35227	3.06	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9848	22888	36487	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9848	22888	36488	1.25	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11883	24871	35598	1.76	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
720	13902	26843	0.94	4.0E-81	AI521435.1	EST_HUMAN	tr60e12.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
1887	15013	28121	1.54	4.0E-81	AW779812.1	EST_HUMAN	hn88d02.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036907 3' similar to SW:COOP_BOVIN
3239	18413	29428	3.91	4.0E-81	AB037766.1	NT	P53820 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds
3718	18879	29884	0.89	4.0E-81	AW004608.1	EST_HUMAN	w69h03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505289 3' similar to TR:O43815 O43815
4276	17421	30408	2.94	4.0E-81	AF263308.1	NT	STRIATIN. ; Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4276	17421	30409	2.94	4.0E-81	AF263308.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7427	20504	33874	0.91	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
7559	20631	34108	0.59	4.0E-81	11420544	NT	Homo sapiens ets variant gene 1 (ETV1), mRNA
8482	21663	35098	2.36	4.0E-81	X05989.1	NT	Human mRNA for amyloid A4(761) protein
8742	21821	35355	2.2	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8742	21821	35356	2.2	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9427	22501	36087	3.35	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10306	23341	36846	1.4	4.0E-81	11425281	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10374	23409	37018	0.65	4.0E-81	11436086	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10374	23409	37019	0.65	4.0E-81	11436085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11481	24520	38189	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
11481	24520	38190	4.74	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B), mRNA
12200	26039	31682	8.38	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12200	26039	31683	8.38	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12796	25632	32009	1.63	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12796	25632	32010	1.63	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12956	26623	31978	4.21	4.0E-81	11417974	NT	Homo sapiens NF2 gene
1296	14452	27516	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1296	14452	27517	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2444	15572	28701	1.72	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3055	16231	29250	6.11	3.0E-81	4508280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3055	16231	29251	6.11	3.0E-81	4508280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2894	16073	29080	2.29	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2894	16073	29091	2.29	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3873	17032	30031	0.8	2.0E-81	AW614542.1	EST_HUMAN	hg85601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
8144	21226	34746	0.69	2.0E-81	8923839	NT	Homo sapiens hypothetical protein (LOC55586), mRNA
13129	17032	30031	5.68	2.0E-81	AW614542.1	EST_HUMAN	hg85601.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
4638	17774	30754	2.86	1.0E-81	AA040370.1	EST_HUMAN	ZK45H09.r1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4768	17903	30885	9.54	1.0E-81	BE047998.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly;
5241	18363	31331	0.6	1.0E-81	9969844	NT	tz45604.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526 5'
5351	18479	38821	6.18	1.0E-81	U87928.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
5469	18669	31648	3.8	1.0E-81	11432366	NT	Human aconitase hydratase (ACO2) gene, exon 3
5469	18669	31649	3.8	1.0E-81	11432366	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5619	18813	31881	0.76	1.0E-81	AA255569.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5771	18963	32284	3.18	1.0E-81	U52351.1	NT	z85006.r1 Soares_NihMPu.S1 Homo sapiens cDNA clone IMAGE:882475 5' similar to SW:PR12_HUMAN P49843 DNA PRIMASE 58 KD SUBUNIT
							Homo sapiens arm-repeat protein NPRAP/neurotrophin (CTNND2) mRNA, partial cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5771	18983	32265	3.18	1.0E-81	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurexophilin (CTNND2) mRNA, partial cds
6274	19448	32797	1.81	1.0E-81	BF674641.1	EST_HUMAN	602137864F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274536 5'
8877	20029	33439	1.09	1.0E-81	AJ133269.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7849	20699	34509	7.94	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7872	21022	34935	0.81	1.0E-81	AJ250408.1	NT	Homo sapiens GLI3 gene for GLI3 protein
9878	23017	36810	0.89	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9878	23017	36611	0.89	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
10174	23211	36804	5.13	1.0E-81	BE594387.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
10308	23343	36948	0.81	1.0E-81	A4630734.1	EST_HUMAN	6014308 a1 StrataGene Hela cell c83 837216 Homo sapiens cDNA clone IMAGE:866427 3' similar to SW:YB36_YEAST_P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.1
10310	23345	36930	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10310	23345	36951	3.72	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10726	23759	37387	1.41	1.0E-81	AW897550.1	EST_HUMAN	CM3-NN0089-140400-147-at12 NN0089 Homo sapiens cDNA
10864	23896	37519	0.49	1.0E-81	AW250322.1	EST_HUMAN	2822127 Sp1me NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822127 5'
11182	24251	37886	1.97	1.0E-81	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11347	24409	38061	1.56	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11347	24409	38082	1.56	1.0E-81	AW844986.1	EST_HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA
11362	24414	38058	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-280200-011-a06 UM0046 Homo sapiens cDNA
11362	24414	38083	2.93	1.0E-81	AW798167.1	EST_HUMAN	RC3-UM0046-280200-011-a06 UM0046 Homo sapiens cDNA
11950	18490	31529	2.48	1.0E-81	AW900558.1	EST_HUMAN	EST372729 IMAGE resequencing, MAGF Homo sapiens cDNA
11812	24802	38501	1.89	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12417	25285	32086	3.6	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13251	26251	1.59	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
108	13251	26251	1.35	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
274	13482	26523	1.58	8.0E-82	U08998.1	NT	Human CRFB4 gene, partial cds
837	14015	27070	1.87	8.0E-82	U08998.1	NT	Human CRFB4 gene, partial cds
910	14085	27180	1.84	8.0E-82	U08998.1	NT	Human CRFB4 gene, partial cds
1520	14673	27755	2.24	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1890	14842	27927	1.39	8.0E-82	8715601	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4188	17348	30339	0.74	8.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4358	17501	30483	0.83	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA

Page 392 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1481	14634		1.18	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
2825	15839	26049	1.62	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
1705	14857	27044	22.54	4.0E-82	AF081494.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5613	18807	31874	0.87	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5613	18807	31875	0.87	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-108 HT0540 Homo sapiens cDNA
5878	19066	32374	1.1	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
12016	25000	38702	4.71	4.0E-82	AI937900.1	EST_HUMAN	wf75a09.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276
12683	25455		3.78	4.0E-82	AF029701.2	NT	O75276 PKD1;
							Homo sapiens presenilin-1 gene, exons 1 and 2
288	13506	26540	15.3	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
721	13803	26944	2.5	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
810	13988	27043	8.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
893	14069	27134	5.31	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1086	14252		15.73	3.0E-82	AA725848.1	EST_HUMAN	al23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1386	14541	27617	1.22	3.0E-82	AW675073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1484	14847	27729	5.59	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1950	15033	28194	2.14	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2062	15202	28318	1.11	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type 1 (ADCYAP1R1) mRNA
3345	16518		2.42	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8346	21427	34952	2.66	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8763	21832	35371	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8763	21832	35372	0.89	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
10029	23067	36665	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10029	23067	36666	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
610	13799	28818	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
610	13799	26819	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1720	14870	27962	2.23	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3949	17107	30104	0.83	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4131	17284	30279	0.88	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprease mRNA, complete cds
4348	17491	30473	0.9	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4690	17815	30803	1.52	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4880	17815	30804	1.62	2.0E-82	AB026019.1	NT	Homo sapiens mRNA for KIAA1086 protein, partial cds
4992	18121	31100	2.86	2.0E-82	AF045555.1	NT	Homo sapiens wbcscr1 (WBCSCR1) and wbcscr5 (WBCSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5191	18313	31280	1.58	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5191	18313	31281	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5587	18792	31827	2.89	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6304	19471	32832	4.53	2.0E-82	AF234892.1	NT	Homo sapiens FAM44A1 splice variant a (FAM44A1) mRNA, complete cds
7858	26222		1.19	2.0E-82	AI476428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7988	21038	34550	0.8	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8500	21591	35117	1.81	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
8869	21948	35482	0.58	2.0E-82	7657340	NT	Homo sapiens micrarchidia (mouse) homolog (MORC), mRNA
8869	21948	35483	0.58	2.0E-82	7657340	NT	Homo sapiens micrarchidia (mouse) homolog (MORC), mRNA
10315	23350	36956	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10315	23350	36957	1.16	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11547	24603	38279	1.74	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11547	24603	38280	1.74	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11588	24641	38322	2.6	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11588	24641	38323	2.9	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12230	25177		2.81	2.0E-82	N94950.1	EST_HUMAN	z631d10.s1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:306203 3'
12818	25545		3.72	2.0E-82	AA011276.1	EST_HUMAN	z101g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428568 5'
605	13794	26813	1.69	1.0E-82	11543921	EST_HUMAN	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1235	14394		3.19	1.0E-82	BE886106.1	EST_HUMAN	607610859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1314	14470	27536	1.38	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1315	14471	27537	0.8	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8143	22222	36766	0.9	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9853	22693	36474	0.51	1.0E-82	AB014582.1	NT	Homo sapiens mRNA for KIAA0862 protein, partial cds
10451	23486		1.4	1.0E-82	BF515638.1	EST_HUMAN	U1H-BW1-ape-4-03-0-J1.e1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084083 3'
10984	24083	37698	2.49	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C008
11258	24327	37666	1.49	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
5307	18424	31394	1.05	9.0E-83	AF224969.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3' (UBE2D3) genes, complete cds
8912	21991	35630	4.99	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291861 5'
10481	23516	37128	0.72	9.0E-83	BE253347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3367734 5'
1446	14599	27676	2.97	8.0E-83	BE383973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 6'

Page 394 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1715	15992	27956	10.59	8.0E-83	N66951.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:285823 3'
1388	14543	27618	1.2	7.0E-83	AW385629.1	EST_HUMAN	QV4.LT0016-271299-068.n11 LT0016 Homo sapiens cDNA
2928	16105		1.64	7.0E-83	AA584655.1	EST_HUMAN	nc12h01.s1 NCI_QGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4936	18066		6.95	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.s1 NCI_QGAP_Pr28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
6176	18352	32699	0.95	7.0E-83	11428657	NT	DJ207H1.1;
416	13611	26660	1.39	6.0E-83	M33320.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
1828	14676	28071	1.79	8.0E-83	AW573088.1	EST_HUMAN	Human platelet Glycoprotein IIB (GPIIb) gene, exons 2-29
3082	16258	29277	0.68	8.0E-83	AW816405.1	EST_HUMAN	h31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to
3116	16282		0.7	6.0E-83	AF231919.1	NT	h31h03.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to
3653	16816	29828	0.92	6.0E-83	11430241	NT	SW:YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034.;
5408	18610	31582	1.73	6.0E-83	4507886	NT	QV4.ST0234-181199-037-105 ST0234 Homo sapiens cDNA
6147	19324	32669	1.31	6.0E-83	AJ010770.1	NT	Homo sapiens chromosome 21 unknown mRNA
7671	20737	34215	2	6.0E-83	11422024	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA,
9878	22918	36503	3.51	6.0E-83	4503314	NT	and translated products
9071	23010	36604	0.71	6.0E-83	11430647	NT	Homo sapiens hyperion gene, exons 1-50
9971	23010	36605	0.71	6.0E-83	11430647	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
11821	24810		2.31	6.0E-83	AA486105.1	EST_HUMAN	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
12179	25139		4.14	6.0E-83	AF240786.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
958	14142		1.24	5.0E-83	U17883.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
2108	15938		3	5.0E-83	AF006305.1	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
3726	16869	29893	0.91	5.0E-83	AL133207.2	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
4015	17172	30180	0.73	5.0E-83	4885190	NT	ab14e10.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains
4554	17892	30672	0.61	5.0E-83	AL163210.2	NT	THR.L2 THR repetitive element;
5190	18312	31278	13.87	5.0E-83	4567013	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
5190	18312	31279	13.87	5.0E-83	4567013	NT	genes, complete cds
657	13843	26870	1.87	4.0E-83	AF224689.1	NT	Human succinate dehydrogenase iron-protein subunit (adhB) gene, exon 5
1022	14193		4.09	3.0E-83	AA368311.1	EST_HUMAN	Human succinate dehydrogenase iron-protein subunit (adhB) gene, exon 5

Page 395 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2837	15951		1.6	3.0E-83	AA632654.1	EST_HUMAN	np87c07.s1 NCL_CGAP_Thyl Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element;
6708	10866		0.82	3.0E-83	AI217228.1	EST_HUMAN	qf73603.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1756882 3'
1843	14989	28089	1.37	2.0E-83	AA983492.1	EST_HUMAN	q64g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q82814
1843	14989		1.37	2.0E-83	AA983492.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
1978	15121	28222	9.11	2.0E-83	N66951.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
2251	15384	28512	1.57	2.0E-83	AB033098.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
2913	16091	29103	1.33	2.0E-83	BE828694.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
3342	16515		2.16	2.0E-83	11430834	NT	Q82814 MYELOBLAST KIAA0216. ;
3874	17033		0.94	2.0E-83	AL163202.2	NT	Q82814 MYELOBLAST KIAA0216. ;
4466	17598	30578	4.95	2.0E-83	AF202879.1	NT	Q82814 MYELOBLAST KIAA0216. ;
4776	17910	30883	3.19	2.0E-83	7706398	NT	Q82814 MYELOBLAST KIAA0216. ;
4775	17910	30894	3.19	2.0E-83	7706398	NT	Q82814 MYELOBLAST KIAA0216. ;
5385	18587	31559	0.91	2.0E-83	U06879.1	NT	Q82814 MYELOBLAST KIAA0216. ;
5967	19153	32468	0.97	2.0E-83	11428081	NT	Q82814 MYELOBLAST KIAA0216. ;
6086	19288	32587	1.2	2.0E-83	BE885401.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
6885	20037	33448	0.72	2.0E-83	AF128533.1	NT	Q82814 MYELOBLAST KIAA0216. ;
7593	20584	34140	5.15	2.0E-83	AF128533.1	NT	Q82814 MYELOBLAST KIAA0216. ;
7987	21036	34548	0.58	2.0E-83	BF105097.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
8028	21109	34629	0.63	2.0E-83	AB001025.1	NT	Q82814 MYELOBLAST KIAA0216. ;
8028	21109	34627	0.63	2.0E-83	AB001025.1	NT	Q82814 MYELOBLAST KIAA0216. ;
8175	21257	34779	1.48	2.0E-83	U66707.1	NT	Q82814 MYELOBLAST KIAA0216. ;
8509	21590	35124	2.52	2.0E-83	AF011920.1	NT	Q82814 MYELOBLAST KIAA0216. ;
8509	21590	35125	2.52	2.0E-83	AF011920.1	NT	Q82814 MYELOBLAST KIAA0216. ;
8783	22833	36412	0.54	2.0E-83	5453881	NT	Q82814 MYELOBLAST KIAA0216. ;
9793	22833	36413	0.54	2.0E-83	5453881	NT	Q82814 MYELOBLAST KIAA0216. ;
10240	23275	36886	3.2	2.0E-83	M22094.1	NT	Q82814 MYELOBLAST KIAA0216. ;
10240	23275	36887	3.2	2.0E-83	M22094.1	NT	Q82814 MYELOBLAST KIAA0216. ;
10322	23357	36887	1.35	2.0E-83	AU117659	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
10392	23427	37034	0.78	2.0E-83	AW50500.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;
11086	24160	37796	3.24	2.0E-83	11436448	NT	Q82814 MYELOBLAST KIAA0216. ;
11168	24239	37870	1.64	2.0E-83	AL134482.1	EST_HUMAN	Q82814 MYELOBLAST KIAA0216. ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1168	24239	37871	1.84	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
12559	25570		3.26	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1444	14597	27673	2.26	1.0E-83	4604328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoadyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1444	14597	27674	2.26	1.0E-83	4504328	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketoadyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2076	15216	28335	1.15	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FAGVL1) mRNA
2722	15840	28951	1.21	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908764 5'
3251	18425	29443	0.72	1.0E-83	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIA00868), mRNA
3972	17129	30132	7.76	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4359	17502	30484	2.22	1.0E-83	Z25822.1	NT	H.sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
5008	18137	31111	2.74	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6835	19888	33397	1.59	1.0E-83	AI027614.1	EST_HUMAN	0498008.x1 Sceres_testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3897	17056	30056	3.62	7.0E-84	BE801209.1	EST_HUMAN	PROTEIN (HUMAN).
1323	14479	27544	2.98	6.0E-84	BE838864.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3968863 5'
1323	14479	27545	2.96	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
2471	15598	28723	17.98	6.0E-84	AA176574.1	EST_HUMAN	RC2-FN0119-200600-011-g05 FN0119 Homo sapiens cDNA
5354	18481		2.18	6.0E-84	AL042833.2	EST_HUMAN	ae86g03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5635	18828	31905	1.91	6.0E-84	AA897339.1	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5777	18969	32273	0.99	6.0E-84	11428718	NT	af47g03.s1 Sceres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480500 3' similar to gb:M14338
5777	18969	32274	0.99	6.0E-84	11428718	NT	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
7642	20711	34190	3.14	6.0E-84	BE810371.1	EST_HUMAN	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7868	20922	34429	1.05	6.0E-84	AF088391.1	EST_HUMAN	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
8284	21346	34851	2	6.0E-84	BE770189.1	EST_HUMAN	PMO-LT0019-180600-004-F02 LT0019 Homo sapiens cDNA
732	13914	26956	1.32	5.0E-84	AA382811.1	EST_HUMAN	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
3079	16255		1.91	5.0E-84	AF109718.1	NT	PMO-LT0054-160600-004-e10 FT0054 Homo sapiens cDNA
							EST56094 Testis 1 Homo sapiens cDNA 5' end
							Homo sapiens chromosome 3 subtelomeric region
6232	19407	32756	0.62	5.0E-84	AA167678.1	EST_HUMAN	zq39a07.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632100 5' similar to
							TR-G483915 G483915 RETROTRANSPOSABLE L1 ELEMENT LRE2 FROM CHROMOSOME 1Q.;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11638	24927	38518	2.85	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11952	24938	38640	1.99	6.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11952	24938	38641	1.99	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1407	14561	27635	1.34	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1443	14596	27672	4.47	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302083 3' similar to SW:NRDC_HUMAN O43847 NARDILYSIN PRECURSOR;
5064	18192	31167	0.66	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5065	18193	31168	1.62	4.0E-84	AF069801.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5377	18579	31448	1.62	4.0E-84	AF022835.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5880	18674	32162	1.8	4.0E-84	11385188	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5880	18674	32163	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6398	19537	32928	2.14	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7825	20880	34381	13.68	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9112	22191	35735	1.12	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9112	22191	35736	1.12	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11158	24229	37859	4.76	4.0E-84	AB032856.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
326	13540	26572	2.16	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1178	14341	27395	1.63	3.0E-84	4798081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2015	15165	28260	2.39	3.0E-84	5463855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2063	15203	28319	2.38	3.0E-84	AL098990.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3843	17002	30005	5.53	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRSP) mRNA, complete cds
11118	24190		6.78	3.0E-84	AI683801.1	EST_HUMAN	wu20d05.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to
2172	15307	28435	6.48	2.0E-84	BE695397.1	EST_HUMAN	gb:U06083 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2172	15307	28436	6.46	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190900-272-b08 BT0795 Homo sapiens cDNA
3009	15185	29209	9.21	2.0E-84	AF036943.1	NT	CM1-BT0795-190900-272-b08 BT0795 Homo sapiens cDNA
3027	16203	29228	1.22	2.0E-84	X89211.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
5643	18837	31914	0.93	2.0E-84	BF511575.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
5643	18837	31915	0.93	2.0E-84	BF511575.1	EST_HUMAN	U1-P-B14-adv-a-02-Q-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
8774	19929	33325	0.92	2.0E-84	H63370.1	EST_HUMAN	U1-P-B14-adv-a-02-Q-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
8247	21329		1.55	2.0E-84	AI298674.1	EST_HUMAN	y56e11.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:209324 3'
8579	21660	35200	0.68	2.0E-84	AL163204.2	NT	qms87c09.x1 NCL CGAP_Sub8 Homo sapiens cDNA clone HS21C004
8579	21660	35201	0.68	2.0E-84	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9548	22811	38179	1.24	2.0E-84	AU120280.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
							AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9893	22972	36564	0.64	2.0E-84	H22841.1	EST_HUMAN	ym49e11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT P26844 BETA-2-GLYCOPROTEIN1;
12449	25316	32092	1.81	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
12449	25316	32093	1.81	2.0E-84	BF448000.1	EST_HUMAN	nae30a02.x1 Lupski, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to TR:Q9UGS3 Q9UGS3 DJ756G23.1;
322	13538	26568	1.5	1.0E-84	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
563	13756	26781	10.87	1.0E-84	4607952	NT	Homo sapiens complement component 5 (C5), mRNA
738	13820	27542	1.19	1.0E-84	AA984379.1	EST_HUMAN	em85b11.s1 Siralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
1321	14477	27542	2.83	1.0E-84	AA984379.1	EST_HUMAN	em85b11.s1 Siralagene echizo brain S11 Homo sapiens cDNA clone IMAGE:1629885 3'
2114	16252	28371	3.11	1.0E-84	BE392137.1	EST_HUMAN	601308000F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3628257 5'
2288	16430	28562	1.53	1.0E-84	11427197	NT	Homo sapiens pericardial material 1 (PCM1), mRNA
3846	17005	30007	2.76	1.0E-84	AA720851.1	EST_HUMAN	nm12a06.s1 NO1 CGAP_S51 Homo sapiens cDNA clone IMAGE:1239106 3'
4538	17676	30659	5.89	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4821	17954	30939	3.03	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
4821	17954	30940	3.03	1.0E-84	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
5031	17676	30659	3.56	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
6043	19226	32549	0.88	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA uterine water channel-28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6319	19491	32849	2.84	1.0E-84	S73482.1	NT	Novel human gene mapping to chromosome 13
7020	20156	33676	1.42	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7020	20156	33577	1.42	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7256	20339	33789	2.53	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7637	20706	34185	10.45	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed) alpha (POLA), mRNA
7737	20798	34287	1.07	1.0E-84	11430846	NT	Homo sapiens NGF1A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7777	20798	34287	2.34	1.0E-84	11430846	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
9736	22800	36608	2.78	1.0E-84	5031984	NT	Homo sapiens Ca2+-binding protein CABP3 (CABP3), gene, exon 6 and partial cds
9972	18488	31527	1.6	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9994	18488	31528	1.6	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
12325	25235	32088	2.82	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
12438	25311	32088	3.77	1.0E-84	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
889	14161		1.94	8.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment H521C009

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088	14263	27319	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skp mRNA, complete cds
1088	14263	27320	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skp mRNA, complete cds
1609	14762	27841	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1609	14762	27842	1.12	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1709	14860	27949	3.59	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
3870	17029		0.8	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4368	17509	30480	0.92	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5001	18130	31105	0.99	9.0E-85	5901878	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5032	18160	31137	1.18	9.0E-85	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
13048	14860	27949	1.78	9.0E-85	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
1159	14323	27378	4.64	7.0E-85	L06094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11943	24929		5.61	7.0E-85	AF113210.1	NT	Homo sapiens MS1P030 mRNA, complete cds
11702	24699	38391	2.59	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11702	24699	38392	2.56	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
12080	25041	38760	2	6.0E-85	AA403053.1	EST_HUMAN	z62b01.71 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3862402 5'
2410	15540	28668	4.09	5.0E-85	AL163284.2	NT	G1335769 GAG-POL POLYPROTEIN ;
4652	17690		0.71	5.0E-85	AF211189.1	NT	Homo sapiens chromosome 21 segment HS21C084
5567	18784	31804	1.59	5.0E-85	BF036674.1	EST_HUMAN	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
5567	18784	31805	1.59	5.0E-85	BF036674.1	EST_HUMAN	601458646F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862402 5'
11381	24442	38101	2.31	5.0E-85	AF224659.1	NT	601458646F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3862402 5'
13127	17690		1.72	5.0E-85	AF211189.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
6276	19450	32798	1.39	4.0E-85	BF677610.1	EST_HUMAN	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
6276	19450	32799	1.39	4.0E-85	BF677610.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
8021	21074	34586	3.43	4.0E-85	BE882304.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
10798	23831		1.8	4.0E-85	BE079263.1	EST_HUMAN	601505022F2 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3806940 5'
1327	14484	27561	0.91	3.0E-85	AF098157.1	NT	RC1-B170623-120200-011-c07 B170623 Homo sapiens cDNA
1821	14970	28082	4.8	3.0E-85	T07495.1	EST_HUMAN	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
5019	18148	31126	1.03	3.0E-85	11024695	NT	y65309.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:121504 5'
							Homo sapiens F-box only protein 24 (FBXO24), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5019	18148	31128	1.03	3.0E-85	11024895	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5080	18208	31180	0.91	3.0E-85	7363442	NT	Homo sapiens ciliary receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5517	18715	31729	6.35	3.0E-85	11436001	NT	Homo sapiens lactoferrin rich protein (LPRP), mRNA
6210	19395	32734	0.72	3.0E-85	11420204	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6282	19436	32782	4.92	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6282	19436	32783	4.92	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7091	20185		7.95	3.0E-85	AJ404463.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7555	20827	34103	0.84	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
8056	21139	34659	1.44	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8706	21786	35319	0.48	3.0E-85	11525829	NT	Homo sapiens CGI-81 protein (LOC511108), mRNA
9178	22256	35798	4.39	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9506	22772	36343	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
9508	22772	36344	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
10700	23733	37338	0.72	3.0E-85	AF09842.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11798	24786	38484	1.48	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discordin like domains 3 (EDIL3), mRNA
12998	25948		3.02	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
985	14157	27218	0.62	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1056	14231	27289	2.35	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1436	14939	27682	1.19	2.0E-85	7708205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1451	14904	27682	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1451	14904	27683	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2304	15436	28568	2.92	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2894	14523		4.22	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3087	16263	29280	3.57	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4454	17594	30574	4.66	2.0E-85	4503860	NT	Homo sapiens plasminogen (PLG) mRNA
4687	17822	30810	0.74	2.0E-85	4828977	NT	Homo sapiens retin (RELN) mRNA
5030	18159	31136	1.21	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9473	22530	36094	1.78	2.0E-85	A1760820.1	EST_HUMAN	w67808.x1 NCL CGAP_K1412 Homo sapiens cDNA clone IMAGE:2388431 3' similar to contains element MSR1 repetitive element;
9849	22889	36469	0.82	2.0E-85	A1914459.1	EST_HUMAN	w449c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331451 3'
10489	23504	37118	0.94	2.0E-85	A1886384.1	EST_HUMAN	wm94412.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2360	15491		3.55	1.0E-86	BE794309.1	EST_HUMAN	601591415F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2467	15594	28719	9.36	1.0E-85	BE818392.1	EST_HUMAN	801462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:386021 5'
2467	15594	28720	9.38	1.0E-85	BE818392.1	EST_HUMAN	801462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:386021 5'
7983	21032	34545	0.61	1.0E-85	BE082851.1	EST_HUMAN	MRO-BT0284-221199-002-103 BT0284 Homo sapiens cDNA
9984	23023	36816	2.13	1.0E-85	BE257917.1	EST_HUMAN	801109739F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350583 5'
10415	23450	37055	0.76	1.0E-85	AW813525.1	EST_HUMAN	RC1-ST0166-081099-011-c05 ST0166 Homo sapiens cDNA
11164	24235	37865	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z45103.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11164	24235	37868	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z45103.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11245	24314	37953	1.98	1.0E-85	BF311552.1	EST_HUMAN	801897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
11245	24314	37954	1.98	1.0E-85	BF311552.1	EST_HUMAN	801897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
12088	25049	38757	3.29	1.0E-85	AI98420.1	EST_HUMAN	q55a07.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860488 3'
12301	25404	32045	4.68	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12601	25404	32045	2.92	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1480	14613	32774	0.62	8.0E-88	11424140	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
8254	19428	26480	2.2	7.0E-86	7692247	NT	qj88108.s1 Soares_parathyroid_tumor_NbHFA Homo sapiens cDNA clone IMAGE:1403559 3'
233	13454	26480	1.03	7.0E-86	AA860801.1	EST_HUMAN	qj88108.s1 Soares_parathyroid_tumor_NbHFA Homo sapiens cDNA clone IMAGE:1403559 3'
960	14133	27163	1.03	7.0E-86	AA860801.1	EST_HUMAN	qj88108.s1 Soares_parathyroid_tumor_NbHFA Homo sapiens cDNA clone IMAGE:1403559 3'
6325	19497	32853	0.97	7.0E-86	9896888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6326	19497	32854	0.97	7.0E-86	9896888	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7116	18542	31499	0.43	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
8943	22022	35562	3.98	7.0E-86	136557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
8901	22941	35562	1.13	7.0E-86	545097	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9960	22998	35595	1.68	7.0E-86	11526307	NT	Homo sapiens DGeorge syndrome critical region gene 6 (DGCR6), mRNA
11204	24273	37909	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11204	24273	37910	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
12117	25097	38802	1.99	7.0E-86	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
1322	14478	27543	1.87	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH), mRNA
217	13439	28471	2.15	4.0E-86	BE547173.1	EST_HUMAN	801072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3488880 5'
6159	18335	32080	11.61	4.0E-86	BE265943.1	EST_HUMAN	801178865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:34531953 5'
11517	13439	28471	2.34	4.0E-86	BE547173.1	EST_HUMAN	801072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3488880 5'
4404	17947	30531	0.94	3.0E-86	BE967703.1	EST_HUMAN	801443262F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3847485 5'
5713	18908	32201	6.19	3.0E-86	AW340846.1	EST_HUMAN	x282h12.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8457	21538	35087	1.21	3.0E-86	AV723239.1	EST_HUMAN	AV723239 HTB Homo sapiens cDNA clone HTBBS004 5'
10425	23460	37065	3.54	3.0E-86	BE88478.1	EST_HUMAN	801509698F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10425	23490	37066	3.54	3.0E-86	BE886476.1	EST_HUMAN	601506896F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11720	23906	37529	4.87	3.0E-86	AI659240.1	EST_HUMAN	tu18002.x1 NC1_CGAP_Py28 Homo sapiens cDNA clone IMAGE:2261371 3'
11803	24763	38491	1.37	3.0E-86	AV690469.1	EST_HUMAN	AV690469 GKCC Homo sapiens cDNA clone GKCBSE02 5'
12300	25971		3.38	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3630753 5'
277	13495	26525	1.56	2.0E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells V1 Homo sapiens cDNA 5' end
427	13622		2.68	2.0E-86	AL163203.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
1217	14378	27437	3.33	2.0E-86	N58977.1	EST_HUMAN	yz18a08.11 Soares_multiple_sclerosis_ZNblHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2265	15398	28529	8.53	2.0E-86	9635487	EST_HUMAN	Human endogenous retrovirus, complete genome
2342	15473	28607	1.56	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3302	16689	28878	1.61	2.0E-86	AW966142.1	EST_HUMAN	EST178216 IMAGE resequences, MAGI Homo sapiens cDNA
3840	16989	30001	2.29	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3840	16999	30002	2.29	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4151	17303		2.59	2.0E-86	AW515742.1	EST_HUMAN	nd87g08.x1 NC1_CGAP_GCC Homo sapiens cDNA clone IMAGE:2816542 3'
4910	18040	31030	3.21	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5993	19178	32489	1.32	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5993	19178	32500	1.32	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7221	25837	33501	0.78	2.0E-86	11410429	NT	Homo sapiens similar to octonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8199	21281	34803	0.58	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8772	21851	35392	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8772	21851	35393	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
9104	22183	35728	0.68	2.0E-86	10653876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9519	22584	36153	1.96	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10664	23698	37307	2.9	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10664	23698	37308	2.9	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10667	23701	37311	0.48	2.0E-86	11417120	NT	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA
10721	23754	37360	1.25	2.0E-86	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11143	24216	37842	1.78	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KAS) mRNA
12789	25527	32008	6.3	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (c22p1), mRNA
12980	25638		2.56	2.0E-86	AB011399.1	NT	Homo sapiens gene for AFB, complete cds
1627	14779	27864	2.15	1.0E-86	4926855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3231	16405	29417	1.69	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3307	16481	29502	2.39	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3368	16540	29563	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3368	16540	29564	1.74	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4380	17523	30504	5.41	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17878	30861	0.94	1.0E-86	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
5670	18864	32149	1.85	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11805	18864	32149	1.53	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5472	18672		1.84	9.0E-87	AI150703.1	EST_HUMAN	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7606	20676	34150	1.82	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7606	20676	34151	1.82	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
482	13686	26720	49.59	8.0E-87	X62245.1	NT	O.cuniculus mRNA for elongation factor 1 alpha
2369	15500	28628	3.27	7.0E-87	BF063211.1	EST_HUMAN	7h8502.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2369	15500	28627	3.27	7.0E-87	BF063211.1	EST_HUMAN	7h8502.x1 NCI CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6530	18694	33067	1.38	7.0E-87	AW890336.1	EST_HUMAN	MRO-NT0039-020600-004-a11 NT0039 Homo sapiens cDNA
8384	21465	34980	3	7.0E-87	BF352776.1	EST_HUMAN	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA
9653	21096	34610	0.86	7.0E-87	BE112961.1	EST_HUMAN	IL5-HT0702-180600-103-d08 HT0702 Homo sapiens cDNA
10270	23311	36907	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
10276	23311	36908	3.38	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
10686	28865		0.53	7.0E-87	AI081595.1	EST_HUMAN	ox58h01.x1 Soares NIH-MPU_S1 Homo sapiens cDNA clone IMAGE:1680657 3'
11129	24201	37825	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 16 gene with homology to MHC-HLA-SB-1 Intron A
11129	24201	37826	6.59	7.0E-87	K03002.1	NT	Human mRNA from chromosome 16 gene with homology to MHC-HLA-SB-1 Intron A
3815	18779	29794	1.19	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
8551	19713	33089	1.47	6.0E-87	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
10963	24044		4.48	6.0E-87	11432444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1184	14347	27404	1.62	5.0E-87	AA33281.1	EST_HUMAN	EST16094 Testis 1 Homo sapiens cDNA 5' end
12603	14347	27404	2.58	6.0E-87	AA33281.1	EST_HUMAN	EST16094 Testis 1 Homo sapiens cDNA 5' end
988	14160	27220	1.37	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1199	14361	27420	7.91	4.0E-87	AB037635.1	NT	Homo sapiens mRNA for KIAA1474 protein, partial cds
1461	14614	27686	1.31	4.0E-87	R18133.1	EST_HUMAN	y80710.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146579 5' similar to contains Alu repetitive element
2086	15226	28348	2.28	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds

Page 404 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2143	15279	28402	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2143	15279	28403	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2493	15620	28738	0.99	4.0E-87	7706298	NT	Homo sapiens CGI-80 protein (LOC51626), mRNA
2493	15620	28739	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-80 protein (LOC51626), mRNA
3553	16718	29732	3.61	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MILL T4) mRNA
5562	18759	31798	4.6	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5969	19059	32366	0.59	4.0E-87	U85429.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6170	19346	32692	4.34	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
7848	20903	34406	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7848	20903	34407	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7950	21000	34510	3.64	4.0E-87	L48524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
11437	24468	38165	3.42	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
12705	26023	31671	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12705	26023	31672	1.27	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12898	25593		58.7	4.0E-87	11417812	NT	Homo sapiens putative receptor P2X-like 1, orphan receptor (P2RX1), mRNA
2836	13950	29057	14.35	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
3884	17043	30042	1.02	2.0E-87	AU116935.1	EST_HUMAN	Homo sapiens HEMBA1 Homo sapiens cDNA clone HEMBA100307 5'
5033	18161	31138	3.2	2.0E-87	BF376311.1	EST_HUMAN	CM6-TN0038-150900-352-h08 TN0038 Homo sapiens cDNA
5076	18204	31176	0.8	2.0E-87	BE175478.1	EST_HUMAN	RC5-HT0380-200300-031-G04 HT0380 Homo sapiens cDNA
5778	18970	32275	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
5778	18970	32276	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6456	18923		4.87	2.0E-87	BE587193.1	EST_HUMAN	601341383F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6838	18991	33399	0.79	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
6920	20235	33668	0.75	2.0E-87	AV654143.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone GLCDSG04 3'
7324	20408	33668	1.35	2.0E-87	AV654143.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7374	20453	33918	0.7	2.0E-87	BE294432.1	EST_HUMAN	Homo sapiens heat domain and RLD 2 (HERC2), mRNA
7611	20691	34157	36.59	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
7864	20918	34424	35.3	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'
8589	21670	36208	3.35	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
8988	23027		4.86	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1208	15989		2.2	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1483	14616	27698	1.61	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141098-001-g04 CT0265 Homo sapiens cDNA
1483	14616	27698	1.61	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141098-001-g04 CT0265 Homo sapiens cDNA
3801	16862	28963	5.18	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3828	16988	29891	2.3	1.0E-87	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
6366	19526	32883	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6366	19526	32884	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7303	20414	33878	1.09	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7558	20630	34105	1.05	1.0E-87	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7707	20772	34267	0.92	1.0E-87	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8307	21389	34912	0.93	1.0E-87	AF214682.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9110	22189	35732	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8110	22189	35733	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8833	22873	36456	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
8833	22873	36457	2.92	1.0E-87	BE818183.1	EST_HUMAN	RC8-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10364	23619	37228	0.88	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
10970	24050	37683	2.11	1.0E-87	5729887	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
11247	24316		1.66	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12701	26190		2.37	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
13228	26798	31890	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
13228	26798	31891	1.22	1.0E-87	AF169558.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
1130	14295	27350	8.48	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1380	14535	27609	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1380	14535	27610	2.94	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2189	16324	28449	0.96	9.0E-88	7681701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3717	16878	29883	1	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4384	17527	30508	2.97	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
4384	17527	30509	2.97	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)
9223	22301	36845	4.04	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1875	15019		1.22	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2704	15822	28639	3.65	5.0E-88	N88399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3084	16240	28290	0.82	5.0E-88	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds

Page 406 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3075	16251	29272	0.71	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3075	16251	29273	0.71	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3476	16643		2.78	5.0E-88	AF114488.1	EST_HUMAN	wf88h08.xt.NCI.CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element/contains element MER22 MER22 repetitive element;
3625	16789	29806	0.75	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4859	17692	30979	0.71	5.0E-88	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
6910	20226	33656	2.67	5.0E-88	H10932.1	EST_HUMAN	ym06b10.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:47123 5'
8114	21196	34715	2.67	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9512	22977	36143	0.63	5.0E-88	BF680206.1	EST_HUMAN	602154959F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4295775 5'
1360	14515	27589	0.96	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
1360	14515	27590	0.96	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-F10 TN0028 Homo sapiens cDNA
5244	18365	31333	0.65	4.0E-88	BF070714.1	EST_HUMAN	90214976ZF1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4290975 5'
7392	20470	33936	1.7	4.0E-88	11416685	NT	Homo sapiens transforming growth factor, beta-induced, 88kD (TGFB1), mRNA
11150	24221	37849	1.54	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11779	24769	38464	1.72	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11779	24769	38465	1.72	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
750	13931	28974	1.25	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1855	15001		3.09	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
3073	16189	29214	6.08	3.0E-88	N66951.1	EST_HUMAN	z448f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4355	17498	30477	0.81	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4355	17498	30478	0.81	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4600	17737		4.81	3.0E-88	11428200	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5414	18816	31590	2.79	3.0E-88	11429597	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5703	18896	32188	3.63	3.0E-88	9988888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5822	19012	32318	3.9	3.0E-88	11420697	NT	Homo sapiens viral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6290	19463	32815	0.72	3.0E-88	11417370	NT	Homo sapiens Interleukin 13 (IL13), mRNA
6543	25826	33080	0.84	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6543	25826	33081	0.84	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7211	20070	33459	15.52	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7712	20777	34263	5.53	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
8105	21187	34707	9.3	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8390	21471	34897	1.58	3.0E-88	AF034374.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein A and molybdenum cofactor biosynthesis protein C mRNA, complete cds

Page 407 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9634	21077	34589	2.14	3.0E-88	11529252	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10132	23170	36767	0.76	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10132	23170	36768	0.76	3.0E-88	AB016228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
10102	23189	36784	0.8	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12424	26301		2.49	3.0E-88	11417874	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
12439	26300	31676	1.63	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13223	25786	31889	1.31	3.0E-88	11529140	NT	Homo sapiens proteinase, serine, 7 (entrikinase) (PRSS7), mRNA
1061	14227	27283	6.85	2.0E-88	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1653	14906	27891	4.24	2.0E-88	AF248218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1789	14938	28031	6.83	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3554	16719	28733	2.9	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4545	17883	30686	1.93	2.0E-88	5031688	NT	Homo sapiens dynamin, axonemal, light polypeptide 4 (DNAL4), mRNA
6032	19215	32536	4.68	1.0E-88	AW139555.1	EST_HUMAN	U1H-B11-ase-4-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6032	19215	32537	4.98	1.0E-88	AW139555.1	EST_HUMAN	U1H-B11-ase-4-04-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6783	19538	33334	21.66	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6783	19538	33335	21.66	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7271	20354	33807	1.52	1.0E-88	AB69034.1	EST_HUMAN	wq70a12.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2476608 3'
7334	20415	33877	3.7	1.0E-88	AA488981.1	EST_HUMAN	aa44a11.s1 NCL_CGAP_GC61 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2
8331	21413	34839	0.51	1.0E-88	AF135183.1	NT	CE00851 ; Homo sapiens Recq helicase 5 (RECQ5) gene, alternative splice products, complete cds
9443	22559	36122	0.76	1.0E-88	AA190388.1	EST_HUMAN	zp87c02.r1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:627170 5' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POLYPROTEIN ;
9778	22818	36306	2.83	1.0E-88	AL04314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N0323 5'
11730	23916	37541	3.35	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612766 3' similar to gb:M16342
12885	28442		4.28	1.0E-88	AL163248.2	NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
13232	25900	31650	1.54	1.0E-88	AW451790.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
11184	24283	37898	8.14	9.0E-89	11421238	NT	Homo sapiens transglutinin 2 (TAGLN2), mRNA
2795	15910	28019	1.75	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508188 5'
7072	20125	33541	1.14	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC88232), mRNA
446	13642	26680	1.41	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
446	13642	26681	1.41	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5005	18134	31108	2.71	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA

Table 4

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							DKFZP434E246.t1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZP434E248.5'
5048	18174	31151	7.29	7.0E-89	AL045748.1	EST_HUMAN	H.sapiens CLN3 gene, complete CDS
5547	18744	31778	1.22	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
5547	18744	31779	1.22	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
5547	18744	31779	1.22	7.0E-89	X99832.1	NT	H.sapiens CLN3 gene, complete CDS
6473	19840	33000	1.57	7.0E-89	7549808	NT	Homo sapiens plasmin 3 (T isoform) (PLS3), mRNA
6473	19840	33001	1.57	7.0E-89	7549808	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
6473	19840	33001	1.57	7.0E-89	11420754	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7668	20734	34211	1.84	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8063	21145	34664	0.68	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8063	21145	34665	0.68	7.0E-89	J02923.1	NT	Human GSK-III-related phosphoprotein (p65) mRNA, complete cds
8674	21784	35288	0.53	7.0E-89	J02923.1	NT	H.sapiens Weet hu gene
8674	21784	35289	1.34	7.0E-89	X62048.1	NT	H.sapiens Weet hu gene
10750	23763	37396	1.34	7.0E-89	X62048.1	NT	H.sapiens miRNA for KIAA0823 protein, partial cds
10750	23763	37396	1.34	7.0E-89	X62048.1	NT	H.sapiens miRNA for KIAA0823 protein, partial cds
10750	23763	37396	1.34	7.0E-89	AB020630.1	NT	H.sapiens miRNA for KIAA0823 protein, segment 2
10768	23801	37423	1.35	7.0E-89	AB020630.1	NT	Human aldose reductase (AR) gene, segment 1
10768	23801	37423	1.35	7.0E-89	M59783.1	NT	H.sapiens inner membrane protein, mitochondrial (IMMT), mRNA
10768	23801	37423	1.35	7.0E-89	M59783.1	NT	H.sapiens inner membrane protein, mitochondrial (IMMT), mRNA
11515	24572	38260	2.66	7.0E-89	5803114	NT	H.sapiens ornithine decarboxylase enzyme E2L 3 (UBE2L3) mRNA
1048	14214	27271	1.39	6.0E-89	4506124	NT	H.sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2287	15419	28551	2.52	6.0E-89	4507788	NT	H.sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2504	15531	28750	1.61	6.0E-89	4507788	NT	H.sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2504	15531	28751	1.61	6.0E-89	AB007786.2	NT	H.sapiens miRNA for KIAA0406 protein, partial cds
4759	17894	30873	3.79	6.0E-89	AB007786.2	NT	H.sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4759	17894	30874	3.79	6.0E-89	6806918	NT	H.sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5295	18413	31379	0.81	6.0E-89	6806918	NT	H.sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5295	18413	31380	0.81	6.0E-89	6806918	NT	H.sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5186	18308	31273	3.35	5.0E-89	BE244323.1	EST_HUMAN	TGBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia BAYlor-HGSC project=TCBA Homo sapiens cDNA clone TCBAPO0383
5186	18308	31274	3.36	5.0E-89	BE244323.1	EST_HUMAN	cDNA clone TCBAPO0383
7761	20820	34310	1.02	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080500-219-g03 NT0022 Homo sapiens cDNA
2941	16118	28131	1.63	3.0E-89	AW976181.1	EST_HUMAN	GVS-NT0022-080500-219-g03 NT0022 Homo sapiens cDNA
7280	20372	33828	1.3	3.0E-89	AJ217359.1	EST_HUMAN	QV3-NT0022-080500-219-g03 NT0022 Homo sapiens cDNA
11039	24118	37751	2.29	3.0E-89	N57367.1	EST_HUMAN	yw86e11.r1 Soares_placenta_8to9weeks_2NHBPACGW Homo sapiens cDNA clone IMAGE:259148 5' similar to SW:P14K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
12790	25918	31863	1.52	3.0E-89	AV708431.1	EST_HUMAN	AV708431 ADG Homo sapiens cDNA clone ADCARE02 5'
2598	25587	31989	1.82	3.0E-89	AV705749.1	EST_HUMAN	qht17606.x1 Scores_NFL_I_GBC_ST Homo sapiens cDNA clone ADBBGA01 5'

Page 409 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
129	13616	26660	0.73	2.0E-89	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
129	13616	26657	0.73	2.0E-89	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26656	0.89	2.0E-89	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26657	0.89	2.0E-89	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13738	26760	0.63	2.0E-89	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2945	16122	29135	1.53	2.0E-89	EST_HUMAN	q99c08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 (GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
4263	17408	30394	1.18	2.0E-89	NT	Homo sapiens topoisomerase-related function protein (TRF-4-2) mRNA, partial cds
4269	17414	30402	5.14	2.0E-89	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4269	17414	30403	5.14	2.0E-89	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4469	17609	30587	1.13	2.0E-89	NT	Homo sapiens chromosome 21 segment HS21C003
4619	17759	30738	1	2.0E-89	NT	Homo sapiens GGT gene, exon 5
5469	18659	31642	1.39	2.0E-89	EST_HUMAN	60106596F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5598	18793	31842	3.95	2.0E-89	NT	Homo sapiens gene for LECT2, complete cds
5909	19098	32412	1.5	2.0E-89	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
6339	19509	32865	0.79	2.0E-89	NT	Homo sapiens chromosome 21 segment HS21C085
7847	20902	34405	5.28	2.0E-89	NT	Human GT24 (GT24) mRNA, partial cds
8119	21201	34722	3.11	2.0E-89	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
8612	21692	35228	0.9	2.0E-89	NT	Homo sapiens partial mRNA for PEX3 related protein
9453	22669	36136	0.72	2.0E-89	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10015	23053	36847	1.22	2.0E-89	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
10015	23063	36648	1.22	2.0E-89	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
11655	24734	38425	2.63	2.0E-89	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11871	24859	38554	3.52	2.0E-89	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12017	25001	38703	1.64	2.0E-89	NT	Human IMAGE-7 antigen (IMAGE7) pseudogene, complete cds
12877	25884		4.25	2.0E-89	NT	Homo sapiens human endogenous retrovirus W gagC3 3' gag (gag) gene, complete cds
11877	24865	38561	6.88	1.0E-89	EST_HUMAN	hr81d09.x1 NCI_CGAP_KH11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778
11877	24865	38562	6.88	1.0E-89	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN; hr81d09.x1 NCI_CGAP_KH11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 054778
11877	24865	38562	6.88	1.0E-89	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;

Page 410 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8422	21603	36036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8422	21603	36036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1089	14254	27308	4.38	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1089	14254	27308	2.91	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1361	16035	27591	3.26	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1361	16035	27592	3.26	8.0E-90	BE670561.1	EST_HUMAN	7c36f08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8757	21836	35377	0.6	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-12040-022-b08 HT0598 Homo sapiens cDNA
10939	24021	37854	1.38	8.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10939	24021	37655	1.38	8.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
859	14036		6.81	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8619	21699		2.14	7.0E-90	AA782977.1	EST_HUMAN	al63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
9166	22244	36787	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
9166	22244	36788	2.13	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10220	23256	36844	0.46	7.0E-90	AW273794.1	EST_HUMAN	xx24a02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814026 3'
10340	23375	36985	4.2	7.0E-90	H68849.1	EST_HUMAN	y86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10340	23375	36986	4.2	7.0E-90	H68849.1	EST_HUMAN	y86e04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;
10672	23706	37314	0.62	7.0E-90	BF526089.1	EST_HUMAN	602071208F1 NCI CGAP Bm84 Homo sapiens cDNA clone IMAGE:4214257 5'
3136	16312	29324	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
3136	16312	29325	1.16	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6)
4342	17485	30467	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4342	17485	30468	11.21	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6105	19285	32618	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
6105	19285	32619	2.84	6.0E-90	U77700.1	NT	Homo sapiens HsGCN1 mRNA, partial cds
8522	21603	35140	4.01	6.0E-90	4504794	NT	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 3 (ITPR3) mRNA
8522	21603	35141	4.01	6.0E-90	4504794	NT	Homo sapiens Inositol 1,4,5-trisphosphate receptor, type 3 (ITPR3) mRNA
159	13384		27.59	5.0E-90	AB035344.1	NT	Homo sapiens TGL6 gene, exon 1-10b
1219	14380	27439	6.22	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds

Page 411 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1864	15010	28116	1.07	5.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Scaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
1864	15010	28117	1.07	5.0E-90	AI222095.1	EST_HUMAN	q996c08.x1 Scaree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN);contains Alu repetitive element;
2622	16745	28859	2.37	5.0E-90	AF114487.1	NT	Homo sapiens intercalin long isoform (ITSN) mRNA, complete cds
4662	17787	30784	4.51	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4683	17818	30806	0.78	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6708	18901	32188	2.85	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5726	18919		0.72	5.0E-90	AF008815.1	NT	Homo sapiens EVI6 homolog mRNA, complete cds
6810	19000	32307	1.32	5.0E-90	AB015817.1	NT	Homo sapiens ELKS mRNA, complete cds
6866	18901	32188	1.88	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6868	20021	33430	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC58934), mRNA
6889	20021	33431	0.95	5.0E-90	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC58934), mRNA
7364	20443	33905	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7364	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7736	20767	34286	7.98	5.0E-90	4657258	NT	Homo sapiens adenylylase 9 (ADCY9) mRNA
8488	21668	35107	4.89	5.0E-90	11345483	NT	Homo sapiens hypodermal protein FL13222 (FL13222), mRNA
9882	22922	36508	1.17	5.0E-90	11419429	NT	Homo sapiens similar to ecdysiotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10488	23523	37133	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10663	23697	37306	0.68	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10723	23756	37362	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37363	0.53	5.0E-90	7662051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12948	25659		1.77	5.0E-90	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
13000	25949		4.54	5.0E-90	AI523366.1	EST_HUMAN	ar78h05.x1 Barstead actin HPLRB6 Homo sapiens cDNA clone IMAGE:2128781 3'
313	13329	26582	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13329	26583	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1110	14275	27332	4.36	4.0E-90	4506316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1724	14874	27866	13.42	4.0E-90	X99033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 10
2823	16101	29114	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2923	16101	29115	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Page 412 of 550

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3088	16284	29281	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3088	16284	29282	0.93	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4779	17814	30900	3.63	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4919	18049	31037	2.1	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cdo
4939	18059	31047	1.91	4.0E-90	M55967.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
12885	16101	29114	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12885	16101	29115	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8036	21119	34638	0.91	3.0E-90	BF516168.1	EST_HUMAN	UIH-BW 1-any-b-04-Q-UJ.s1 NCI_GGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
8036	21119	34639	0.91	3.0E-90	BF516168.1	EST_HUMAN	UIH-BW 1-any-b-04-Q-UJ.s1 NCI_GGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11830	24916	38619	28.7	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
220	13442	26473	4.5	2.0E-90	BE537913.1	EST_HUMAN	601087378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1200	14362	27421	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGI7), mRNA
1200	14362	27422	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGI7), mRNA
3048	17106	30103	2.95	2.0E-90	A1138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8tc6weeks_2NbltP8tc6w Homo sapiens cDNA clone IMAGE:1713410 3'
4811	17944	30930	1.05	2.0E-90	AB006627.1	NT	similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3 ;
5029	18158	31135	10.16	2.0E-90	5728855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5896	19084	32395	0.6	2.0E-90	11625901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5896	19084	32396	0.6	2.0E-90	11625901	NT	Homo sapiens Rap2 interacting protein 8 (RPI8p), mRNA
5803	19092	32406	3.89	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPI8p), mRNA
9893	23032	38623	0.99	2.0E-90	11427320	NT	be49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2899881 5' similar to TR:O75208 O76208 HYPOTHETICAL 35.5 KD PROTEIN ;
9998	23032	38624	0.99	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23202	36795	1.46	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
10165	23202	36796	1.46	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBAA1004795 5'
11758	23944	37571	3.06	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBAA1004795 5'
287	13505	26536	4.1	1.0E-90	4502168	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
385	15983	26828	2.28	1.0E-90	AF231920.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
386	15983	26828	1.96	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26932	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26933	1.92	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial

Page 413 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
748	13928	26971	17.93	1.0E-90	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
748	13929	26972	17.93	1.0E-90	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1134	14289		2.25	1.0E-90	4507628	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1334	14491	27560	3.48	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1334	14491	27561	3.46	1.0E-90	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1701	14853		2.61	1.0E-90	BE379894.1	EST_HUMAN	601159563F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511118 5'
1951	15094	28195	3.73	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila))-like (LOC57167), mRNA
2915	16093	29106	6.46	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3054	17112	30112	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3954	17112	30113	0.59	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4543	17681	30663	1.68	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5782	18983	32286	2.08	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5959	19145	32480	0.9	1.0E-90	11426810	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7220	20065	33500	0.73	1.0E-90	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7849	20904	34408	2.31	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9021	22100	35640	3	1.0E-90	11422038	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9493	22560		0.92	1.0E-90	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9516	22581	36148	1.4	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9516	22581	36149	1.4	1.0E-90	11422108	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4313	17456	30444	8.29	8.0E-91	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s381 3'
8501	21582	35118	1.14	7.0E-91	11419234	NT	Homo sapiens makorin, fing finger protein, 1 (MKRN1), mRNA
10607	23542	37153	0.65	7.0E-91	AI904151.1	EST_HUMAN	GM-BT043-090289-075 BT043 Homo sapiens cDNA
3593	16728	28744	1.85	5.0E-91	AA702794.1	EST_HUMAN	z60b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4030	17775	30755	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4639	17775	30756	1.14	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4930	18060	31042	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4930	18060	31043	0.67	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6760	19906	33300	1.25	5.0E-91	AI879995.1	EST_HUMAN	eu49/09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASFG_FNAME_Q47698 N4-(BETA-N-ACETYL-GLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR
8400	21481	35009	1.33	5.0E-91	BF314882.1	EST_HUMAN	601907624F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8980	22039	35581	1.47	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLOCYF08 3'

Page 414 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8960	22039	35582	1.47	5.0E-91	AV648878.1	EST_HUMAN	AV648878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12971	25631		1.61	5.0E-91	AI193588.1	EST_HUMAN	qet011.x1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:1744366 3' similar to contains MIR b2 MIR MIR repetitive element;
3272	16446	29465	1.58	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3272	16446	29466	1.56	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
11171	24242	37875	3.22	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12376	25267	32074	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12378	25267	32119	3.27	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12685	25457	32020	1.16	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1647	14800	27885	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1847	14800	27886	2.17	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1832	15983	28077	1.1	3.0E-91	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3420	15389	29605	1.29	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3551	16716	29729	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3551	16716	29730	4.85	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3888	17047	30047	0.93	3.0E-91	AF094530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4714	17849	30832	4.41	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5094	18222	31193	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5094	18222	31194	1.48	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5803	18993	32296	3.55	3.0E-91	11434964	NT	Homo sapiens epididymal secretory protein (19.5kD) (HE1), mRNA
6434	18902		2.56	3.0E-91	4602740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6713	19871	33262	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6713	19871	33263	2.98	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7816	20871	34368	4.48	3.0E-91	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
7816	20871	34369	4.48	3.0E-91	U96959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8132	21214	34735	0.69	3.0E-91	6601689	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8970	22048	35592	2.73	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9488	22345	36108	0.73	3.0E-91	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11480	24539	38207	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11480	24539	38208	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
13037	18486	31430	8.54	3.0E-91	AF169556.1	NT	Homo sapiens beta-ureidopropionase (BUP-1) gene, exon 6
13037	18486	31431	8.54	3.0E-91	AF169556.1	NT	Homo sapiens beta-ureidopropionase (BUP-1) gene, exon 6
49	13288	26300	2.94	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1274	14431	27502	2.74	1.0E-91	AW449749.1	EST_HUMAN	U1H-B15-aka-4-01-0-U1.1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5529	18726	31742	0.78	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1856 (PRO1856), mRNA
6983	20211	33640	1.98	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4157804 5'
6983	20211	33641	1.96	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4157804 5'
12190	25110	38814	1.48	1.0E-91	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSBEC05 5'
12540	26114		1.5	1.0E-91	H15212.1	EST_HUMAN	ym30403.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:49687 5'
1270	14428	27406	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
1270	14428	27497	5.77	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
5309	18428	31396	0.66	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5579	18774	31820	5.98	9.0E-92	U03007.1	NT	Human Na ⁺ K ⁺ ATPase alpha-subunit mRNA, partial cds
5722	18915	32210	2.82	9.0E-92	11427149	NT	Homo sapiens NALP1 mRNA, complete cds
6583	19745	33127	3.77	9.0E-92	AF310105.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34644	0.65	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34645	0.55	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8569	21650	35191	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21650	35192	1.53	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9474	22531	36095	1.83	9.0E-92	W26387.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13330	26357	6.63	8.0E-92	BE386363.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
296	13513	26547	3.09	8.0E-92	11434722	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814987 5'
1866	15012	28119	1.43	8.0E-92	11434722	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814987 5'
1866	15012	28120	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90kD) (DGKG), mRNA
5508	18707	31722	0.69	8.0E-92	AB048820.1	NT	Homo sapiens mRNA for KIAA1500 protein, partial cds
5615	18809	31877	0.9	8.0E-92	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6677	19838	33225	1.28	8.0E-92	AJ000975.1	NT	Homo sapiens MCP-4 gene
6680	19839	33228	0.91	8.0E-92	AF179426.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8283	21365		0.55	8.0E-92	11416961	NT	Homo sapiens AIM-1 protein (LOC61151), mRNA
8820	21700	35235	5.05	8.0E-92	L04163.1	NT	Human lens membrane protein (mp18) gene, exon 11

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8620	21700	35236	5.05	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8721	21801	35337	0.71	8.0E-92	11428569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
9262	22339	35889	2.53	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10232	22267	36857	0.91	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
11043	24121	37755	2.88	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11842	24722	38415	1.93	8.0E-92	4503940	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
12740	25491	32028	1.59	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
68	13305	26328	1.91	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
246	18008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	18008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
604	13793	27533	1.68	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepsis truncated isoform mRNA, complete cds
1309	14465	27533	1.94	7.0E-92	4503384	NT	Homo sapiens B-cell CLL/lymphoma 75 (BCL75) mRNA
2260	15393	28619	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2260	15393	28520	3.85	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2630	15753	28688	6.13	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2787	15903	28010	5.84	7.0E-92	6003738	NT	Homo sapiens NRAS-related gene (DTS165E), mRNA
3426	18466	29609	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3426	18466	29610	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
5294	18403	31371	0.98	7.0E-92	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5376	18578	31448	5.51	7.0E-92	AA446206.1	EST_HUMAN	z668412.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'
2178	15313	28441	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2178	15313	28442	0.96	3.0E-92	11434814	NT	Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), mRNA
2824	15938	26048	2.74	3.0E-92	BE908714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
5997	19182	32504	3.96	3.0E-92	AA378336.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
11002	24081	37716	3.28	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11002	24081	37717	3.28	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12878	26108		1.67	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-011 GN0021 Homo sapiens cDNA
26	13264	26268	1.54	2.0E-92	4501898	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
183	13405	26433	4.28	2.0E-92	11422848	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
183	13405	26434	4.28	2.0E-92	11422848	NT	Homo sapiens hypothetical protein dJ482O23.2 (dJ482O23.2), mRNA
768	13549	26897	5.48	2.0E-92	BE289190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
768	13549	26898	5.49	2.0E-92	BE289190.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14901		1.82	2.0E-92	S78653.1	NT	mif-1nas-related [human, Genomic, 2416 nt]
1890	15132	28238	2.53	2.0E-92	AI818119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1890	15132	28237	2.53	2.0E-92	AI818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2020	15161	28285	1.01	2.0E-92	4507484	NT	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2020	15161	28286	1.01	2.0E-92	4507484	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;
2108	16245	28369	5.35	2.0E-92	4506860	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2725	16843	28954	22.36	2.0E-92	6812457	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
3701	16862	28984	1.02	2.0E-92	AF231919.1	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
3701	16862	28985	1.02	2.0E-92	AF231919.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3777	16938	29944	7.02	2.0E-92	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4403	17548	30530	1.17	2.0E-92	M10976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
5108	18236		4.1	2.0E-92	AL040437.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
5879	19069	32377	0.64	2.0E-92	AF016535.1	NT	DKFZp334C0414.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp334C0414 5'
6431	19599		7.19	2.0E-92	4504756	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6748	19904	33297	2.8	2.0E-92	AB028991.1	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7627	20697		0.81	2.0E-92	U67780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
7657	20697		0.64	2.0E-92	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
9058	22135	35860	1.28	2.0E-92	AW940174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
10897	24076	37709	4.68	2.0E-92	11434900	NT	h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808371 3' similar to TR:O02711
11257	24328	37803	3.22	2.0E-92	11434759	NT	O02711 PRO-POL-OUTPASE POLYPROTEIN ;
11409	24470	38134	5.71	2.0E-92	AW838290.1	EST_HUMAN	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11409	24470	38135	5.71	2.0E-92	AW838290.1	EST_HUMAN	Homo sapiens zinc finger protein 188 (ZNF188), mRNA
12768	25502	32035	8.46	2.0E-92	AB029016.1	NT	GM4-LT0028-161289-062-g08 LT0028 Homo sapiens cDNA
							GM4-LT0028-161289-062-g08 LT0028 Homo sapiens cDNA
							Homo sapiens mRNA for KIAA1083 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12782	25624	32005	1.36	2.0E-92	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
13086	15843	28654	73.58	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1897	15040	28150	2.95	1.0E-92	R78078.1	EST_HUMAN	y80e08.11 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145574 5'
1897	15040	28151	2.95	1.0E-92	R78078.1	EST_HUMAN	y80e08.11 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145574 5'
2135	15271	28392	35.12	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8441	21522	35051	0.82	1.0E-92	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
							ig01b02.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
							Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element/contains element
9365	22440	35899	3.24	1.0E-92	AI380356.1	EST_HUMAN	MER17 repetitive element
							ig01b02.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
9365	22440	36000	3.24	1.0E-92	AI380356.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element/contains element
2085	15225	28347	3.53	9.0E-93	AL121881.1	EST_HUMAN	MER17 repetitive element
							ig01b02.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
2100	15240		20.41	9.0E-93	AA316723.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element/contains element
							EST188414 HOC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
2712	15830		1.69	9.0E-93	AF223391.1	NT	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
3703	16884	29867	1.35	9.0E-93	BE388571.1	EST_HUMAN	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
11947	24933		7.79	9.0E-93	11418523	NT	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
6723	19880	33271	2.4	8.0E-93	BF036364.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
256	13476	26506	7.25	7.0E-93	AF231919.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
3144	16320	29332	0.74	6.0E-93	11526176	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6819	19972	33360	0.97	6.0E-93	AB033083.1	NT	Homo sapiens PTH-responsive osteosarcoma B1 protein (B1) mRNA, complete cds
7056	20109	33525	7.64	6.0E-93	AF095771.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1412	14566	27840	0.99	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1439	14592	27666	4.61	5.0E-93	AB014511.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1439	14592	27667	4.61	5.0E-93	AI674184.1	EST_HUMAN	wc09c08.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2314670 3'
1504	14657		4.17	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
1889	16049	28123	1.03	5.0E-93	AJ297710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3305	16478	29500	3.73	5.0E-93	X04201.1	NT	Human skeletal muscle 1 3 kb mRNA for tropomyosin
5920	16107	32420	1.09	5.0E-93	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
							Homo sapiens vbscr1 (WBSCR1) and vbscr5 (WBSCR5) genes, complete cds, alternatively spliced and
							replication factor C subunit 2 (RFC2) gene, complete cds
6235	16410		1.75	5.0E-93	AF045555.1	NT	

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20944	34450	3.52	6.0E-93	AF067138.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8804	21883	35422	0.73	5.0E-93	4557626	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8804	21883	35423	0.73	5.0E-93	4557626	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9822	22862	36443	2.02	5.0E-93	AF274983.1	NT	Homo sapiens secretory pathway component Sec3B-1 mRNA, alternatively spliced, complete cds
10012	23090	36844	1.38	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10275	23310	36908	1.78	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11084	24140	37778	1.92	5.0E-93	11439589	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12851	25791	31921	2.31	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
90	13325		6.63	4.0E-93	AA459933.1	EST_HUMAN	z60e09.61 Scanes_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW:CLPA_RAT
458	13653	26660	2.38	4.0E-93	4557879	NT	P37387 CALPONIN, ACIDIC ISOFORM 1
458	13653	26691	2.38	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
793	13972	27024	1.18	4.0E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PEST1), mRNA
793	13972	27025	1.16	4.0E-93	7657454	NT	Homo sapiens pascadillo (zebrafish) homolog 1, containing BRCT domain (PEST1), mRNA
1210	14371	27431	2.12	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
2039	15174	28284	4.37	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2318	15450	28562	1.19	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2672	15792	28909	1.16	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3656	16816	29831	0.73	4.0E-93	7705395	NT	Homo sapiens tumor antigen SLP-8p (HCC9), mRNA
4159	17310	30306	1.61	4.0E-93	4504854	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5136	16819	29831	0.75	4.0E-93	7705395	NT	Homo sapiens tumor antigen SLP-8p (HCC9), mRNA
5760	18952	32265	5.01	4.0E-93	T46864.1	EST_HUMAN	y84c12.r1 Stratagene liver (4937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11398	24459	38123	10.47	4.0E-93	AY692051	EST_HUMAN	AV692051 GKG Homo sapiens cDNA clone GKGDFF07 5'
3742	16803	29906	12.26	3.0E-93	BF690630.1	EST_HUMAN	602246564F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3742	16803	29907	12.28	3.0E-93	BF690630.1	EST_HUMAN	602246564F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4350	17493		2.6	3.0E-93	AF226896.1	NT	Homo sapiens tensin mRNA, complete cds
6693	18851	33242	1.31	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
11040	24119	37762	2.86	3.0E-93	AB24829.1	EST_HUMAN	wb2405.x1 NCI_GGAP GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
185	13418	26447	5.59	2.0E-93	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds

Page 420 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
185	13418	26448	5.69	2.0E-93	AB015610.1	NT	Chlorobius aethiops mRNA for ribosomal protein S4X, complete cds
333	13547	26578	13.77	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
334	13547	26578	6.74	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1846	14799	27884	3.9	2.0E-93	AF225696.1	NT	Homo sapiens tensin mRNA, complete cds
2169	16334	28461	2.23	2.0E-93	U40763.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyp mRNA, complete cds
2555	15680	28805	1.02	2.0E-93	BE252982.1	EST_HUMAN	601117566F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5254	18374	31340	1.19	2.0E-93	BE253201.1	EST_HUMAN	601116810F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5533	18730	31746	5.08	2.0E-93	AW964365.1	EST_HUMAN	EST976458 IMAGE resequences, MAGH Homo sapiens cDNA
5544	18741	31775	0.7	2.0E-93	4758153	NT	Homo sapiens deafness, autosomal dominant 5 (DFNA5), mRNA
5660	18854		0.84	2.0E-93	BF351469.1	EST_HUMAN	QV3-HT0513-280300-128-H04 HT0513 Homo sapiens cDNA
5754	18946	32248	1.08	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5768	18960	32261	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-98
6922	19975		1.2	2.0E-93	AW502002.1	EST_HUMAN	UJHF-BND-aks-g-09-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11333	24396	38044	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11333	24396	38045	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12625	25358		1.78	2.0E-93	AA128735.1	EST_HUMAN	229c10.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:503346 3'
12624	25420		3.25	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12930	25613		6.34	2.0E-93	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'
105	13341	26368	1.38	1.0E-93	AF238997.1	NT	Homo sapiens GTR1 pseudogene
105	13341	26369	1.38	1.0E-93	AF238997.1	NT	Homo sapiens GTR1 pseudogene
531	13724	26750	7.76	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.G1.1), mRNA
613	13802	26822	3.32	1.0E-93	A1146755.1	EST_HUMAN	cy84b08.x1 NCJ_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
896	14071	27136	3.43	1.0E-93	D87876.1	NT	ZINC FINGER PROTEIN ;
1194	14356	27414	0.6	1.0E-93	4903872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1265	14422	27487	7.22	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 87kD) (GAD1), transcript variant GAD67, mRNA
1265	14422	27488	7.22	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1376	14531	27604	9.7	1.0E-93	AF16706.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2414	15544	28672	1.08	1.0E-93	AF231081.1	NT	Homo sapiens cysteine-rich repeat-containing protein S82 precursor, mRNA, complete cds
2534	15669	28783	3.06	1.0E-93	AF05096.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2576	15702		1.29	1.0E-93	AL137200.1	NT	Homo sapiens MHC class 1 region
2883	14480	27546	1.32	1.0E-93	BE297369.1	EST_HUMAN	Novel human gene mapping to chromosome 1
2883	14480	27547	1.32	1.0E-93	BE297369.1	EST_HUMAN	601177886F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3000	16176	29197	5.86	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3287	16461		1.23	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4549	17687	30668	3.28	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5348	18461	31426	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5348	18461	31427	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
5684	18878	32167	2.39	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5684	18878	32168	2.39	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5885	19074	32383	1.2	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6037	19220	32543	10.78	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Waisson disease) (NF1) mRNA
6326	19498	32855	4.8	1.0E-93	7662241	NT	Homo sapiens KIAA0872 gene product (KIAA0872), mRNA
6931	20246	33679	1.94	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7400	20478	33946	3.24	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8455	21536	35066	2.29	1.0E-93	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8740	21819	35353	1.15	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEVD protein
8850	21929	35468	1.14	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9651	21094	34608	2.03	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9655	21098	34612	1.14	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9787	22827	36403	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9787	22827	36404	3.9	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9926	22966	36556	1.24	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10349	23384	36994	0.59	1.0E-93	11433646	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
12820	25547		1.62	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12923	25608		3.71	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
13108	25723	31941	1.36	1.0E-93	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13123	26173		1.42	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10819	23852		1.13	8.0E-94	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4070	17226	30233	1.94	6.0E-94	AF142462.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
5483	16682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5483	16682	31698	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
6173	18349	32695	2.24	5.0E-94	AA722434.1	EST_HUMAN	cg87906.s1 Soares_fetal_hart_NBHH18W Homo sapiens cDNA clone IMAGE:409564 3'
7150	20285	33726	1.45	5.0E-94	A015900.1	EST_HUMAN	ol83d05.s1 Soares_totat_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'

Page 422 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8840	21919	35457	0.85	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180023 5'
11215	24284	37922	1.43	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11215	24284	37923	1.43	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12503	26177	31558	3.8	5.0E-94	T89398.1	EST_HUMAN	Y08850.4.s1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:116239 3'
1890	15034		16.49	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2723	15941	28952	0.99	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3762	16923	29925	1.12	4.0E-94	AW197851.1	EST_HUMAN	X189112.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3762	16923	29926	1.12	4.0E-94	AW197851.1	EST_HUMAN	X189112.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4840	17973	30963	3.06	4.0E-94	AI691312.1	EST_HUMAN	U011110.x1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q16265 Q16265 PROTEIN TYROSINE PHOSPHATASE ;
6597	19757	33144	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6597	19757	33145	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7052	20106		0.9	4.0E-94	L27388.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
626	13811	26833	1.76	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
739	13921	26961	1.13	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1779	14928	28021	12.9	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1779	14928	28022	12.9	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1813	14962	28055	3.18	3.0E-94	4567556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4306	17449	30435	0.67	3.0E-94	AA464605.1	EST_HUMAN	ZW63008.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:774782 5'
4437	17577	30567	0.72	3.0E-94	AA781836.1	EST_HUMAN	AI65806.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376163 3'
5799	18988	32292	3.21	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6279	19453	32801	1.13	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6581	19743	33125	3.84	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7978	21027	34541	0.63	3.0E-94	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8393	21474	35001	0.99	3.0E-94	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8787	21866	35408	4.41	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9791	22831	36410	7.29	3.0E-94	AF087042.1	NT	Homo sapiens glycoengin-1L mRNA, complete cds
11362	24423	35079	1.94	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11975	24960	36692	2.11	3.0E-94	U26711.1	NT	Human cbl-b truncated form 1 lacking leucine zipper mRNA, complete cds
9954	22993	36587	0.67	2.0E-94	AI910393.1	EST_HUMAN	W30h11.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2391813 3'
9954	22993	36588	0.67	2.0E-94	AI910393.1	EST_HUMAN	W30h11.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2391813 3'
153	13376	26410	3.07	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631038 5'

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3158	16333	28342	2.05	1.0E-94	BE263433.1	EST_HUMAN	60111696F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352559 5'
3158	16333	28343	2.05	1.0E-94	BE263433.1	EST_HUMAN	60111696F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3352559 5'
4478	17618	30800	1.11	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6188	16373	32724	0.89	1.0E-94	AE000283.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6396	16565	32925	1.91	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	16574	32936	0.82	1.0E-94	H08270.1	EST_HUMAN	Y08702.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:45033 5'
6648	19807	33184	0.86	1.0E-94	AV725992.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HTCBEF05 5'
8304	21386	34908	0.9	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34909	0.9	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8458	22572	36138	2.17	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
8980	23028	36620	1.35	1.0E-94	BE760478.1	EST_HUMAN	601468748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872089 5'
11321	24384	38028	3.11	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11597	24550	38334	1.88	1.0E-94	AI272244.1	EST_HUMAN	ap22a02.X1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q62845
12051	25032	38738	1.34	1.0E-94	11418871	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
12639	13378	26410	2.02	1.0E-94	BE285714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
12668	13378	26410	1.73	1.0E-94	BE285714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1506	14659	27741	6.05	9.0E-95	AF027302.1	NT	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3224	16386	28408	1.09	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3224	16398	28410	1.09	9.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95	X82569.1	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31734	1.46	9.0E-95	X82569.1	NT	Musculus glyt1 gene (exons 1c and 2)
8448	21527	35054	1.58	9.0E-95	AF274753.1	NT	Musculus glyt1 gene (exons 1c and 2)
149	13374	26407	2.0	8.0E-95	AF154830.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
4658	17794	30779	1.68	8.0E-95	AI700998.1	EST_HUMAN	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4658	17794	30780	1.68	8.0E-95	AI700998.1	EST_HUMAN	we08e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
7087	20181	33805	0.73	8.0E-95	11418378	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7390	20488	33934	1.4	8.0E-95	11428529	NT	we08e04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340806 3' similar to gb:K00558
7390	20488	33935	1.4	8.0E-95	11428529	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
9391	21472	34988	2.08	8.0E-95	AF032897.1	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
9565	22707	36273	1.98	8.0E-95	11420944	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens KIAA0255 gene product (KIAA0255), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9565	22707	36274	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10053	23091	36693	2.45	8.0E-95	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH), mRNA
10083	23121		2.92	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1305 protein, partial cds
10440	23475	37079	0.81	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10953	24035	37670	1.59	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11773	24765	38461	1.72	8.0E-95	10864024	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
11982	24957	38669	1.32	8.0E-95	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
11982	24967	38670	1.32	8.0E-95	7019572	NT	Homo sapiens zinedin (ZIN), mRNA
12887	25588		17.21	8.0E-95	AA629056.1	EST_HUMAN	zu84b01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.1 L1 repetitive element;
286	13504	26537	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
286	13504	26538	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2519	15845	28767	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
2519	15845	28768	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
4486	17626	30608	15.92	7.0E-95	M95708.1	NT	Homo sapiens Ly-8-like protein (CD59), mRNA, complete cds
4535	17673		1.09	7.0E-95	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
9418	22492	36058	0.62	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
215	13438	26468	0.82	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GI.CBIF01 3'
5558	18756	31794	1.52	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCI_CGAP_Bm54 Homo sapiens cDNA clone IMAGE:4214147 5'
5791	25811	32285	0.94	3.0E-95	4503354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1), mRNA
7315	20397	33859	0.73	3.0E-95	AA412321.1	EST_HUMAN	z897d01.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	0.73	3.0E-95	AA412321.1	EST_HUMAN	z897d01.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7525	20598	34071	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC resequences, MAGC Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC resequences, MAGC Homo sapiens cDNA
9555	22620	36190	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9555	22620	36191	1.62	3.0E-95	7662289	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9948	22987	36581	0.86	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
1676	14828	27911	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1676	14828	27912	3.52	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1995	15136	28242	73.27	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1998	15139	28246	3.97	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658862 5'
2497	15624	28743	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA
2497	15624	28744	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2536	15861	28784	3.62	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2582	15707	28826	1.34	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2892	15794		0.99	2.0E-95	R16245.1	EST_HUMAN	ya49d08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53393 3'
3226	16400	29412	2.1	2.0E-95	AF019452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3555	16818	28828	3.6	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3655	16818	28830	3.6	2.0E-95	7709900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3706	16867	28870	0.81	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3844	17004	30008	0.62	2.0E-95	AI290264.1	EST_HUMAN	qm01c02.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:12367.4
4481	17621	30602	1.36	2.0E-95	7657185	NT	CE03705
5151	18273	31242	3.5	2.0E-95	7661979	NT	Homo sapiens hypothetical protein (H33222B1A), mRNA
5230	18352	31321	0.99	2.0E-95	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5597	18792	31840	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51098), mRNA
5597	18792	31841	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51098), mRNA
5815	19005	32310	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5815	19005	32311	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5855	19045	32352	0.63	2.0E-95	11525883	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6270	19444	32793	3.86	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6579	19741	33122	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant, hepatic nuclear factor (TCF2), mRNA
6579	19741	33123	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant, hepatic nuclear factor (TCF2), mRNA
6700	19858	33249	3.25	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6903	20218	33647	1.47	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9343	22419	35973	1.48	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10592	23827	37236	0.56	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10992	24043	37678	1.68	2.0E-95	4757863	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A) mRNA
11138	24210	37836	1.35	2.0E-95	7661993	NT	Homo sapiens Ste20-related serine/threonine kinase (KIAA0204), mRNA
12002	24987	38691	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12002	24987	38692	1.69	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	25083		1.57	2.0E-95	AF161420.1	NT	Homo sapiens HSPC302 mRNA, partial cds
12608	25407	32047	2.31	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Table 4 Single Exon Probes Expressed in Placenta							
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12721	25480			1.3	11417680	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
13067	25698	31966		7.4	11418164	NT	Homo sapiens adenylsuccinate lyase (ADSL), mRNA
							z123h04.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
							TR:G1067084 G1067084 F55H2.6;
						EST_HUMAN	z123h04.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to
5732	18925	32219		8.06	AA284651.1		TR:G1067084 G1067084 F55H2.6;
						EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5732	18925	32220		8.06	AA284651.1		RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
7683	20748	34229		4.11	BF370000.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:31763 5'
7683	20748	34230		4.11	BF370000.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3322423 5'
7683	20748	34230		4.11	BF370000.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3322423 5'
9663	22626	36187		0.45	R17806.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3999761 5'
9663	22626	36187		0.45	BE897259.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3999761 5'
9663	22626	36187		0.45	BE897259.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3999761 5'
8388	21469	34996		1.56	BE907607.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3999761 5'
8388	21469	34996		1.56	BE907607.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA clone IMAGE:3999761 5'
455	16012	26687		0.88	BE907607.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
455	16012	26688		0.88	BE907607.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
455	16012	26688		0.88	BE907607.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5628	18822			2.8	AF236047.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5628	18822			2.8	AF236047.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
4018	17175	30183		1.25	AF231920.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
4018	17175	30183		1.25	AF231920.1	EST_HUMAN	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
2334	15465	28600		2.48	BE117984.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
2334	15465	28600		2.48	BE117984.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3394	16564	29579		0.71	AL163201.2	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3394	16564	29579		0.71	AL163201.2	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3571	16735	29751		10.25	M26873.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3571	16735	29751		10.25	M26873.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11839	24828	38517		2.41	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11839	24828	38517		2.41	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11839	24828	38518		2.41	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11839	24828	38518		2.41	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11891	24879	38576		1.94	8923939	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
11891	24879	38576		1.94	8923939	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
12084	25045	38753		1.32	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
12084	25045	38753		1.32	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
12084	25045	38754		1.32	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
12084	25045	38754		1.32	7662289	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
330	13544	26574		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
330	13544	26574		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
865	14041	27104		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
865	14041	27104		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
865	14041	27105		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
865	14041	27105		3.4	AB032998.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
2884	18804	28284		1.72	11416767	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
2884	18804	28284		1.72	11416767	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3092	18268			0.71	6912735	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
3092	18268			0.71	6912735	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5024	18153	31381		1.69	X60812.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5024	18153	31381		1.69	X60812.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5286	18414	33341		0.79	AF264750.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
5286	18414	33341		0.79	AF264750.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6798	19843			1.1	AF149773.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6798	19843			1.1	AF149773.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6851	20004	33413		0.58	AJ277557.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6851	20004	33413		0.58	AJ277557.1	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6921	20236	33659		3.68	11424399	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6921	20236	33659		3.68	11424399	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6921	20236	33670		3.68	11424399	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
6921	20236	33670		3.68	11424399	NT	RC9-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7163	20298	33740	0.91	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7684	20749	34231	0.76	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8297	21379	34800	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8297	21379	34901	1.87	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 6
12063	25063	38768	1.33	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4308	17451		15.95	3.0E-96	H68656.1	EST_HUMAN	y87h12.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:212327 5'
428	13823		5.76	2.0E-96	4503098	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
768	13947	26894	1.1	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834	14981	28078	1.03	2.0E-96	7708205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4980	18011	30895	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-H1T0230-040500-110-g02 HT0230 Homo sapiens cDNA
7820	20590	34165	0.59	2.0E-96	BF368731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
7820	20590	34166	0.59	2.0E-96	BF368731.1	EST_HUMAN	QV4-GN0120-250800-427-512 GN0120 Homo sapiens cDNA
9181	22259		4.9	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKC/FMD07 5'
12288	28214		2.54	2.0E-96	AW246440.1	EST_HUMAN	2819351.Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2819351 6'
638	13823	26845	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
638	13823	26846	0.86	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
988	13872	26905	3.08	1.0E-96	Y18800.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822	14971	28083	9.97	1.0E-96	AW95054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
1822	14971	28084	9.97	1.0E-96	AW95054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
6331	18444		1.59	1.0E-96	5453913	NT	Homo sapiens phospholipid transfer protein (PLTP) mRNA
7105	16532	31487	1.19	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7184	20099	33470	0.71	1.0E-96	6912455	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407	21488	35017	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8407	21488	35018	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8913	21892	35531	21.44	1.0E-96	11418429	NT	Homo sapiens similar to ectoronucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
9051	22130	35674	2.22	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10362	23397	37007	0.88	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10362	23397	37008	0.88	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
12274	13823	26845	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12274	13823	26846	3.29	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3403	16575	28590	0.72	6.0E-97	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7730	20792		3.4	6.0E-97	BE141848.1	EST_HUMAN	IL5-HT0117-011098-004-D07 HT0117 Homo sapiens cDNA

Page 428 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9134	22213	35757	0.75	6.0E-97	BE899012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9134	22213	35758	0.75	6.0E-97	BE899012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37476	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, while II Homo sapiens cDNA 5' end
10821	23854	37478	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST22872 Adipose tissue, while II Homo sapiens cDNA 5' end
11692	24690	38381	2.42	6.0E-97	X15904.1	NT	Human mRNA for alpha-actinin
8204	21286	34809	1.73	6.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
8336	21417	34943	11.21	6.0E-97	AA418028.1	EST_HUMAN	z07e12.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
9877	22917	36502	3.12	6.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA ;
11840	24829	38519	1.68	6.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-409 BT0812 Homo sapiens cDNA
11840	24829	38520	1.68	6.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
982	14135	27198	2.13	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
1959	15102	28202	1.41	4.0E-97	545367.2	NT	CMD-BN0108-170300-293-a06 BN0108 Homo sapiens cDNA
6883	18877	32166	0.92	4.0E-97	4557326	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6882	20190	33615	6.47	4.0E-97	Y11339.2	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6862	20190	33616	6.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7161	20294	33737	1.06	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7214	20079	33492	0.92	4.0E-97	11422155	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8328	21411	34937	1.06	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8553	21634	35171	1.43	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8778	21858	35401	0.51	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NIM), mRNA
8820	21889	35438	0.82	4.0E-97	11423233	NT	Homo sapiens cytochrome P450, subfamily IVB, polypeptide 1 (CYP4B1), mRNA
9449	22585	36128	1.06	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9449	22585	36129	1.06	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23686	37296	0.55	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NIM), mRNA
11435	24496	38162	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11435	24496	38163	1.99	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11719	23905	37528	4.51	4.0E-97	AB042657.1	NT	Homo sapiens mRNA, similar to rat myrmecalin, complete cds
12472	25325		5.26	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTS2E1), mRNA
253	13473	26504	1.58	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
897	14073	27138	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
887	14073	27139	7.16	3.0E-97	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1473	16039	27712	1.64	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2508	15998	28759	2.4	3.0E-97	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3333	16506	28623	0.96	3.0E-97	5174478	NT	Homo sapiens perlecanin (PCNT), mRNA
4902	18032	31021	22.23	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
6567	18719	33095	2.72	1.0E-97	BE566486.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3661821 5'
7039	20092	33609	0.69	1.0E-97	5453881	NT	Homo sapiens phosphotyrosine kinase, gamma 1 (muscle) (PHKG1), mRNA
9666	23005	36600	1.02	1.0E-97	R10887.1	EST_HUMAN	y38c08.s1 Scarsa fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:129134 3'
10946	24027	37663	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0049 gene product (KIAA0049), mRNA
10946	24027	37684	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0049 gene product (KIAA0049), mRNA
11569	24642	38324	1.38	1.0E-97	AA553761.1	EST_HUMAN	nk29g02.s1 NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014962 3'
11756	23942	37668	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11756	23942	37569	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
924	14099	27163	2.34	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-at2 BT0724 Homo sapiens cDNA
1305	14461	27528	1.32	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6432	19600		0.78	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
8020	21072	34583	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
8020	21072	34584	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1638 protein, partial cds
8109	21191	34711	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8109	21191	34712	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9316	22392	35943	1.78	9.0E-98	X05989.1	NT	Human mRNA for amyloid A4(751) protein
9425	22499	36064	1.12	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9482	22549	36112	1.6	9.0E-98	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9540	22805		0.81	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9667	22709	36276	1.28	9.0E-98	4607070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9667	22709	36277	1.28	9.0E-98	4607070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10467	23502	37115	0.87	9.0E-98	AF141326.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10378	23610	37213	0.5	9.0E-98	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
11253	24322	37982	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11253	24322	37983	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12487	14099	27163	4.97	9.0E-98	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-at2 BT0724 Homo sapiens cDNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1403	14557	27631	0.93	8.0E-08	AB033788.1	NT	Homo sapiens hPAD-cdony10 mRNA for peptidylarginine deiminase type I, complete cds
1591	14743	27825	1.1	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1591	14743	27826	1.1	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1765	14914	28009	2.79	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1765	14914	28010	2.79	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3896	17055	30055	6.45	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT1) gene, complete cds
6207	19382	32732	0.96	5.0E-08	BE889573.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908097 5'
2247	15380	28508	1.35	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2873	16793	28910	2.1	3.0E-08	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2807	15921		5.04	3.0E-08	AA077488.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7085	20179	33602	1.99	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7085	20179	33603	1.99	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8851	22030	35571	4.07	3.0E-08	H46698.1	EST_HUMAN	y017609.1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9497	22553	36116	0.54	3.0E-08	8922098	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10087	23125	36726	1.82	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10087	23125	36727	1.82	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10691	23724	37330	0.89	3.0E-08	BEG00454.1	EST_HUMAN	601673886F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11185	24264	37899	2.56	3.0E-08	U59309.1	NT	Human fumarate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11819	24808	38504	2.22	3.0E-08	AH159975.1	EST_HUMAN	qb80h02.x1 Soares fetal_NbHH19W Homo sapiens cDNA clone IMAGE:1706451 3'
13138	25739		3.01	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
754	13935	26980	0.67	2.0E-08	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2141	15277	28399	4.06	2.0E-08	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2311	15443	28578	2.21	2.0E-08	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C0002
4411	17553	30538	0.82	2.0E-08	AF032897.1	NT	Homo sapiens polessium channel subunit (HERG-3) mRNA, complete cds
4459	17599	30577	4.23	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4948	18078	31052	1.39	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4948	18078	31053	1.39	2.0E-08	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5492	18691	31708	4.78	2.0E-08	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6793	18948	33347	1.7	2.0E-08	4505788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A), mRNA
7801	20857	34348	1.25	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7801	20857	34349	1.25	2.0E-08	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8807	21886	35428	4.44	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8807	21886	35427	4.44	2.0E-08	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA

Page 431 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8889	21088	35503	0.8	2.0E-08	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
8889	21088	35504	0.8	2.0E-08	L76656.1	NT	Homo sapiens NKAT4b mRNA, complete cds
9737	22802	36376	1.56	2.0E-08	X12864.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10624	23688		1.65	2.0E-08	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
12136	25116		1.61	2.0E-08	AB046813.1	NT	Homo sapiens mRNA for KIAA1593 protein, partial cds
12492	25340	32082	2.23	2.0E-08	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
418	13613	28653	27.52	1.0E-08	AI852007.1	EST_HUMAN	W36804.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
467	13662	26998	3.27	1.0E-08	AW998511.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A. ;
1840	14986	28086	28.16	1.0E-08	N49818.1	EST_HUMAN	PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
5432	18632	31610	3.3	1.0E-08	AA195854.1	EST_HUMAN	Y23905.r1 Soares fetal liver spleen INF.S Homo sapiens cDNA clone IMAGE:243585 5' similar to
5687	18861	32172	0.97	1.0E-08	BE390827.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L29 - human ;
5687	18861	32173	0.97	1.0E-08	BE390827.1	EST_HUMAN	Z98809.r1 Stragene muscle 637209 Homo sapiens cDNA clone IMAGE:028240 5' similar to TR:G806862
9199	22277	35816	0.69	1.0E-08	AF141349.1	NT	G806562 NEBULIN. ;
9199	22277	35816	0.69	1.0E-08	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5939	19125	32439	1.05	9.0E-09	AI905004.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
5939	19125	32439	1.05	9.0E-09	AI905004.1	EST_HUMAN	QV-BT073-191288-012 BT073 Homo sapiens cDNA
6166	19341	32888	4.01	9.0E-09	AW968635.1	EST_HUMAN	QV-BT073-191288-012 BT073 Homo sapiens cDNA
11384	24445	38105	1.86	9.0E-09	AI479829.1	EST_HUMAN	EST380711 MAGC resequences, MAGC Homo sapiens cDNA
11384	24445	38106	1.85	9.0E-09	AI479829.1	EST_HUMAN	Im68h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:RID_HUMAN
11700	24697	38989	1.72	9.0E-09	AA134604.1	EST_HUMAN	Im68h07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:RID_HUMAN
8924	22003	35542	1.19	8.0E-09	9635487	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
5956	19142	32458	9.25	7.0E-09	AF035808.1	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11809	24996	38999	1.91	7.0E-09	AF001886.1	NT	TR:G662994 G662994 GPI-ANCHORED PROTEIN P137. ;
484	13678	28713	0.72	8.0E-09	U10951.1	NT	Human endogenous retrovirus, complete genome
2196	15331	28458	6.2	6.0E-09	11430555	NT	Homo sapiens oscillin (hcn) gene, exon 5
2196	15331	28457	6.2	6.0E-09	11430555	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
3995	17152	30160	2.8	6.0E-09	AW976364.1	EST_HUMAN	Human G2 protein mRNA, partial cds
4870	18003	30986	1.42	6.0E-09	4502660	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
							Homo sapiens cysteine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
							EST388473 MAGC resequences, MAGC Homo sapiens cDNA
							Homo sapiens CD34 antigen (CD34) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	19888	33280	0.94	6.0E-99	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6816	19889	33376	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6816	19889	33377	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8298	21378	34899	1.85	6.0E-99	X98101.1	NT	H. sapiens mRNA for estrogen receptor
8314	21398	34921	0.59	6.0E-99	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8964	22043	35588	2.67	6.0E-99	AB038428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/sulfotransferase 4, complete cds
9084	22143	35688	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
9084	22143	35689	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
9123	22202	35744	0.59	6.0E-99	11431984	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9123	22202	35745	0.59	6.0E-99	11431984	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
10968	24039	37674	3.15	6.0E-99	11526269	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11742	23928	37553	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11742	23928	37554	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
2022	15163	28268	1	5.0E-99	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4686	17821	30809	1.81	5.0E-99	AF005660.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S3A2 to TORBV12S2 region
12502	25346		2.49	5.0E-99	BE890177.1	EST_HUMAN	601613157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8516	21597		4.95	3.0E-99	M65566.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1268	14426		7.26	2.0E-99	AW274792.1	EST_HUMAN	xp09506.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
3331	16504	29522	1.4	2.0E-99	M30938.1	NT	LIGHT CHAIN ALKAL, NON-MUSCLE ISOFORM (HUMAN); Human Ku (p70/p80) subunit mRNA, complete cds
4665	17800	30787	1.82	2.0E-99	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7851	20906	34410	0.76	2.0E-99	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8904	21983	35523	10.79	2.0E-99	W23507.1	EST_HUMAN	zb46406.t1 Soares_Tetal_Jung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to
9353	22428	35986	0.75	2.0E-99	R78254.1	EST_HUMAN	gb:M1618182 BETA-GLUCURONIDASE PRECURSOR (HUMAN); y181b09.t1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11367	24428	38085	3.16	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12081	25081	38767	1.64	2.0E-99	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
325	13539	26571	1.49	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
390	13596	26632	1.75	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1452	14605	27684	3.61	1.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1587	14739	27819	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1587	14739	27820	1.16	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1980	15123	28224	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products

Page 433 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1880	15123	28225	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3164	16328	29339	0.93	1.0E-99	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Ree) mRNA, complete cds
4489	17639	30821	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4499	17639	30822	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6943	20256	33694	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943	20256	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289	25842	33827	0.81	1.0E-99	X98022.1	NT	H. sapiens EG-AP gene exon 2
9400	22474		0.75	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9720	22785	36359	1.7	1.0E-99	AW340174.1	EST_HUMAN	h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
11403	24464	38128	2.56	1.0E-99	7427514	NT	002711 PRO-POL-DUTASE POL YPROTEIN:
11403	24464	38129	2.56	1.0E-99	7427514	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462	24521	38191	1.68	1.0E-99	5901979	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11659	24738	38429	2.83	1.0E-99	AB023222.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSP2BP), mRNA
11998	24981	38687	2.45	1.0E-99	11417161	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12287	25193		4.52	1.0E-99	AF240786.1	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
1	13241	26241	1.7	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	13241	26241	2.91	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26329	1.62	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26330	1.82	1.0E-100	11418230	NT	Homo sapiens testis-specific XK-related protein on Y (XKRY), mRNA
89	13324	26363	0.82	1.0E-100	AW276237.1	EST_HUMAN	Homo sapiens testis-specific XK-related protein on Y (XKRY), mRNA
173	13397	26425	0.89	1.0E-100	AL163208.2	NT	xv78b11.x1 NC1_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
327	13541	26573	1.84	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
333	13564	26692	1.87	1.0E-100	T05087.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
450	13646		2.24	1.0E-100	AF003528.1	NT	EST02975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCCR32
502	13697		5.88	1.0E-100	X89631.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
522	13716	26742	1.21	1.0E-100	BE180809.1	EST_HUMAN	G. gorilla DNA for ZNF80 gene homolog
1044	14210	27266	4.57	1.0E-100	7661685	NT	RC3-HT0625-040500-022-509 HT0625 Homo sapiens cDNA
1044	14210	27267	4.57	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1577	14730		1.3	1.0E-100	AW207555.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1581	14733	27814	1.66	1.0E-100	AI200857.1	EST_HUMAN	UHH-B11-atk-c-07-q-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
							qf6209.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
							P81081 CYSTATIN1

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2315	15447		1.14	1.0E-100	D63349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2507	15634	28754	1.41	1.0E-100	X62468.1	NT	H. sapiens mRNA for IFN-gamma (KC-4)
2771	15886	28096	2.5	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIA0957), mRNA
3083	16259		6.55	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4326	17469	30456	1.87	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4351	17494	30474	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5202	18323	31291	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5202	18323	31292	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5404	18606	31578	1.74	1.0E-100	BF244218.1	EST_HUMAN	601883184F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4080899 5'
5625	18819	31893	0.76	1.0E-100	AW075983.1	EST_HUMAN	xa8201.x1 NCI_CGAP_CVIL1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
5818	19008	32314	1.45	1.0E-100	AU118182.1	EST_HUMAN	PROTEIN PHPS1-2 (HUMAN);
5854	19054	32361	1.78	1.0E-100	AF135116.1	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5860	19146	32461	0.85	1.0E-100	X14680.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6292	19465	32817	0.9	1.0E-100	4557568	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6292	19465	32818	0.9	1.0E-100	4557568	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6626	19788	33174	5.62	1.0E-100	AU140214.1	EST_HUMAN	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6824	19977	33384	1.36	1.0E-100	R10887.1	EST_HUMAN	AL140214 PLAGE2 Homo sapiens cDNA clone PLACE2000137 5'
6908	20223	33653	1.77	1.0E-100	7382479	NT	y98c08.s1 Soares fetal liver spleen TNF-LS Homo sapiens cDNA clone IMAGE:129134 3'
6982	20210	33638	1.02	1.0E-100	AA496841.1	EST_HUMAN	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6982	20210	33639	1.02	1.0E-100	AA496841.1	EST_HUMAN	ae33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7026	20162	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7026	20162	33584	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN ;
7033	20169	33591	6.2	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8729	21809	35345	3.53	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8768	21845	35837	5.59	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9216	22294	35837	0.47	1.0E-100	AU116951.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:39831310 5'
9216	22294	35838	0.47	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9433	22507	36073	3.88	1.0E-100	AB040518.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9510	22776		1.65	1.0E-100	AJ972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9633	21076	34586	2.28	1.0E-100	AW698611.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
							MR22 repetitive element ;
							PM0-BN0065-100300-001-c05 BN0065 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9857	22736		0.84	1.0E-100	AU127720.1	EST_HUMAN	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9782	22822	36400	2.17	1.0E-100	AB046848.1	NT	Homo sapiens mRNA for KIAA1628 protein, partial cds
9782	22822	36401	2.17	1.0E-100	AB046848.1	NT	Homo sapiens mRNA for KIAA1628 protein, partial cds
10048	23086	36687	1.81	1.0E-100	AW530487.1	EST_HUMAN	h83c11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2863388 5'
10048	23086	36688	1.81	1.0E-100	AW530487.1	EST_HUMAN	h83c11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2863388 5'
10688	23121	37327	0.64	1.0E-100	BF347618.1	EST_HUMAN	802020554F1 NCL CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4166165 5'
10782	23115		1.35	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10906	24076	37708	6.64	1.0E-100	BF327292.1	EST_HUMAN	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11584	24619	38300	1.55	1.0E-100	X94633.1	NT	H. sapiens GD97 gene exon 4
11584	24619	38301	1.35	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
11635	24715	38406	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
11635	24715	38406	3.91	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
11665	13241	26241	3.07	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11977	24682		2.21	1.0E-100	AF266285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
12128	25108	38812	1.93	1.0E-100	AJ131034.1	NT	Homo sapiens class gene, exon 12
12177	25137	38832	7.59	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12312	26037		1.78	1.0E-100	BF446549.1	EST_HUMAN	7q88h03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to TR:Q21987 Q21997
12493	26341	32063	4.97	1.0E-100	11545732	NT	COSMID R151. [2] TR:Q9JAO8
12754	25500	32033	1.31	1.0E-100	11418123	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13195	25778	31835	6.91	1.0E-100	11417874	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
78	13315	26342	0.82	1.0E-101	7110714	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
78	13315	26343	0.82	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13887	26919	1.4	1.0E-101	AB007915.2	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
722	13904	26945	6.12	1.0E-101	7110734	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
722	13904	26948	6.12	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
792	13971	27023	1.37	1.0E-101	7657454	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
876	14062	27117	1.35	1.0E-101	4503914	NT	Homo sapiens pascadillo (zbrashish) homolog 1, containing BRCT domain (PES1), mRNA
948	14121	27182	0.85	1.0E-101	Z20656.1	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylhydrazide synthetase (GART) mRNA
1008	14180	27243	6.07	1.0E-101	BF881218.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1077	14243	27289	1.39	1.0E-101	A1221878.1	EST_HUMAN	602155474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287281 5'
1674	14767	27849	1.44	1.0E-101	5821460	NT	q98909.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
							Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1614	14787	27850	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1785	14934	28028	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1785	14934	28028	1.57	1.0E-101	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1090	15140	28247	2.07	1.0E-101	4602996	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2116	16254	28373	2.76	1.0E-101	BE843070.1	EST_HUMAN	RC3-ST0281-160900-018-109 ST0281 Homo sapiens cDNA
2425	16082	28880	1.2	1.0E-101	5729882	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2690	15800	28917	4.62	1.0E-101	X72993.1	NT	H. sapiens EWS gene, exon 5
2802	15916	29025	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2802	15916	29026	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3020	16186		20.15	1.0E-101	AJ262312.1	NT	Homo sapiens genomic downstream Rhesus box
3273	16447	29467	2.97	1.0E-101	4865270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3313	16486		2.3	1.0E-101	BF053327.1	EST_HUMAN	601458331F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3468	16635	29654	1.82	1.0E-101	AW965556.1	EST_HUMAN	EST377629 MAGC resequences, MAGI Homo sapiens cDNA
3487	15916	29025	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3487	15916	29026	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3981	17138	30142	3.81	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5147	18269	31239	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5147	18269	31240	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5248	18369	31336	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5248	18369	31337	0.6	1.0E-101	BE612554.1	EST_HUMAN	601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5433	18633	31611	1.94	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGC resequences, MAGI Homo sapiens cDNA
6126	19305	32645	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6126	19305	32646	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6834	19987	33398	0.98	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7423	20500		1.26	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7473	20548	34019	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7473	20548	34020	4.22	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7645	20714	34182	7.65	1.0E-101	AW008475.1	EST_HUMAN	w55f12x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7749	20809		1.98	1.0E-101	BE267384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3348901 5'
7900	20952	34459	6.54	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-112 BT0313 Homo sapiens cDNA
8097	21179	34696	0.74	1.0E-101	BE275821.1	EST_HUMAN	601121821F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348869 5'
8097	21179	34697	0.74	1.0E-101	BE275821.1	EST_HUMAN	601121821F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3348869 5'
8245	21327	34843	1.6	1.0E-101	BF029174.1	EST_HUMAN	601764886F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'

Page 437 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21598	35132	0.71	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8517	21598	35133	0.71	1.0E-101	AW630070.1	EST_HUMAN	hh74g10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
9212	22280	35832	1.1	1.0E-101	AA036800.1	EST_HUMAN	z128g08.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471898 5' similar to PIR:S54640 S54640 YD9335.03c protein - yeast;
9531	22556	36167	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9531	22556	36168	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9651	21103	34618	17.35	1.0E-101	X60089.1	NT	Human mRNA for pancreatic gemma-glutamyltransferase
9651	21103	34620	17.38	1.0E-101	X60089.1	NT	Human mRNA for pancreatic gemma-glutamyltransferase
9876	22638	36209	19.41	1.0E-101	8845482	NT	Homo sapiens gemma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9899	22698	36593	3.38	1.0E-101	BE616657.1	EST_HUMAN	501472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9959	22698	36594	3.38	1.0E-101	BE616657.1	EST_HUMAN	501472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
10088	23138	36737	0.68	1.0E-101	10883960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10620	23654	37284	1.84	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10656	23690	37289	4.37	1.0E-101	A1570293.1	EST_HUMAN	h677d11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10656	23690	37300	4.37	1.0E-101	A1570293.1	EST_HUMAN	h677d11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10771	23804	37426	0.83	1.0E-101	BE973648.1	EST_HUMAN	501680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23804	37427	0.83	1.0E-101	BE973648.1	EST_HUMAN	501680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
11371	24432	38089	1.31	1.0E-101	AB020628.1	NT	Homo sapiens mRNA for KIAA0819 protein, partial cds
12059	25040	38748	1.85	1.0E-101	A1808168.1	EST_HUMAN	RC-BT163-280499-085 BT163 Homo sapiens cDNA
12059	25040	38749	1.85	1.0E-101	A1808168.1	EST_HUMAN	RC-BT163-280499-085 BT163 Homo sapiens cDNA
12738	25489		2.24	1.0E-101	BE163587.1	EST_HUMAN	QV3-HT0460-230200-101-d03 HT0460 Homo sapiens cDNA
12793	25529		12.79	1.0E-101	AW939051.1	EST_HUMAN	QV1-DT0088-240200-085-a01 DT0088 Homo sapiens cDNA
40	13278	26284	0.81	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
351	13562	26599	4.57	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
635	13820	26844	0.61	1.0E-102	BE252470.1	EST_HUMAN	601108282F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
796	13975	27028	1.06	1.0E-102	4657534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1141	14306	27392	1.8	1.0E-102	M10876.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1297	14453	27518	2.05	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1287	14453	27518	2.05	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	14603	27881	355.8	1.0E-102	BE408447.1	EST_HUMAN	60126882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629801 6'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2383	15514	28642	1.91	1.0E-102	A1124668.1	EST_HUMAN	am80c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
2383	15514	28643	1.91	1.0E-102	A1124668.1	EST_HUMAN	am80c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3090	16286		0.74	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3133	16309	29322	1.47	1.0E-102	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3203	16378	29387	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3203	16378	29388	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4347	17490	30472	1.74	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4533	17871	30655	2.57	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
6224	18346	31316	1.28	1.0E-102	R69488.1	EST_HUMAN	y82c04.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:140934 5'
5487	18886	31704	1.6	1.0E-102	AF087133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5857	19057		6.87	1.0E-102	AB034951.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5905	19094	32408	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	19094	32409	3.25	1.0E-102	7705398	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5912	19100	32414	0.81	1.0E-102	11433046	NT	Homo sapiens head domain and RLD 2 (HERC2), mRNA
6422	19591	32956	2.81	1.0E-102	A459825.1	EST_HUMAN	ar82109.x1 Barstead codon HPLR87 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
7227	20090	33507	0.7	1.0E-102	AW451643.1	EST_HUMAN	Q13137 NDP52. ;
7236	20369	33823	0.91	1.0E-102	BE729323.1	EST_HUMAN	UI-P-B13-aj-d-10-0-UJ.st NCI CGAP_Sub56 Homo sapiens cDNA clone IMAGE:2736835 3'
7314	20396	33858	1.02	1.0E-102	BE386106.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7429	20506	33877	1.5	1.0E-102	AB023177.1	NT	60127216F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7510	20584	34057	8.03	1.0E-102	AJ238994.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
7802	20858	34350	2.61	1.0E-102	AV710738.1	EST_HUMAN	Homo sapiens mRNA for Centaurin-alpha2 protein
8418	21499	35031	3.85	1.0E-102	BE763051.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAD03 5'
8691	21771	35301	1.71	1.0E-102	AV694817.1	EST_HUMAN	QV3-NT0025-210600-238-108 NT0025 Homo sapiens cDNA
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKc Homo sapiens cDNA clone GKCEEE11 5'
8802	21861	35419	0.81	1.0E-102	AB007923.1	NT	Homo sapiens cDNA clone GKCEEE11 5'
9131	22210	35754	1.2	1.0E-102	BE388063.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
9481	22538	36102	0.84	1.0E-102	AV765842.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9522	22587	36155	2	1.0E-102	T70393.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9522	22587	36156	2	1.0E-102	T70393.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD06 5'
9611	22666	36237	3.11	1.0E-102	AU124628.1	EST_HUMAN	y13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
							y13d07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
							AU124628 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10593	23828		0.64	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10647	23681	37281	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10647	23681	37282	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
10687	23720	37325	3.28	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-280499-014 BT074 Homo sapiens cDNA
10687	23720	37328	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-BT074-280499-014 BT074 Homo sapiens cDNA
10748	23781	37394	1.5	1.0E-102	AA970786.1	EST_HUMAN	on67h04.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to
11323	24386	38030	1.37	1.0E-102	BE997468.1	EST_HUMAN	SW:CAV2_HUMAN P61686 CAVEOLIN-2 [1];
11327	24390	38035	2.44	1.0E-102	4507822	NT	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824166 5'
11327	24390	38036	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11600	24633	38337	1.47	1.0E-102	AA886675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11680	24688	38378	2.47	1.0E-102	BF359243.1	EST_HUMAN	ak9h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406347 3'
12009	24694	38869	2.83	1.0E-102	U41302.1	NT	RC8-ET0072-150600-011-F01 E10072 Homo sapiens cDNA
12182	25142		5.69	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12775	25517	32000	6.87	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12831	25553	32015	1.25	1.0E-102	11419159	NT	K007c12.x1 NCI_CGAP_Cox20 Homo sapiens cDNA clone IMAGE:2686038 3'
71	13308	26331	0.85	1.0E-103	BE908158.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4), mRNA
71	13308	26332	0.85	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
102	13339	26395	8.24	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
213	13436	26486	0.84	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1004	14176	27234	74.34	1.0E-103	AJ276348.1	NT	Homo sapiens nuclear protein (KKE/D repeat) (NOP58) mRNA
1272	14428	27500	7.08	1.0E-103	BE877541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1626	14778	27863	3.61	1.0E-103	AF012872.1	NT	601485389F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1984	15107	28207	1.02	1.0E-103	7657692	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
2031	15172	28280	0.95	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2031	15172	28281	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2379	15510	28638	1.95	1.0E-103	AU134991	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2523	16848	28772	1.84	1.0E-103	AF060568.1	NT	AU134991 PLACE1 Homo sapiens cDNA clone IMAGE:1000965 5'
2885	15805	28921	1	1.0E-103	N32770.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3137	16313		2.76	1.0E-103	BE744722.1	EST_HUMAN	yy91d08.s1 Soares_placenta_8to9weeks_2NblHP8b9W Homo sapiens cDNA clone IMAGE:2686680 3'
3487	16834	29863	5.33	1.0E-103	AW288245.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
							UI-HBW0-ajl-h-11-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733166 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3526	16691	29700	0.95	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3850	17010		5.45	1.0E-103	AF023891.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3894	17053	30053	0.9	1.0E-103	AA485553.1	EST_HUMAN	ab10412.s1 Stralagene lung (#337210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3933	17092	30090	1.54	1.0E-103	11430878	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4110	17284	30264	4.63	1.0E-103	T23683.1	EST_HUMAN	seq340 b4-IB3MA-Cor109+10-Bio Homo sapiens cDNA clone b4-IB3MA-Cor109+10-Bio-7 3'
5325	18438		0.63	1.0E-103	AA451616.1	EST_HUMAN	z43304.1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:789199 5' similar to TR:G292352 G292352 COLLAGEN CHAIN RH ;
6056	18238	32563	0.9	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4310573 5'
6063	19245	32571	1.87	1.0E-103	AF179906.1	NT	Homo sapiens septin 2 (SEPT2) mRNA, partial cds
6397	19568	32926	0.8	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6397	19568	32927	0.8	1.0E-103	11435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19748	33130	0.84	1.0E-103	AW94599.1	EST_HUMAN	EST366636 IMAGE ressequences, MAGC Homo sapiens cDNA
6587	19748	33131	0.84	1.0E-103	AW954566.1	EST_HUMAN	EST366636 IMAGE ressequences, MAGC Homo sapiens cDNA
6725	25531	33273	1.15	1.0E-103	AA781442.1	EST_HUMAN	q26603.s1 Soares, testis, NHT Homo sapiens cDNA clone 1391452 3'
6768	19824	33318	0.91	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6859	20011	33422	1.68	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6859	20011	33423	1.66	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6987	18506	31521	1.77	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6987	18506	31522	1.77	1.0E-103	5032282	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7108	18535	31490	1.04	1.0E-103	11431100	NT	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7178	20310	33753	0.96	1.0E-103	AJ288880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
7375	20454	33919	1.88	1.0E-103	AW95778.1	EST_HUMAN	EST377849 IMAGE ressequences, MAGI Homo sapiens cDNA
7488	20563	34032	3.6	1.0E-103	BE748158.1	EST_HUMAN	601571537F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:3838545 5'
7951	21001	34511	4	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
7951	21001	34512	4	1.0E-103	AI590071.1	EST_HUMAN	tm58605.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21565	35101	0.59	1.0E-103	T31080.1	EST_HUMAN	EST27103 Human Brain Homo sapiens cDNA 5' end similar to None
8822	21901	35440	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8822	21901	35441	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8900	21978	35518	1.34	1.0E-103	BF109244.1	EST_HUMAN	700e03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525954 3' similar to SW_PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1;
9307	22383	35934	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
9307	22383	35935	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF Interacting) (TRIO), mRNA
9349	22425	35980	0.97	1.0E-103	AA581088.1	EST_HUMAN	nd13c02.s1 NCL CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:U02428 26S
10283	23298	36896	2.04	1.0E-103	Z37976.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10304	23339	36944	2.07	1.0E-103	AW963676.1	EST_HUMAN	EST375749 IMAGE:3525954 3' similar to gb:U02428 26S
10443	23478	37083	10.79	1.0E-103	A1878956.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518328 5' similar to TR:Q02084 Q02084
10878	23963	37691	1.52	1.0E-103	BE549706.1	EST_HUMAN	7b41f03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10971	24051	37684	9.5	1.0E-103	A1782759.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING ;
11072	24147	37785	2.45	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11072	24147	37786	2.45	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37794	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11083	24157	37795	2.4	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11656	24735	38426	2.87	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone IMAGE:1003923 5'
11731	23917	37542	4.1	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11968	24653		1.71	1.0E-103	AB024769.1	NT	Homo sapiens TSA305 gene, exon 16
12044	25025	38730	2.26	1.0E-103	BE844611.1	EST_HUMAN	7e68a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29, 13 MER29 repetitive element;
12178	25138		3.4	1.0E-103	AF224669.1	NT	Homo sapiens marmosinase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12209	25162		1.22	1.0E-103	11526281	NT	(UBE2D3) genes, complete cds
12414	25203	32083	1.71	1.0E-103	AB011369.1	NT	Homo sapiens gene for AF-6, complete cds
243	13465	26494	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 584 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
243	13465	26495	2.46	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.1 584 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 5'
1937	15080	28182	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2267	15400	28528	33.29	1.0E-104	AA132975.1	EST_HUMAN	zo22c06.s1 Stratagene clone (#937204) Homo sapiens cDNA clone IMAGE:587628 3' similar to gb:Z14116.maf CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2277	15409	28540	4.55	1.0E-104	BE744628.1	EST_HUMAN	601577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2442	15570	28698	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2442	15570	28699	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-f12 CT0249 Homo sapiens cDNA
2508	15633	28763	2	1.0E-104	5091570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2634	16111	28125	17.99	1.0E-104	M34671.1	NT	Human lymphocyte antigen CD59/MEM43 mRNA, complete cds
2883	16159		2.15	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II
3337	16610	29526	0.99	1.0E-104	AU133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000936 5'
3478	16645		2.33	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3690	16832	29860	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3690	16832	29861	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209	30219	0.71	1.0E-104	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4248	17394	30383	0.71	1.0E-104	F11745.1	EST_HUMAN	HS031A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4496	17636	30618	33.95	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4732	17867	30849	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4732	17867	30850	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	19243	32567	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6061	19243	32568	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6108	19288	32623	0.93	1.0E-104	AB017332.1	NT	Homo sapiens aik3 mRNA for Aurora/Ip1-related kinase 3, complete cds
6596	19756	33142	8.5	1.0E-104	A1768797.1	EST_HUMAN	w03b12.x1 NCJ CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TRQ14145 Q14145
6596	19756	33143	8.5	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element
6786	19941	33338	0.74	1.0E-104	77068512	NT	w03b12.x1 NCJ CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TRQ14145 Q14145
6942	20255	33692	3.39	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6942	20255	33693	3.39	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
7373	20452	33917	2.01	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
8766	21875	35414	0.87	1.0E-104	BF509244.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9368	22443	36004	2.41	1.0E-104	BF448230.1	EST_HUMAN	U1-H-BJ4-aw-b-09-f-U1.s1 NCJ CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086176 3'
9463	22520	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	hnd18g11.x1 NCJ CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9484	22541		1.03	1.0E-104	T74219.1	EST_HUMAN	z88b05.at Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9515	22580	36146	5	1.0E-104	AF091395.1	NT	yc8302.r1 Soares infant brain T1N1B Homo sapiens cDNA clone IMAGE:22440 5'
9515	22580	36147	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
							Homo sapiens Trio isoform mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9841	21084	34597	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9841	21084	34598	4.14	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9856	22994	36389	0.82	1.0E-104	AW103846.1	EST_HUMAN	xd76d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9856	22994	36389	0.82	1.0E-104	AW103846.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
9856	22994	36389	0.82	1.0E-104	AW103846.1	EST_HUMAN	xd76d02.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9856	22994	36389	0.82	1.0E-104	AW103846.1	EST_HUMAN	Q24116 HYPOTHETICAL 29.4 KD PROTEIN. ;
10163	23190	36787	0.49	1.0E-104	AF113514.1	NT	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10298	23333	36937	3.15	1.0E-104	BE791713.1	EST_HUMAN	601881503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939977 5'
10298	23333	36938	3.16	1.0E-104	BE791713.1	EST_HUMAN	601881503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939977 5'
10611	23645	37253	1.49	1.0E-104	AV728070.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10657	23691	37301	4.47	1.0E-104	AU130765.1	EST_HUMAN	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10757	23790	37407	0.54	1.0E-104	AA931321.1	EST_HUMAN	co08a10.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1666370 3'
10757	23790	37408	0.54	1.0E-104	AA931321.1	EST_HUMAN	co08a10.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1666370 3'
10774	23807	37430	6.4	1.0E-104	U66535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25
10781	23824		0.74	1.0E-104	11427757	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11577	24632	38310	44.86	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11577	24632	38311	44.86	1.0E-104	BE720191.1	EST_HUMAN	RCO-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11611	24663	38350	4.1	1.0E-104	BF684288.1	EST_HUMAN	802141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
12082	29062	38768	48.12	1.0E-104	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS9KA5), mRNA
13073	26702		1.32	1.0E-104	BE393892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658678 5'
289	15881	26641	2.67	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
438	13238	26238	6.69	1.0E-105	4605150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
607	13798	26816	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
607	13798	26816	2.51	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1865	15011	28118	10.24	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1879	18122	28223	2.39	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2263	15396	28624	3.08	1.0E-105	AA318399.1	EST_HUMAN	EST20608 Spleen I Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p80 subunit
2298	15529		1.18	1.0E-105	BE891706.1	EST_HUMAN	601434161F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919611 5'
2784	15900		0.98	1.0E-105	AA584808.1	EST_HUMAN	no10005.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3071	16247		2.79	1.0E-105	AJ229041.1	NT	Homo sapiens 959 kb config between AML1 and CBR1 on chromosome 21q22; segment 1/3
3432	16600	29618	0.86	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
3432	16600	29619	0.86	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4213	17362	30350	2.23	1.0E-105	AW961988.1	EST_HUMAN	EST373781 IMAGE resequences, MAGG Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5053	18181		5.34	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5259	18378	31344	1.08	1.0E-105	AB020873.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5445	18645	31623	1.18	1.0E-105	AF016704.1	NT	Homo sapiens EB-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5513	18711		1.12	1.0E-105	11420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7045	20098	33513	1.44	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7045	20098	33514	1.44	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7121	18547	31458	3.78	1.0E-105	11419196	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7121	18547	31459	3.78	1.0E-105	11419198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7167	20300	33743	0.72	1.0E-105	AW051834.1	EST_HUMAN	EST363689 MAGE resequences, MAGB Homo sapiens cDNA
7436	20513	33086	0.72	1.0E-105	BE902618.1	EST_HUMAN	601677278F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
8043	21126	34847	0.93	1.0E-105	X12556.1	NT	Human mRNA for dkl proto-oncogene
8217	21298	34820	11.05	1.0E-105	T05087.1	EST_HUMAN	EST02875 Fetal brain, Striatogene (cat5936206) Homo sapiens cDNA clone HFB0R32
8592	21673	35211	1.63	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:2600626 3' similar to
9128	22207	35750	0.82	1.0E-105	AW840817.1	EST_HUMAN	SW/ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
9250	22327	35874	2.51	1.0E-105	AW016879.1	EST_HUMAN	RC1-CN0008-070100-011-e05 CN0008 Homo sapiens cDNA
9404	22478	36041	0.83	1.0E-105	AW882372.1	EST_HUMAN	UHH-B10p-4b1b-12-0-U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9404	22478	36042	0.83	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9767	22764	36333	0.75	1.0E-105	BE867793.1	EST_HUMAN	QV2-OT0062-140300-083-d09 OT0062 Homo sapiens cDNA
9767	22764	36334	0.75	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11173	24243	37876	4.82	1.0E-105	AF254822.1	NT	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11508	24564	38241	1.42	1.0E-105	D63548.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11569	24814	38283	1.85	1.0E-105	77058936	NT	Homo sapiens COL4A6 gene for a(IV) collagen, exon 31
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11972	24957	38659	1.48	1.0E-105	BF430921.1	EST_HUMAN	wy74f07.x1 Soares_thymus_NHfTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
12111	25091	38794	1.3	1.0E-105	AF218896.1	EST_HUMAN	P87892 PROTEASE ;
156	13380		0.88	1.0E-106	AW503208.1	EST_HUMAN	7o18c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P87880 P87880
210	13433	26464	5.14	1.0E-106	AW503208.1	EST_HUMAN	RIN1. ;
555	13748	26774	1.89	1.0E-106	AW936556.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 8
620	13807	26828	0.8	1.0E-106	J00146.1	NT	U1-HF-BND-ak-8-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
621	13807	26828	1.13	1.0E-106	J00146.1	NT	U1-HF-BND-ak-8-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
1554	14707	27787	8.84	1.0E-106	AF145712.1	NT	U1-HF-BND-ak-8-07-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	14885	27878	7.83	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1757	14806	28000	1.33	1.0E-108	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1846	14992	28093	5.51	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element LTR3 repetitive element;
1846	14992	28094	5.51	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:837352 3' similar to contains element LTR3 repetitive element;
2181	15326	28481	1.84	1.0E-108	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2391	15522	28651	3.82	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2574	15599	28821	2.19	1.0E-108	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2667	15788	28804	1.93	1.0E-106	U04675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2669	15790	28806	2.01	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3602481 5'
2815	15929	29041	8.05	1.0E-108	A1278526.1	EST_HUMAN	q176h10.x1 Soares_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:1876307 3'
2886	14817	27700	1.84	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	14817	27701	1.84	1.0E-108	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2939	16116	29128	1.18	1.0E-108	BE384296.1	EST_HUMAN	601272875F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
3007	16182	29204	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3007	16182	29205	5.7	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3248	18422	29438	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	18422	29439	2.5	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3461	16828	29548	1.04	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3527	16692	29701	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3527	16692	29702	1.07	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4149	17301	30293	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4149	17301	30294	9.2	1.0E-106	AW074650.1	EST_HUMAN	EST386875 MAGe resequences, MAGN Homo sapiens cDNA
4723	17859	30840	2.27	1.0E-106	BE144286.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5485	18684	31701	2.95	1.0E-106	AA781155.1	EST_HUMAN	aj24309.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1-2 (HUMAN);
5978	19161	32480	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
5978	19161	32481	0.95	1.0E-106	AU130113.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6028	19209	32529	0.61	1.0E-106	AA434166.1	EST_HUMAN	zw28412.s1 Soares ovary tumor N5HOT Homo sapiens cDNA clone IMAGE:770615 3'
6116	19296	32631	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6116	19296	32632	1	1.0E-106	AU143428.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6227	19402	32752	8.39	1.0E-106	BF979574.1	EST_HUMAN	602164012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'

Page 446 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Accession No.	Top Hit Descriptor
6336	19507	32864	0.81	1.0E-106	EST_HUMAN	BE897112.1	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6526	19507	32864	0.66	1.0E-106	EST_HUMAN	BE897112.1	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6549	19711	33087	15.91	1.0E-106	NT	11545913	Homo sapiens xylosyltransferase II (XT2), mRNA
6549	19711	33088	15.91	1.0E-106	NT	11545913	Homo sapiens xylosyltransferase II (XT2), mRNA
7528	20601	34075	5.69	1.0E-106	EST_HUMAN	AA663779.1	KINESIN HEAVY CHAIN (HUMAN);
7582	20654	34130	4.17	1.0E-106	NT	11429817	Homo sapiens XPMC2 protein (LOC57109), mRNA
7672	20738	34216	1.64	1.0E-106	EST_HUMAN	BE292722.1	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2888345 5'
7787	20843	34335	8.06	1.0E-106	NT	11425503	Homo sapiens sorting nexin 11 (SNX11), mRNA
7787	20843	34336	8.06	1.0E-106	NT	11425503	Homo sapiens sorting nexin 11 (SNX11), mRNA
7894	21044	34596	0.6	1.0E-106	EST_HUMAN	AU118850.1	AU118850 HEMBA1 Homo sapiens cDNA clone HEMBA1000129 5'
8173	21255	34776	3.62	1.0E-106	EST_HUMAN	BE741408.1	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8173	21255	34777	3.62	1.0E-106	EST_HUMAN	BE741408.1	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8368	21449	34972	2.21	1.0E-106	EST_HUMAN	AI523066.1	ar68a07.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X66233
8830	21909	35447	0.64	1.0E-106	EST_HUMAN	BE387950.1	CALGRANULIN B (HUMAN);
8830	21909	35448	0.64	1.0E-106	EST_HUMAN	BE387950.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8903	21982	35522	2.77	1.0E-106	EST_HUMAN	AI654123.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9252	22329	35876	0.83	1.0E-106	EST_HUMAN	AW838831.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9348	22424	35978	2.34	1.0E-106	EST_HUMAN	AA825307.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9348	22424	35979	2.34	1.0E-106	EST_HUMAN	AA825307.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9486	22543	36108	0.77	1.0E-106	EST_HUMAN	AI750447.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9629	22684	36255	1.94	1.0E-106	EST_HUMAN	AI479569.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
9629	22684	36256	1.94	1.0E-106	EST_HUMAN	AI479569.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10205	23241	36832	0.6	1.0E-106	EST_HUMAN	BE388234.1	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
10289	23324	36928	1.09	1.0E-106	EST_HUMAN	BF027310.1	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10289	23324	36929	1.09	1.0E-106	EST_HUMAN	BF027310.1	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10448	23481	37088	10.7	1.0E-106	EST_HUMAN	AA60447.1	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10448	23481	37089	10.7	1.0E-106	EST_HUMAN	AA60447.1	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10492	23527	37136	1.83	1.0E-106	EST_HUMAN	AW363289.1	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10497	23532	37141	0.66	1.0E-106	11436432	NT	Homo sapiens multimetric (MMRN), mRNA
10497	23532	37142	0.66	1.0E-106	11436432	NT	Homo sapiens multimetric (MMRN), mRNA
10878	23712	37320	0.65	1.0E-106	AL030886.1	EST_HUMAN	DKFZp434F0712.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434F0712 5'
10807	23840	37464	4.26	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11135	24207	37832	4.81	1.0E-106	BF032753.1	EST_HUMAN	601463481F1 NIH_MGC 86 Homo sapiens cDNA clone IMAGE:3857366 5'
11135	24207	37833	4.81	1.0E-106	BF032753.1	EST_HUMAN	601463481F1 NIH_MGC 86 Homo sapiens cDNA clone IMAGE:3857366 5'
11317	24380	38025	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11317	24380	38026	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11694	24692	38383	1.35	1.0E-106	BE257385.1	EST_HUMAN	601109219F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3349897 5'
11837	24826	38514	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11837	24826	38515	1.89	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12353	25048	32059	4.3	1.0E-106	AW410405.1	EST_HUMAN	fn05h11.1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:2861644 5'
12484	25338	32060	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918524 5'
12484	25338	32060	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3918524 5'
12717	25477		3.71	1.0E-106	BE865005.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
244	13468		4.52	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
276	13493		0.9	1.0E-107	X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
637	13822		1.03	1.0E-107	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
647	13832	28858	2.34	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-28 antigen mRNA, partial cds
838	14014	27086	1.02	1.0E-107	X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
908	14084	27149	1.38	1.0E-107	X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
991	14163	27223	6.71	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1307	14463	27531	1.08	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1600	14753	27836	3.81	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-388-a05 HT0540 Homo sapiens cDNA
1791	14940	28033	5.42	1.0E-107	AF138275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1887	15031	28138	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1887	15031	28139	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2282	16414	28546	3.77	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2435	15503	28691	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
2435	15503	28692	4.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29288	8.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3072	16248	29289	8.14	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-190100-001-d03 CN0031 Homo sapiens cDNA
3169	16344	29352	2.9	1.0E-107	5802087	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3931	17090	30087	4.89	1.0E-107	AF020871.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
5742	18935	32235	0.64	1.0E-107	AW686038.1	EST_HUMAN	EST381115 IMAGE resequences, MAGK Homo sapiens cDNA
5986	19171	32493	2.71	1.0E-107	BE887469.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849494 5'
7520	20593	34067	1.33	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BN0-aif-c-08-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7520	20593	34068	1.33	1.0E-107	AW503913.1	EST_HUMAN	U1HF-BN0-aif-c-08-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7688	20783	34247	1.36	1.0E-107	AW503978.1	EST_HUMAN	W556h04.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384791 3'
7909	20981	34467	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7909	20981	34468	0.59	1.0E-107	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
9587	22728	36299	0.99	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10880	23973	37604	1.92	1.0E-107	BE168726.1	EST_HUMAN	QV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA
10944	24028	37682	2.96	1.0E-107	AI92850.1	EST_HUMAN	1910d06.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
11189	24258	37894	1.58	1.0E-107	L49141.1	NT	P05095 ALPHA-ACTININ 3, NON MUSCULAR
11202	24271	37907	2.3	1.0E-107	BF688511.1	EST_HUMAN	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
11603	24656	38341	3.91	1.0E-107	BE94050.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11678	23604	37526	4.29	1.0E-107	11419701	NT	601096681F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11678	23904	37527	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12322	28100		7.14	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
13211	25760	31920	1.24	1.0E-107	BE798189.1	EST_HUMAN	2a45e01.s1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
977	14160	27210	1.72	1.0E-108	BE296042.1	EST_HUMAN	THR repetitive element
1294	14450	27515	2.41	1.0E-108	Y18000.1	NT	601582652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937188 5'
2140	15276	28398	1.02	1.0E-108	BF026728.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
2407	15538	28665	12.11	1.0E-108	AI686040.1	EST_HUMAN	Homo sapiens NF2 gene
2407	15538	28668	12.11	1.0E-108	AI686040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2499	15626	28746	11.96	1.0E-108	BE206694.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3025	16201	29224	0.84	1.0E-108	6005979	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3430	16598	29614	0.64	1.0E-108	AF032897.1	NT	1891e10.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248938 3' similar to qb:M14219 BONE
3430	16598	29615	0.64	1.0E-108	AF032897.1	NT	PROTEOLYCAN II PRECURSOR (HUMAN);
							1891e10.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248938 3' similar to qb:M14219 BONE
							PROTEOLYCAN II PRECURSOR (HUMAN);
							bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S
							RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
							Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
							Homo sapiens potassium channel subunit 1 (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit 1 (HERG-3) mRNA, complete cds

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4273	17418	30408	1.57	1.0E-108	AW664438.1	EST_HUMAN	h12a11.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW:3BP1_MOUSE
4847	17783	30765	2.62	1.0E-108	U72961.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1;
4847	17783	30768	2.62	1.0E-108	U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4927	18057	31040	3.37	1.0E-108	7681979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
5037	18165	31141	0.63	1.0E-108	AW504799.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5063	18181	31166	3.18	1.0E-108	AJ008003.1	NT	UJHF-BNC-ah-e-04-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
5598	18791	31839	1.24	1.0E-108	AJ008003.1	NT	Homo sapiens PSN1 gene, alternative transcript
5844	18838	31916	2.56	1.0E-108	BE869016.1	EST_HUMAN	RCO-HT0372-241199-031-c03 HT0372 Homo sapiens cDNA
5844	18838	31917	2.56	1.0E-108	BE869016.1	EST_HUMAN	RCO-HT0372-241199-031-c03 HT0372 Homo sapiens cDNA
6049	19232	32644	0.66	1.0E-108	AF012623.1	NT	601444922F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3848980 5'
6125	19304	32644	0.74	1.0E-108	BF334851.1	EST_HUMAN	601444922F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3848980 5'
6287	19441	32789	6.14	1.0E-108	AF264717.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6287	19441	32790	6.14	1.0E-108	AF264717.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6392	19591	32821	1.22	1.0E-108	AJ133269.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6489	19304	32844	1.09	1.0E-108	BF334851.1	EST_HUMAN	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6753	19909	33302	0.84	1.0E-108	AF016706.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6753	19909	33303	0.84	1.0E-108	AF016706.1	NT	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
7308	20390	33850	4.52	1.0E-108	11431857	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7597	20687	34143	2.12	1.0E-108	4768333	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7646	20715	34193	1.32	1.0E-108	BE252607.1	EST_HUMAN	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7674	20739	34218	0.73	1.0E-108	BF528912.1	EST_HUMAN	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7674	20739	34219	0.73	1.0E-108	BF528912.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354084 5'
8264	21336	34910	1.72	1.0E-108	AF083500.1	NT	602043384F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181037 5'
8306	21388	34911	0.61	1.0E-108	AF083500.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181037 5'
8306	21388	34911	0.61	1.0E-108	AF083500.1	EST_HUMAN	602043384F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181037 5'
9247	22324	35989	0.77	1.0E-108	AF203977.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
9287	22363	35912	0.46	1.0E-108	NA4974.1	EST_HUMAN	UJHF-BMO-ads-e-12-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
10847	23880	37500	1.08	1.0E-108	11428165	NT	UJHF-BMO-ads-e-12-Q-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3082878 5'
							Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
							y33h10.r1 Scarsa melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR-A46773
							A45773 kalch protein, long form - fruit fly;
							Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10904	21037	34549	2.09	1.0E-108	BE53227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3443361 5'
11066	18501	31537	2.67	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11319	24382	38027	1.35	1.0E-108	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11549	24605	38283	3.46	1.0E-108	AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
11805	24658	38343	1.71	1.0E-108	AV708780.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAE03 5'
11805	24658	38344	1.71	1.0E-108	AV708780.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAE03 5'
11852	24731		2.77	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11698	15538	28665	2.99	1.0E-108	AI686040.1	EST_HUMAN	H81e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb.M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11698	15538	28666	2.99	1.0E-108	AI686040.1	EST_HUMAN	H81e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb.M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
11712	24752	38446	1.72	1.0E-108	D63539.1	NT	Homo sapiens COL4A8 gene for $\alpha 1(V)$ collagen, exon 23
12489	25344	32064	4.15	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12940	25618		5.09	1.0E-108	BF346356.1	EST_HUMAN	602016571F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4154297 5'
43	13281	26287	1.01	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-260400-079-D06 UM0077 Homo sapiens cDNA
68	13303	26328	1.17	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
225	13447	26475	3.34	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
235	13456	26482	2.77	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
479	13674	28705	2.28	1.0E-109	4507712	NT	Homo sapiens tetratricopeptide repeat domain 2 (TTC2), mRNA
611	13800	26820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
611	13800	26821	14.77	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1037	14205	27262	1.62	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1229	14389	27451	8.5	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1230	14389	27451	6.38	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1573	14728	27808	0.99	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1573	14728	27807	0.99	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959636 5'
1923	15066	28170	2.3	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2314	15446	28580	5.46	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2326	15457	28589	3.65	1.0E-109	Y17123.1	NT	Homo sapiens SNF3/NIN1 gene, exon 6
2687	15907	28923	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN, ;
2687	15907	28924	19.35	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:1654538 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN, ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2688	15808	28925	2.68	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3126	16301	26314	3.37	1.0E-109	N65190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC
3475	16842	29881	2.08	1.0E-109	AW893192.1	EST_HUMAN	FINGER PROTEIN HNF43
3475	16842	29682	2.08	1.0E-109	AW893192.1	EST_HUMAN	GM3-NN0009-180400-150-f10 NN0009 Homo sapiens cDNA
3506	16770	29785	1.1	1.0E-109	AF240698.1	NT	GM3-NN0009-180400-150-f10 NN0009 Homo sapiens cDNA
3945	17104		1.31	1.0E-109	BE146144.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
4264	17409	30395	4.35	1.0E-109	AI655417.1	EST_HUMAN	MRD-HT0209-110400-108-a04 HT0209 Homo sapiens cDNA
4824	17663	30690	2.67	1.0E-109	4504208	NT	ts98e06.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP.F63A2.8
4722	17857	30839	1.7	1.0E-109	7682083	EST_HUMAN	CE16100
5165	18287	31282	0.72	1.0E-109	BE293673.1	EST_HUMAN	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
5165	18287	31253	0.72	1.0E-109	BE293673.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377) mRNA
5381	18584	31440	0.67	1.0E-109	AU137292	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5374	18677	31445	0.92	1.0E-109	BF073718.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5428	18828	31604	2.92	1.0E-109	5174622	NT	AU137292 PLACE1 Homo sapiens cDNA clone PLACE1006169 5'
5724	18917		1.23	1.0E-109	BE179358.1	EST_HUMAN	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
6060	18817	32556	1.23	1.0E-109	BF379688.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6119	18817		1.41	1.0E-109	BE179358.1	EST_HUMAN	RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA
6721	18878	33269	0.85	1.0E-109	AI221385.1	EST_HUMAN	GM1-UT0038-060900-399-h07 UT0038 Homo sapiens cDNA
6907	20222	33651	0.69	1.0E-109	11024711	NT	RC1-HT0615-200400-022-004 HT0615 Homo sapiens cDNA
6907	20222	33652	0.69	1.0E-109	11024711	NT	qg86h03.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
7389	20467	33933	0.67	1.0E-109	AB046811.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7738	20769	34288	3.76	1.0E-109	11432574	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7740	20801	34290	4.91	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens mRNA for KIAA1691 protein, partial cds
7740	20801	34291	4.91	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8368	21447	34970	1.35	1.0E-109	AL049784.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8480	21561	35096	1.39	1.0E-109	AW749130.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8857	21836		2.84	1.0E-109	AA077498.1	EST_HUMAN	Novel human gene mapping to chromosome 13
8932	22011	35549	4.36	1.0E-109	BE787540.1	EST_HUMAN	PMO-BT0340-091298-002-e05 BT0340 Homo sapiens cDNA
9392	22011	35550	4.36	1.0E-109	BE787540.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
9177	22256	35787	0.57	1.0E-109	BE145672.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
9439	22513	36077	1.66	1.0E-109	H84860.1	EST_HUMAN	601479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
							IL0-HT0205-071198-142-p01 HT0205 Homo sapiens cDNA
							ye80g08.r1 Scores retina N255HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP.A63491
							A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9650	22815	36184	0.64	1.0E-109	BE397088.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9650	22815	36185	0.64	1.0E-109	BE397088.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9685	22734	36304	1.37	1.0E-109	F06804.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone c-10012
11013	24082	37730	1.8	1.0E-109	BE540909.1	EST_HUMAN	601083030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11013	24082	37731	1.8	1.0E-109	BE540909.1	EST_HUMAN	601083030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11046	24123	37757	19.88	1.0E-109	BF694831.1	EST_HUMAN	602008724F2 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4245341 5'
11387	24448	38108	1.57	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002590 5'
11661	24730	38422	2.18	1.0E-109	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
11693	24681	38382	4.5	1.0E-109	W18610.1	EST_HUMAN	z608b12.r1 Soares fetal lung NBHL10W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S43969 S43969 p54-bata stress-activated protein kinases - rat;
11884	24872	38569	1.64	1.0E-109	BE045560.1	EST_HUMAN	h123105.x1 NCI CGAP LU24 Homo sapiens cDNA clone IMAGE:2955989 3' similar to TR:Q8Z124 Q8Z124
11948	24934	38636	1.5	1.0E-109	AL119824.1	EST_HUMAN	YGR163W MRNA HOMOLOGUE, COMPLETE CDS. ;
11984	24969	38673	1.31	1.0E-109	11418618	NT	DKFZp7611124.1 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611124 5'
12126	25106	38810	2.26	1.0E-109	AB007692.1	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12397	15437	28589	2.32	1.0E-109	Y17123.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
12636	15457	28589	3.2	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12762	25008	32036	8.36	1.0E-109	AB011399.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	13242	26242	1.4	1.0E-110	7549804	NT	Homo sapiens gene for AF-6, complete cds
36	13276	26281	3.96	1.0E-110	5803073	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
36	13276	26282	3.96	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
112	13242	26242	1.83	1.0E-110	7549804	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
305	13521	26555	1.31	1.0E-110	D87291.1	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
540	13733	26757	1.04	1.0E-110	U84550.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
1207	14369	27429	0.89	1.0E-110	5031620	NT	Human dystrobrevin (DTN) gene, exon 20
1308	14494	27532	1.02	1.0E-110	AB032283.1	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1973	15116	28217	1.51	1.0E-110	BE379477.1	EST_HUMAN	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
2118	15256		1.96	1.0E-110	BF508896.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2903	16081		7.19	1.0E-110	4503098	NT	UHH-B14-acs-b-05-0-U1 st NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
3166	16331		1.48	1.0E-110	U78027.1	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3264	16438	28457	2.66	1.0E-110	11436041	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3284	16438	28458	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4320	17463	30449	1.08	1.0E-110	M15918.1	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
						NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene

Page 463 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4768	17893	30872	2.04	1.0E-110	AI017213.1	EST_HUMAN	0332b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627863 3' similar to SW:NI21_RAT P52591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4777	17912	30887	3.01	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBAT Homo sapiens cDNA clone HEMBA1002241 5'
5083	18216		2.28	1.0E-110	7692441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5409	18611	31583	2.23	1.0E-110	BE299408.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028638 5'
5843	19033	32339	0.78	1.0E-110	BE621096.1	EST_HUMAN	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895785 5'
5860	19060	32368	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5860	19060	32357	8.61	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6858	20835	33421	5.43	1.0E-110	M55112.1	NT	Human cytic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7179	20311	33754	0.59	1.0E-110	BE251496.1	EST_HUMAN	601106388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7251	20334	33782	0.88	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7251	20334	33783	0.85	1.0E-110	U08888.1	NT	Human GS2 gene, exon 2
7477	20552	34026	0.78	1.0E-110	AI560289.1	EST_HUMAN	bt12408.x1 NCI_CGAP Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN P50646 ETS TRANSLOCATION VARIANT 1 ;
7583	20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7583	20655	34132	16.18	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7613	20683	34169	2.87	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
7743	20804	34283	0.86	1.0E-110	AU137823.1	EST_HUMAN	AU137823 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9536	22601	36174	1.09	1.0E-110	BE302694.1	EST_HUMAN	ba6801.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805561 5' similar to TR:O77268 O77268 EG:114D9.2 PROTEIN. ;
9777	22817	36395	2.46	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-020400-119-e04 LT0053 Homo sapiens cDNA
10529	23564	37171	3.38	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10986	24065	37700	3.2	1.0E-110	Y12337.1	NT	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
11209	24278	37816	3.64	1.0E-110	BE734357.1	EST_HUMAN	601665604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11209	24278	37817	3.64	1.0E-110	BE734357.1	EST_HUMAN	601665604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11608	24661	38347	1.89	1.0E-110	M10051.1	NT	Human Insulin receptor mRNA, complete cds
11728	23914	37639	1.7	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781288 5' similar to TR:G1145816 G1145816 FKBP54 ;
12211	25164		2.47	1.0E-110	BE897218.1	EST_HUMAN	601439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12341	25246		2.86	1.0E-110	AW062388.1	EST_HUMAN	IL0-BT0163-040869-094-g10 BT0163 Homo sapiens cDNA
12594	25400		2.98	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
12746	26113		6.01	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140600-006-f12 NN1082 Homo sapiens cDNA
13071	15256		1.18	1.0E-110	BF608806.1	EST_HUMAN	UI-H-B14-aes-b-05-0-U1.31 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
179	13402		11.92	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
201	13424	28455	1.64	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
753	13934		1.99	1.0E-111	BF05327.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
762	13943	26989	4.13	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
850	14123	27185	2.5	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
4286	17431	30419	1.15	1.0E-111	7861569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4449	17589	30570	4.59	1.0E-111	K02268.1	NT	Human enkephalin B (enkeB) gene, exon 4 and 3' flank and complete cds
5593	18788	31835	0.75	1.0E-111	AA151017.1	EST_HUMAN	Z47607.1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5593	18788	31836	0.75	1.0E-111	AA151017.1	EST_HUMAN	gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5749	18941	32242	0.88	1.0E-111	BE867909.1	EST_HUMAN	gb:M23575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5852	19052	32359	0.66	1.0E-111	U19969.1	NT	Human two-handed zinc finger protein ZEB mRNA, partial cds
6156	19332	32678	2.09	1.0E-111	A1344679.1	EST_HUMAN	qp09g12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS-RELATED PROTEIN RAL-A (HUMAN);
6818	19871	33379	0.96	1.0E-111	AL040762.1	EST_HUMAN	DKFZp434C1815.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1815 5'
6945	20258	33697	1.31	1.0E-111	AW294648.1	EST_HUMAN	U1-H-BW0-ail-d-03-Q-UJ st NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729535 3'
7605	20675	34149	3.04	1.0E-111	BF368228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7704	20769	34254	0.7	1.0E-111	AI761228.1	EST_HUMAN	w168401.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIA5 (HUMAN);
7791	20847	34340	0.83	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8286	21388	34986	0.8	1.0E-111	AA278588.1	EST_HUMAN	z579g03.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR, ;
8286	21388	34989	0.8	1.0E-111	AA278588.1	EST_HUMAN	z579g03.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR, ;
8383	21464	34989	0.63	1.0E-111	11431896	NT	Homo sapiens protein x 0001 (LOC51185), mRNA
8435	21516	35047	3.58	1.0E-111	U66533.1	NT	Human beta2-integrin (ITGB2) gene, exon 13
8878	21957	35492	0.96	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8975	22054	35597	0.64	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9008	22087	35708	8.43	1.0E-111	BF214902.1	EST_HUMAN	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9085	22164	35709	15.93	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9289	22365	35914	3.37	1.0E-111	AF091395.1	NT	Human mRNA for Trf isoform mRNA, complete cds
9518	22583	36152	0.54	1.0E-111	BF333210.1	EST_HUMAN	Homo sapiens Trf isoform mRNA, complete cds
9518	22583	36152	0.54	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-e06 BT0817 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10355	23390	37000	1.56	1.0E-111	AA504160.1	EST_HUMAN	ae58g02.e1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235
10393	23418		1.04	1.0E-111	D10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10479	23514	37127	5.58	1.0E-111	AA131248.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10895	24074	37707	1.34	1.0E-111	AW298467.1	EST_HUMAN	23101.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:903645 5'
11299	24365	38008	3.29	1.0E-111	U68159.1	NT	UI-H-BW0-alc-d-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730278 3'
12187	25130	38828	4.07	1.0E-111	1141790.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12741	25492	32028	4.72	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12881	25888	31866	4.82	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08 5'
13041	18504	31539	1.27	1.0E-111	AB035356.1	NT	72C8 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
623	13808	26829	2.77	1.0E-112	4501864	NT	Homo sapiens mRNA for neuronin -alpha protein, complete cds
628	13810	26831	4.84	1.0E-112	U29103.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Human embryonic acute regulatory protein (SAR) gene, exon 5
649	13834	26860	1.82	1.0E-112	BF509038.1	EST_HUMAN	Human steroidogenic acute regulatory protein (SAR) gene, exon 5
649	13834	26861	1.82	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-act-q-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1026	14187	27255	33.06	1.0E-112	AF157623.1	NT	UI-H-B14-act-q-04-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1087	14253	27308	1.49	1.0E-112	P92742	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1718	14868	27658	7.1	1.0E-112	7662125	NT	ZINC FINGER PROTEIN 135
1718	14868	27659	7.1	1.0E-112	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1863	15009	28115	1.11	1.0E-112	AF248540.1	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2577	15703	26823	2.83	1.0E-112	BE868859.1	EST_HUMAN	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
3147	16323		0.76	1.0E-112	4504116	NT	601442674F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3846858 5'
3444	16612	28630	0.61	1.0E-112	AI826511.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3990	17147	30153	0.63	1.0E-112	BE076073.1	EST_HUMAN	wk45b12.x1 NCI_CGAP_Py22 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gb:M81850_mn1
4726	17861	30843	0.68	1.0E-112	4504116	NT	SEMNOCGELIN 1 PROTEIN PRECURSOR (HUMAN);
4875	18007	30690	5.87	1.0E-112	AB037832.1	NT	MR2-BT0590-090300-113-09 BT0590 Homo sapiens cDNA
4875	18007	30690	5.87	1.0E-112	AB037832.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4875	18007	30691	5.87	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5784	19976	32282	36.7	1.0E-112	N46046.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
6201	19376	32727	1.33	1.0E-112	AF146773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6273	19447	32795	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajls-q-06-0-UI.f1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6273	19447	32796	0.66	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajls-q-06-0-UI.f1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6378	19548	32804	0.93	1.0E-112	BE741666.1	EST_HUMAN	UI-HF-BR0p-ajls-q-06-0-UI.f1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3948557 5'
6568	19749	33102	0.7	1.0E-112	BF672815.1	EST_HUMAN	501594717F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283420 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6773	19928	33323	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505508 5'
6773	19928	33324	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505508 5'
6981	20209	33637	1.51	1.0E-112	BE574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7305	20387	33847	0.68	1.0E-112	AL043299.1	EST_HUMAN	DKFZp434M0523_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434M0523 5'
7491	20566	34037	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7491	20566	34038	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8387	21468	34995	1.79	1.0E-112	AU118051.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
9158	22236	35781	2.64	1.0E-112	BE867835.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9158	22236	35782	2.64	1.0E-112	BE867835.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10097	23135	36736	2.37	1.0E-112	BF111413.1	EST_HUMAN	7130g07.x1 Soares_NSF_F8_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW35 Q9VW35 CG8743 PROTEIN. ;
11017	24086	37735	16.73	1.0E-112	AW663327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
11103	24175	37810	1.31	1.0E-112	T83967.1	EST_HUMAN	Yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11103	24175	37811	1.31	1.0E-112	T83967.1	EST_HUMAN	Yd56d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11191	24260	37896	3.14	1.0E-112	AJ249800.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11389	24421	38077	2.24	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11428	24489	38153	2.28	1.0E-112	AJ792603.1	EST_HUMAN	qk24c08.y4 NCL_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11428	24489	38154	2.28	1.0E-112	AJ792603.1	EST_HUMAN	qk24c08.y4 NCL_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
11460	24519	38188	4.78	1.0E-112	AW377670.1	EST_HUMAN	PMO-CT0237-141098-001-H02 CT0237 Homo sapiens cDNA
12086	25076	38783	1.66	1.0E-112	AJ792603.1	EST_HUMAN	qk24c08.y4 NCL_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12086	25076	38784	1.66	1.0E-112	AJ792603.1	EST_HUMAN	qk24c08.y4 NCL_CGAP_Ki43 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR:Q64362 Q64362 FUSED TOES ;
12727	25484		1.31	1.0E-112	AF106866.1	NT	Homo sapiens adenylocuccinate lyase gene, complete cds
761	13942	26987	6.82	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
761	13942	26988	6.82	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
965	14138	27199	2.93	1.0E-113	M11955.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1572	14725	27805	3.23	1.0E-113	AJ365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1893	18934	28240	1.83	1.0E-113	AF240776.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2161	18287	28422	1.49	1.0E-113	BF515218.1	EST_HUMAN	UIH-BW1-ant-f03-q-UI-st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082878 3'
3200	18375	29386	2.09	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5178	18300	31263	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5178	18300	31264	36.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5359	28930		2.4	1.0E-113	BE780858.1	EST_HUMAN	601468485F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872536 5'
6610	18805	31870	6.37	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6045	19228	32562	3.84	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6072	19254	32583	1.02	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6195	19371	32722	2.57	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T8) (GALNT8), mRNA
6285	19458	32809	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32810	0.8	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6446	19613	32976	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6446	19613	32977	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7474	20549	34021	0.63	1.0E-113	BE262161.1	EST_HUMAN	601162078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
7474	20549	34022	0.63	1.0E-113	BE262161.1	EST_HUMAN	601162078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508382 5'
9093	22172	35717	0.5	1.0E-113	8922819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9286	23372	35921	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627954 5'
9286	23372	35922	2.91	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627954 5'
9601	22668		0.52	1.0E-113	BE172967.1	EST_HUMAN	RC1-FT0134-280600-021-d02 FT0134 Homo sapiens cDNA
10036	23074	36674	1.27	1.0E-113	11428367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10256	23281	36888	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10256	23281	36889	1.01	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10842	23878	37486	0.47	1.0E-113	AW500517.1	EST_HUMAN	UI-HF-BND-ak-b-12-q-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11385	24446	38107	1.89	1.0E-113	AW500519.1	EST_HUMAN	UI-HF-BND-ak-b-12-q-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077323 5'
11396	24457	38119	5.42	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.yt NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868176 5' similar to TR:O60327 O60327
11396	24457	38120	6.42	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.yt NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868176 5' similar to TR:O60327 O60327
11640	24596	38272	2.91	1.0E-113	BE202068.1	EST_HUMAN	KIAA0584 PROTEIN;
59	13297	26314	0.76	1.0E-114	Y117151.2	NT	KIAA0584 PROTEIN;
							Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)

Page 458 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
59	13297	26315	0.76	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
59	13297	26310	0.75	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
662	13848	26876	7.46	1.0E-114	T70551.1	EST_HUMAN	Yd15c01.31 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element
1098	14261	27318	2.54	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1341	14497	27569	4.65	1.0E-114	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1673	14825	27909	1.9	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1706	14858	27945	5.08	1.0E-114	6679073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2145	15281	28408	2.52	1.0E-114	BE171984.1	EST_HUMAN	WFO-HT0559-250200-002-407 HT0559 Homo sapiens cDNA
2330	15462	28595	0.99	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds
2655	13283	26291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2865	13283	26291	0.6	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3201	16376	29388	2.6	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3240	16414	29429	1.03	1.0E-114	BF206374.1	EST_HUMAN	60186932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4124	17278	30278	3.27	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4510	17849	30637	0.7	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
5282	18401	31370	1.1	1.0E-114	AW294203.1	EST_HUMAN	UI-H-B12-aho-d-01-O-U1.s1 NCI_CGAP Sub4 Homo sapiens cDNA clone IMAGE:2726424 3'
5616	18714	31727	1.68	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) SA (SEMASA) mRNA
5516	18714	31728	1.88	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) SA (SEMASA) mRNA
5712	18805	32200	0.9	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTGL1), transcript variant 2, mRNA
7224	20088		0.71	1.0E-114	AB041533.1	NT	Homo sapiens HCMOG T-1 mRNA for sperm antigen, complete cds
7388	20466	33931	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7388	20466	33932	1.09	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7434	20511	33983	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7434	20511	33984	8.2	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
8075	21137	34673	1.94	1.0E-114	4557800	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8360	21431	34963	1.85	1.0E-114	AI803139.1	EST_HUMAN	qy68406.x1 NCI_CGAP Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8380	21441	34964	1.85	1.0E-114	AI363139.1	EST_HUMAN	qy68406.x1 NCI_CGAP Bm25 Homo sapiens cDNA clone IMAGE:2017163 3'
8898	21977	35516	2.99	1.0E-114	U83041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
8968	22045	35589	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8968	22045	35590	5.81	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds

Page 459 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9384	22459	36022	0.87	1.0E-114	BF109832.1	EST_HUMAN	7189g12.x1 Sources_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q8UJH9 Q8UJH9 TRANSMEMBRANE PROTEIN 2.
9614	22669		1.3	1.0E-114	AW327465.1	EST_HUMAN	dc03605.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 6'
9602	21104	34621	2.67	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9748	22812		1.36	1.0E-114	M13538.1	NT	Human ceruloplasmin mRNA
10343	23378	36989	1.02	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10384	23399	37010	1.11	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10762	23795	37415	1.18	1.0E-114	BE171984.1	EST_HUMAN	MRO-HT0859-260200-002-407 HT0859 Homo sapiens cDNA
11027	24108		4.31	1.0E-114	BE302968.1	EST_HUMAN	bat73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse L1 Rep3 protein mRNA from a repetitive element, complete (MOUSE);
11466	24525	38197	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11466	24525	38198	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 6'
11842	24631	38522	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11842	24631	38523	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12843	26187		4.63	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12936	25616	31975	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12936	25616	31976	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13262	26264	3.06	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
132	13358	26391	1.09	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A) mRNA
136	13362		18.42	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
303	13519	26552	2.02	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-F08 UM0094 Homo sapiens cDNA
549	13742	26766	1.68	1.0E-115	AI339206.1	EST_HUMAN	q106801.x1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR:O00538 O00538, TTF-1 INTERACTING PEPTIDE 5;
549	13742	26767	1.68	1.0E-115	AI339206.1	EST_HUMAN	q106801.x1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR:O00538 O00538, TTF-1 INTERACTING PEPTIDE 5;
809	13988	27041	3	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
809	13988	27042	3	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
811	13990	27044	15.24	1.0E-115	4603784	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1590	14742	27823	1.15	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1590	14742	27824	1.15	1.0E-115	AF229180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1888	15032	28140	1.31	1.0E-116	U78027.1	NT	Homo sapiens Brubn's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2142	15278	28400	1.13	1.0E-115	BE745468.1	EST_HUMAN	60167838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'

Page 460 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2142	15278	28401	1.13	1.0E-115	BE745469.1	EST_HUMAN	60157938F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928832 5'
2150	15286	28411	1.1	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2374	15505	28631	1.11	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2912	16080		1.03	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-155-508 UM0094 Homo sapiens cDNA
3184	16359	29365	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3184	16359	29366	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3561	16726	29742	1.8	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4153	17305	30299	4.2	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4821	17660	30647	2.49	1.0E-115	6912659	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4857	17695	30674	4.28	1.0E-115	4786279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
4797	17932	30918	2.86	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4797	17932	30919	2.86	1.0E-115	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5028	18155	31132	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5026	18155	31133	2.99	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5044	18172	31149	1.01	1.0E-115	Y19215.1	NT	Homo sapiens putative psbHbC pseudogene for hair keratin, exons 1 to 9
5304	18421	31391	1.23	1.0E-115	4504688	NT	Homo sapiens interleukin 1 receptor, type I (IL-1R) mRNA
5347	18460	31425	0.92	1.0E-115	AB018311.1	NT	Homo sapiens mRNA for KIAA0768 protein, partial cds
5463	18663	31642	2.8	1.0E-115	AW970335.1	EST_HUMAN	EST382418 IMAGE resequences, MAGK Homo sapiens cDNA
5540	18737	31754	0.97	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4276738 5'
5659	18853	32139	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5659	18853	32137	1.74	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5808	18998	32304	1.15	1.0E-115	AI928799.1	EST_HUMAN	eu84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07802
5808	18998	32305	1.15	1.0E-115	AI928799.1	EST_HUMAN	eu84g01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:L07802
6391	19560	32919	0.68	1.0E-115	11426786	NT	DYNAMIN-1 (HUMAN);
6391	19560	32920	0.88	1.0E-115	11426786	NT	Homo sapiens sperm surface protein (HSS), mRNA
6525	19690	33094	9.49	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63436), mRNA
6558	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
6558	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
7074	20127	33543	0.75	1.0E-115	T88774.1	EST_HUMAN	yd86b08.t1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP-DPOG YEAST P15801 DNA POLYMERASE GAMMA
7428	20505	33975	1.24	1.0E-115	AI076598.1	EST_HUMAN	oz21a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7428	20505	33976	1.24	1.0E-115	AI076598.1	EST_HUMAN	oz21a06.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descrip
7246	20329	33775	1	1.0E-118	AL043781.1	EST_HUMAN	DKFZp434O0127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127 5'
7778	20833	34324	4.7	1.0E-118	11491050	NT	Homo sapiens chromosome 2 open reading frame 3 (C3ORF3), mRNA
7760	20846	34339	0.72	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cdo
8159	21241	34781	1.95	1.0E-118	BE781223.1	EST_HUMAN	601469159F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8577	21658	35198	7	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0283-080200-097-h03 BT0283 Homo sapiens cDNA
8577	21668	35199	7	1.0E-118	BE062856.1	EST_HUMAN	QV0-BT0283-080200-097-h03 BT0283 Homo sapiens cDNA
8583	21684	35204	1.1	1.0E-118	AA443024.1	EST_HUMAN	z88d07_r1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8583	21684	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	z88d07_r1 Scores_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8873	21952	35488	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	21952	35489	0.94	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8918	21997	35536	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8918	21997	35537	1.94	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:31760302 5'
9268	22343	35894	0.56	1.0E-118	AL049474.2	EST_HUMAN	DKFZp586K1824_r1 886 (synonym: huler1) Homo sapiens cDNA clone DKFZp586K1824
8782	22532	36411	1.07	1.0E-118	7687018	NT	Homo sapiens hypothetical protein (DJ328519.G1.1), mRNA
10541	23578	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641803 5'
10541	23578	37186	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641803 5'
10585	23621	37228	1.75	1.0E-118	BF195407.1	EST_HUMAN	7n17608.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3564785 3' similar to SW:ZP3A_HUMAN
10752	23785	37369	0.59	1.0E-118	AW296351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
11555	24610	38290	3.75	1.0E-118	AA315007.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to clyne, light chain 1, cytoplasmic
11855	24843	38539	2.92	1.0E-118	BE908878.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11855	24843	38540	2.92	1.0E-118	BE908878.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
12071	25052	38761	1.81	1.0E-118	BE218235.1	EST_HUMAN	iv36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q8Z2H4
776	13956	27007	2.46	1.0E-119	AF170492.1	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGRA.1 ;
1062	16028	27284	0.93	1.0E-118	7709607	NT	Homo sapiens chloride channel CLCA4 (CLCA4) mRNA, complete cds
1987	15128	28232	2.98	1.0E-119	AB023147.1	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
3171	16348	28353	1.01	1.0E-118	8922205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3312	18485		2.17	1.0E-118	AA918760.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
4083	17219	30227	1.22	1.0E-119	4504116	NT	on1005.a1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WIP:E04F6.2
5453	18553	31632	3.96	1.0E-119	AU133399.1	EST_HUMAN	CE01214 ;
							Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
							AU133399 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'

Page 466 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6468	18668	31645	16.48	1.0E-119	M89914.1	NT	Human neurofibronin (NF1) gene, complete cds
5470	18670	31650	3.28	1.0E-119	BE636121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5550	18747	31782	1.61	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GKCH Homo sapiens cDNA clone GKCDH803 5'
5707	18800	32194	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
5707	18800	32195	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762M0710 5'
6255	19429	32775	6.7	1.0E-119	AI150703.1	EST_HUMAN	qb77c09.x1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:KTCJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10
6414	19883	32944	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6414	19883	32945	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6461	19828	32989	1.22	1.0E-119	AI476732.1	EST_HUMAN	hm23f10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6589	19750	33133	2.39	1.0E-119	X06292.1	NT	Human c-fos/pro proto-oncogene
6801	19761	33149	4.01	1.0E-119	AW974193.1	EST_HUMAN	EST386296 IMAGE resequences, MAGM Homo sapiens cDNA
7588	20640	34116	1.09	1.0E-119	BE796614.1	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8882	21941	35476	0.93	1.0E-119	BE615150.1	EST_HUMAN	601280584F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622526 5'
9957	22966	36592	0.46	1.0E-119	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
10111	23149	36750	0.96	1.0E-119	11036643	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10311	23348	36952	0.61	1.0E-119	AI149796.1	EST_HUMAN	qf43a11.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1752784 3' similar to TR:Q13458
10482	23487	37095	2.29	1.0E-119	AA465124.1	EST_HUMAN	Q13458 GUANINE NUCLEOTIDE EXCHANGE FACTOR PROTEIN TRIO.1
10722	23755	37361	1.13	1.0E-119	AJ297701.1	NT	aa32105.71 NCL CGAP_GCBT Homo sapiens cDNA clone IMAGE:814977 5'
10766	23799	37420	0.77	1.0E-119	11425837	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10768	23799	37421	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10844	23877	37497	0.59	1.0E-119	BE561987.1	EST_HUMAN	601347190F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 5'
10849	23882	37502	0.73	1.0E-119	AB032261.1	NT	Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds
11308	24373	38015	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11308	24373	38016	1.58	1.0E-119	AJ297701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11478	24538		6.62	1.0E-119	BF569571.1	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12490	26098		5.48	1.0E-119	AW847519.1	EST_HUMAN	RC3-CT0212-240999-011-05 CT0212 Homo sapiens cDNA
12845	25982		3.03	1.0E-119	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
247	13468	28500	0.68	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
312	13528	28661	0.97	1.0E-120	4507334	NT	Homo sapiens synaplepinin 1 (SYNJ1), mRNA
1066	14232	27280	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1066	14232	27291	2.74	1.0E-120	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1456	14809	27689	3.26	1.0E-120	N44873.1	EST_HUMAN	iy40g12.1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273766 5'

Page 467 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1831	14783	27868	11.19	1.0E-120	AF167708.1	NT	Homo sapiens cytochrome-rich repeat-containing protein S62 precursor, mRNA, complete cds
1849	14996	28098	8.58	1.0E-120	4657250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2174	15309	28437	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2174	15309	28438	1.83	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
3382	13528	26561	1.61	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4477	17617	30598	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4477	17617	30599	2.05	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4784	17619	30606	3.11	1.0E-120	AF068463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
4784	17619	30607	3.11	1.0E-120	AF068463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5853	19043	32349	16.08	1.0E-120	BF668222.1	EST_HUMAN	Homo sapiens gene for NF-M
5853	19043	32350	16.08	1.0E-120	BF668222.1	EST_HUMAN	Homo sapiens gene for NF-M
7146	20808	34286	1.84	1.0E-120	D34618.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
8078	21160	34677	1.36	1.0E-120	Y00087.1	NT	Human gene for neurofilament subunit M (NF-M)
8078	21160	34678	1.36	1.0E-120	Y00087.1	NT	Human gene for neurofilament subunit M (NF-M)
8527	21608	35147	2.31	1.0E-120	BF337699.1	EST_HUMAN	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21680	35218	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21680	35219	0.9	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8603	21684	35221	1.94	1.0E-120	AB007864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0465
8603	21684	35222	1.94	1.0E-120	AB007864.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0465
8647	21727	35284	1.31	1.0E-120	AB007834.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0465
9701	22750	36319	4.87	1.0E-120	BE392102.1	EST_HUMAN	Homo sapiens mRNA for KIAA0465 protein, partial cds
9701	22750	36320	4.87	1.0E-120	BE392102.1	EST_HUMAN	Homo sapiens mRNA for KIAA0465 protein, partial cds
9948	22885	36578	3.54	1.0E-120	BF306541.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3625544 5'
9948	22885	36578	3.54	1.0E-120	BF306541.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3625544 5'
9962	23001	36687	6.7	1.0E-120	AU133205.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4122878 5'
9979	23018	36612	1.02	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10086	23134	36912	0.55	1.0E-120	AB04151.1	EST_HUMAN	CM-BT043-080299-075 BT043 Homo sapiens cDNA
10281	23318	36918	3.4	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11391	24452	38115	8.68	1.0E-120	BE296387.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3532015 5'
11825	24705	38387	2.12	1.0E-120	BE867619.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3847281 5'
11825	24705	38388	2.12	1.0E-120	BE867619.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3847281 5'
12697	25436	32049	1.42	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
75	13311	26337	0.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
389	13595	26931	1.35	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACET1 Homo sapiens cDNA clone PLAGE1000899 5'
742	16020	26964	1.31	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

Page 468 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2023	15164	28269	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2023	15164	28270	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2189	15304	28431	1.22	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2843	15766	28880	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150286 5'
2843	15766	28881	1.07	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150286 5'
3150	16325	29336	5.8	1.0E-121	Y19208.1	NT	Homo sapiens HHb3 gene for hair keratin, exons 1 to 9
3150	16325	29337	5.8	1.0E-121	Y19208.1	NT	Homo sapiens HHb3 gene for hair keratin, exons 1 to 9
3626	16790	29807	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3626	16790	29808	1.23	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3768	16829	29834	8.25	1.0E-121	AF155158.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4450	17590	30571	1.76	1.0E-121	A1263294.1	EST_HUMAN	q57b01.x1 NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2005417 3'
5091	18219	31189	3.42	1.0E-121	X91937.1	NT	H. sapiens EOE-1 gene (exon 17)
5382	18594	31453	0.84	1.0E-121	BE222250.1	EST_HUMAN	Hu09f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5679	18873	32161	0.73	1.0E-121	BE271424.1	EST_HUMAN	60114048F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6757	19913	33308	0.64	1.0E-121	M91463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7028	20164	33483	0.96	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
7102	18529	31483	0.79	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-102 NN0066 Homo sapiens cDNA
7102	18529	31484	0.79	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-102 NN0066 Homo sapiens cDNA
8123	21203	34725	1.07	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8127	21209	34729	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
8127	21209	34730	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10062	23100	36702	1.02	1.0E-121	AW583858.1	EST_HUMAN	1a05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA;
10062	23100	36703	1.02	1.0E-121	AW583858.1	EST_HUMAN	1a05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA;
11015	24094	37733	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11023	24102	37740	1.94	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11211	24280	37919	5.74	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11243	24312	37950	1.93	1.0E-121	N59624.1	EST_HUMAN	yv74c01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:248448 3'
278	13496	26526	2.64	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
346	13557	26585	2.33	1.0E-122	AF114489.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds

Page 469 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26610	2.56	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
906	14080	27148	3.34	1.0E-122	AF114483.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1247	14406	27468	5.19	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa I)
1728	14878	27869	18.7	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14898	27895	1.81	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14898	27896	1.61	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1857	15003	28110	6.92	1.0E-122	BE906024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899368 5'
2560	15685	28810	7.43	1.0E-122	BF316170.1	EST_HUMAN	601866173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4125234 5'
2600	15885	28811	7.43	1.0E-122	BF316170.1	EST_HUMAN	601866173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2801	16080	29096	4.87	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4871	18100	31076	3.81	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5104	18232		1.41	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BN0-all-a-03-G-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5881	18875	32164	1.2	1.0E-122	BE266039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6896	19875	32164	6.8	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3354232 5'
7363	20442	33904	0.84	1.0E-122	AA868671.1	EST_HUMAN	alk49108.s1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1408339 3'
8996	22075	35614	0.6	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9228	22306	35849	1.17	1.0E-122	11424216	NT	Homo sapiens lethal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9524	22586	36159	0.96	1.0E-122	A1359618.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.
9524	22586	36160	0.96	1.0E-122	A1359618.1	EST_HUMAN	q32h07.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.
10338	23373	36983	0.64	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbi (proto-oncogene)
11233	24302	37839	2.12	1.0E-122	AW955834.1	EST_HUMAN	EST367804 MAGE sequences, MAGE Homo sapiens cDNA
11667	24744	38436	1.83	1.0E-122	AB024088.1	NT	Homo sapiens gene for B120, exon 10
12231	25178		5.28	1.0E-122	11418187	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II (PDK2B), mRNA
789	13968	27019	1.53	1.0E-123	BF346274.1	EST_HUMAN	602018058F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
789	13968	27020	1.53	1.0E-123	BF346274.1	EST_HUMAN	602018058F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1038	14208	27263	6.18	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1047	14213	27270	3.36	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1287	14424	27491	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PDK2B) mRNA, and translated products

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1267	14424	27492	3.83	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2035	15176	28286	0.94	1.0E-123	11422479	NT	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA
2166	15301	28427	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28429	3.21	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2389	15520		4.21	1.0E-123	7705992	NT	Homo sapiens RAB9-like protein (LOC31209), mRNA
3322	16495	29512	0.71	1.0E-123	6912617	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5563	18760	31769	1.82	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5563	18760	31800	1.82	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5569	18893	32185	1.76	1.0E-123	BE799748.1	EST_HUMAN	601591108F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3945433 5'
6598	19768	33146	1.93	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7143	20278	33718	0.91	1.0E-123	H53198.1	EST_HUMAN	Y84a03.11 Soares fetal liver spleen TINFLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7156	20290	33733	1.39	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7344	20424	33887	0.71	1.0E-123	U55258.1	NT	Human hBRAVONIN-CAM precursor (hBRAVONIN-CAM) gene, complete cds
7562	20634	34109	0.83	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7820	20875	34374	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7829	20884	34386	2.22	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:3509162 5'
7836	20891	34393	0.6	1.0E-123	11437202	NT	Homo sapiens hypothetical protein FLJ20184 (FLJ20184), mRNA
7076	21025	34538	0.6	1.0E-123	N35841.1	EST_HUMAN	Y89d11.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S48611
7975	21025	34539	0.6	1.0E-123	N35841.1	EST_HUMAN	S48611 protein kinase Pkpa - Phymocytes blastocyst; Y89d11.11 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S48611
8100	21182	34701	0.79	1.0E-123	AU131881.1	EST_HUMAN	S48611 protein kinase Pkpa - Phymocytes blastocyst; AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8100	21182	34702	0.79	1.0E-123	AU131881.1	EST_HUMAN	AU131881 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8732	21812		0.7	1.0E-123	AW371924.1	EST_HUMAN	RC4-B10311-251199-012-a07 B10311 Homo sapiens cDNA
9569	22111	36279	2.07	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9705	22734	36323	16.77	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
12020	25004	38705	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4250879 5'
12020	25004	38706	4.91	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4250879 5'
12114	25094	38798	2.71	1.0E-123	AW450931.1	EST_HUMAN	U1H-B13-all-10-0-U1.s1 NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'
12114	25094	38799	2.71	1.0E-123	AW450931.1	EST_HUMAN	U1H-B13-all-10-0-U1.s1 NCJ CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'

Page 471 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
279	13497	26927	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	13497	26928	1.02	1.0E-124	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
285	13503		1.49	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
488	13593	28723	2.28	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
709	13881	28928	4	1.0E-124	AA397551.1	EST_HUMAN	281504.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
709	13881	28927	4	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
777	13957	27008	3.72	1.0E-124	AF155054.1	NT	281504.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
831	14009	27086	2.06	1.0E-124	4507500	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
927	14102	27165	2.67	1.0E-124	7705448	NT	Human putative ribosomal protein S1 mRNA
1343	14489	27672	0.66	1.0E-124	11418092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1377	14532	27605	6.42	1.0E-124	AF274892.1	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1377	14532	27606	6.42	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1858	15004	28111	4.06	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2123	15269	28379	2.16	1.0E-124	BE876524.1	EST_HUMAN	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2628	15653	28777	0.98	1.0E-124	AB024089.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (noH81 gene)
3570	16744	29782	1.06	1.0E-124	S78694.1	NT	607497175F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3883954 5'
3739	16900	29904	1.24	1.0E-124	S78694.1	NT	Homo sapiens gene for B120, exon 11
4006	17163	30170	0.64	1.0E-124	X13794.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4179	17329	30321	0.69	1.0E-124	4504116	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4187	17337	30330	0.69	1.0E-124	4504116	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EG 1.1.27) (and joined CDS)
4866	17999	30983	2.51	1.0E-124	AB024089.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5050	18178		15.32	1.0E-124	M18178.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5205	18326	31298	0.74	1.0E-124	AW963390.1	EST_HUMAN	Homo sapiens gene for B120, exon 11
5412	18614	31598	10.48	1.0E-124	8922337	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5789	18881	32284	1.2	1.0E-124	4506786	NT	EST375463 MAGC resequences, MAGH Homo sapiens cDNA
6008	19183	32511	6.89	1.0E-124	BF586135.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6298	19471	32826	0.8	1.0E-124	AV711263.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
							60212464F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
							AV711263 Cu Homo sapiens cDNA clone CuAADF07 5'
6563	19725	33103	1.12	1.0E-124	11420854	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7162	20286	33728	3.15	1.0E-124	Y11717.1	NT	M.musculus mRNA for hoxa3 gene.
7287	20370	33824	0.94	1.0E-124	BE271296.1	EST_HUMAN	60094377F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:266385 5'

Page 472 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7287	20370	33825	0.04	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:2865685 5'
7725	20789	34278	2.38	1.0E-124	AA630331.1	EST_HUMAN	ac08105.s1 Stratagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:855897 3'
8453	21634	35064	2.73	1.0E-124	4506634	NT	Homo sapiens ribosomal protein L6 (RPL6) mRNA
8657	21737	35277	1.24	1.0E-124	AW612106.1	EST_HUMAN	hg04409.x1 NCI_CGAP_K1211 Homo sapiens cDNA clone IMAGE:2863240 3' similar to TR:O95162
8657	21737	35278	1.24	1.0E-124	AW612106.1	EST_HUMAN	hg04409.x1 NCI_CGAP_K1211 Homo sapiens cDNA clone IMAGE:2863240 3' similar to TR:O95162
9363	22438	35996	0.68	1.0E-124	AI769894.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9363	22438	35997	0.68	1.0E-124	AI769894.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9891	22740	36309	1.72	1.0E-124	AV645633.1	EST_HUMAN	hg04409.x1 NCI_CGAP_K1211 Homo sapiens cDNA clone IMAGE:2863240 3' similar to TR:O95162
9891	22740	36310	1.72	1.0E-124	AV645633.1	EST_HUMAN	hg04409.x1 NCI_CGAP_K1211 Homo sapiens cDNA clone IMAGE:2863240 3' similar to TR:O95162
9808	22848	36426	7.77	1.0E-124	AI767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
9808	22848	36427	7.77	1.0E-124	AI767133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
10075	23113	36717	1.46	1.0E-124	AW503755.1	EST_HUMAN	w03102.x1 NCI_CGAP_K1212 Homo sapiens cDNA clone IMAGE:2400891 3'
11302	24368	38009	1.57	1.0E-124	U94776.1	NT	w03102.x1 NCI_CGAP_K1212 Homo sapiens cDNA clone IMAGE:2400891 3'
11817	24688	38356	3.9	1.0E-124	AW665663.1	EST_HUMAN	UHF-BNO-42-b-04-D-U1.1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3078846 5'
11761	23947	37575	2.18	1.0E-124	AI446455.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11761	23947	37576	2.18	1.0E-124	AI446455.1	EST_HUMAN	h05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2860906 3'
12310	13891	28926	4.8	1.0E-124	AA397551.1	EST_HUMAN	YKRS PROTEIN. ;
12310	13891	28927	4.8	1.0E-124	AA397551.1	EST_HUMAN	YKRS PROTEIN. ;
12780	25522	32004	1.99	1.0E-124	AB028016.1	NT	YKRS PROTEIN. ;
13080	26038	31681	2.36	1.0E-124	11417862	NT	YKRS PROTEIN. ;
13080	26038	31681	2.36	1.0E-124	11417862	NT	YKRS PROTEIN. ;
328	13543	28239	4.69	1.0E-125	BE743922.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
439	13239	28239	4.69	1.0E-125	BE743922.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
661	13847	26874	2.02	1.0E-125	AI110656.1	EST_HUMAN	z81b04.r1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
661	13847	26875	2.02	1.0E-125	AI110656.1	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
746	13927	26868	2.42	1.0E-125	AF264750.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	601577981F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3926685 5'
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens ALR-like protein mRNA, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	gb-X65857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN).

Page 473 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1023	14194	27262	1.54	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1177	14340	27394	1.73	1.0E-125	7662278	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1707	18045	27946	1.44	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1864	15000	28106	5.91	1.0E-125	AF019450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1854	15000	28107	5.91	1.0E-125	AF019450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2433	15561	28687	4.81	1.0E-125	AA011278.1	EST_HUMAN	z01g0971 Scores_fetal_liver_spleen_1NF1_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2573	15698	28820	0.96	1.0E-125	AA042813.1	EST_HUMAN	z63c07.s1 Scores_pregnant_uterus_NhrPU Homo sapiens cDNA clone IMAGE:488540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2681	15783	28898	2.34	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH4) mRNA
2681	15783	28899	2.34	1.0E-125	4504696	NT	Homo sapiens inhibin, alpha (INH4) mRNA
3981	17119	30123	1.33	1.0E-125	AA042813.1	EST_HUMAN	z63c07.s1 Scores_pregnant_uterus_NhrPU Homo sapiens cDNA clone IMAGE:488540 3' similar to gb:X65857 cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4672	17807	30796	1.82	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4672	17807	30797	1.82	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4739	17874	30857	0.85	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140786 5'
5877	19067	32375	0.65	1.0E-125	BF683645.1	EST_HUMAN	602138874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
5884	19179	32501	1.39	1.0E-125	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8013	19187	32514	1.2	1.0E-125	BE175169.1	EST_HUMAN	QV2-HT0577-010500-165-506 HT0577 Homo sapiens cDNA
8054	19238	32561	3.53	1.0E-125	BE692660.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918892 5'
8098	19277	32606	0.85	1.0E-125	AI879804.1	EST_HUMAN	tu67c07.x1 NC1_CGAP_Gse4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:G45G9.2 CE01854;
8412	19581	32942	0.72	1.0E-125	BE735055.1	EST_HUMAN	601305970F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
8711	18869	33269	3.71	1.0E-125	BE5692526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688790 5'
8711	18869	33269	3.71	1.0E-125	BE5692526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688790 5'
7207	20072	33483	4.06	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7207	20072	33484	4.06	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7700	20765	34240	1.56	1.0E-125	BE276823.1	EST_HUMAN	601158078F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
7933	20883	34491	0.59	1.0E-126	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8743	21822	35357	1.49	1.0E-125	U90289.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8743	21822	35358	1.49	1.0E-125	U90289.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9316	22394	35945	4.15	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-312 HT0638 Homo sapiens cDNA
9318	22394	35946	4.15	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-312 HT0638 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9561	22723	36293	1.06	1.0E-125	AI566988.1	EST_HUMAN	tn52b03.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10670	23704	37313	0.72	1.0E-125	BE794576.1	EST_HUMAN	HYPOTHETICAL PROTEIN ;
10712	23745	37351	1.06	1.0E-125	AB002298.1	NT	607590345F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3944531 6'
10821	24004	37639	3.03	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds
11091	24165	37802	1.34	1.0E-125	11425570	NT	Homo sapiens LREL gene, exon 5
11357	24419	38076	2.42	1.0E-125	AL040655.1	EST_HUMAN	Homo sapiens ryanodine receptor 1 (skeletal) (RYR1), mRNA
11401	24462	38126	3.35	1.0E-125	AB014567.1	NT	DKFZp434N2414_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434N2414 5'
11538	24594	38303	1.63	1.0E-125	R61450.1	EST_HUMAN	Homo sapiens mRNA for KIAA0667 protein, partial cds
11568	24623	38303	2.13	1.0E-125	7689505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11676	24630	38309	5.32	1.0E-125	AF026026.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11686	24685	38376	2.27	1.0E-125	AW812699.1	EST_HUMAN	RC3-STD186-250200-078-c11 ST0186 Homo sapiens cDNA
11793	24783	38479	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11793	24783	38480	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
795	13874	27027	2.16	1.0E-126	4768007	NT	Homo sapiens CDC-like kinase (CLK), mRNA
798	13977	27030	1.74	1.0E-126	M61638.1	NT	Human laminin B1 chain gene, exon 20
942	14116	27175	1.53	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antichymotrypsin, exon 3
2663	15785	28900	4.55	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3140	16316	29329	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiotes pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3140	16316	29330	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.r1 Stratiotes pancreas (#937208) Homo sapiens cDNA clone IMAGE:592420 5'
3719	16860	29685	0.87	1.0E-126	X53941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3745	16906	29910	2.52	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4908	18038	31026	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4908	18038	31027	1.08	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4956	18086	31062	1.81	1.0E-126	N34078.1	EST_HUMAN	x78c06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:267850 5'
5820	19010	32316	0.68	1.0E-126	T68998.1	EST_HUMAN	ya52b12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66527 3'
6362	19532	32891	2.91	1.0E-126	AA460075.1	EST_HUMAN	z066e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:798444 5' similar to TR:G1145980 G1145980 TITIN ;
6416	19568	32951	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1625 protein, partial cds
6419	19588	32952	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1625 protein, partial cds
7669	20735	34212	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7669	20735	34213	0.9	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34662	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8062	21144	34663	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds

Page 475 of 550

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	21266	34781	2.42	1.0E-126	X15609.1	NT	Human mRNA for ankyrin (variant 2.1)
8377	21458	34982	0.8	1.0E-126	AA483388.1	EST_HUMAN	ne74b12.s1 NCL-OGAP_Ew1 Homo sapiens cDNA clone IMAGE:909883 similar to SW:TS06_HUMAN
10000	23038	36829	0.57	1.0E-128	4505424	NT	P58065 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
11089	24172	37807	2.01	1.0E-128	BF683175.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11806	24798	38484	2.2	1.0E-128	BE281680.1	EST_HUMAN	601149404F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288240 5'
12823	18500	31538	6.48	1.0E-128	BE743822.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
176	13400	26428	2.92	1.0E-127	AB024597.1	NT	601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926885 5'
176	13400	26430	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26428	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	26430	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	26535	2.14	1.0E-127	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
284	13502	26536	2.14	1.0E-127	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
904	14079	27146	1.17	1.0E-127	AF114498.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
939	14113	27174	4.81	1.0E-127	U72821.2	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
1726	14876	27987	2.22	1.0E-127	4827053	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
2127	15283	28382	1.97	1.0E-127	5803065	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2127	15283	28383	1.97	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2273	15406	28535	17.46	1.0E-127	4506620	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2418	15547	28678	3.12	1.0E-127	AF245505.1	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2674	15764	28911	21.46	1.0E-127	X12881.1	NT	Homo sapiens adican mRNA, complete cds
3781	16942	28948	0.61	1.0E-127	AF114498.1	NT	Human mRNA for cyclotactin 18
3913	17072	30070	0.7	1.0E-127	AW161297.1	EST_HUMAN	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
4232	17378	30368	0.59	1.0E-127	AF135188.1	NT	au00008.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN contains element MER22 repetitive element;
4368	17511	30491	24.93	1.0E-127	7706239	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4368	17511	30492	24.93	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4618	17755	30737	0.83	1.0E-127	AF262297.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4725	17860	30842	6.74	1.0E-127	4506384	NT	Homo sapiens cytochrome P450 reductase metabolizing protein P450RAL2 mRNA, complete cds
4755	17890		2.69	1.0E-127	AL163268.2	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4795	17930	30916	4.36	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5824	19014	32320	1.57	1.0E-127	W03547.1	EST_HUMAN	z01a10.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIP6_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5854	19044	32351	0.91	1.0E-127	4828863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5923	19110	32423	4.18	1.0E-127	X85764.1	NT	H sapiens NOS2 gene, exon 6
6291	19464	32816	2.23	1.0E-127	X84060.1	NT	H sapiens TCF11 gene, exon 3-6
6451	19618	32981	5.73	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6797	19952	33352	1.09	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7208	20073	33485	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7994	21014	34525	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7964	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7973	21023	34536	0.63	1.0E-127	BF671355.1	EST_HUMAN	6012151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
9088	22167	35713	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9088	22167	35714	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9840	22880	36462	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9840	22880	36463	3.73	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10077	23116	36718	0.86	1.0E-127	AI288932.1	EST_HUMAN	qm94h09.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1898449 3'
10551	23586	37194	0.99	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11426	24487	38150	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (hsc70-2) (H. sapiens) (LOC63184), mRNA
11426	24487	38151	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (hsc70-2) (H. sapiens) (LOC63184), mRNA
11927	24913	38614	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
11827	24913	38615	1.55	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
12539	13400	26428	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12539	13400	26430	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12763	25507	32037	1.74	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
13170	26044		1.64	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
472	13667	26700	1.56	1.0E-128	BE366817.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3918922 5'
1179	14342	27398	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1179	14342	27397	0.96	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2132	15268	28387	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2132	15268	28388	18.07	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2283	15415	28947	37.91	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2516	15642		1.11	1.0E-128	11497455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3481	16848	29664	1.17	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4786	17821	30909	7.27	1.0E-128	11426873	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5682	18856	32139	0.75	1.0E-128	X69539.1	NT	Homo sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6548	19710	33096	1.5	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7070	20123	33538	6.28	1.0E-128	BF224345.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8745	21824	35360	0.67	1.0E-128	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8745	21824	35361	0.67	1.0E-128	AB007923.1	NT	nc0411.1 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
10341	23376	36987	1.29	1.0E-128	AA630108.1	EST_HUMAN	CHIROMOSOME SEGREGATION GENE HOMOLOG CAS.:
10949	24031	37696	3.54	1.0E-128	11426254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
10957	24038	37673	3.51	1.0E-128	AA926959.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
11210	24278	37918	1.98	1.0E-128	BE887554.1	EST_HUMAN	om88108.s1 NCL CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X64941 CYCLIN
12402	25282		4.26	1.0E-128	AW955290.1	EST_HUMAN	DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
124	13621	25663	1.93	1.0E-128	S37722.1	NT	EST387360 MAGE resequences, MAGE Homo sapiens cDNA
428	13621	25663	1.65	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1755	14905	27999	3.74	1.0E-128	AL096880.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1761	14910	28004	1.66	1.0E-128	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1761	14910	28005	1.66	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
1894	15037	28145	4.07	1.0E-128	11418522	NT	genes, complete cds
2938	16652	29058	2.83	1.0E-128	4505682	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
2938	16652	29059	2.93	1.0E-128	4505682	NT	genes, complete cds
3198	16373	29380	1.43	1.0E-128	Q14585	SWISSPROT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3198	16373	29381	1.43	1.0E-128	Q14585	SWISSPROT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3198	16373	29382	1.43	1.0E-128	Q14585	SWISSPROT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
4278	17424	30413	2.37	1.0E-128	AB040892.1	NT	Homo sapiens platelet-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
4395	17538	30517	2.32	1.0E-128	AW766284.1	EST_HUMAN	ZINC FINGER PROTEIN HZF10
							ZINC FINGER PROTEIN HZF10
							ZINC FINGER PROTEIN HZF10
							Homo sapiens mRNA for KIAA1459 protein, partial cds
							CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
							Cardiomyopathy associated gene 5

Page 478 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4395	17338	30518	2.32	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
6216	18391	32739	3.77	1.0E-129	AJ006345.1	NT	Cardiomyopathy associated gene 5
6634	19813	33201	0.81	1.0E-129	BE88834.1	EST_HUMAN	Homo sapiens KVLQ11 gene
7277	20360	33814	3.88	1.0E-129	AJ006345.1	NT	801513891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7340	20420	33882	4.03	1.0E-129	11420850	NT	Homo sapiens KVLQ11 gene
7697	20762	34245	1.04	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
7697	20762	34246	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8513	21594	36920	3.57	1.0E-129	AB014534.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
10284	23319	36920	1.03	1.0E-129	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
10284	23319	36921	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37370	0.52	1.0E-129	A1189117.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37371	0.52	1.0E-129	A1189117.1	EST_HUMAN	q140408.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
11497	24555	38230	3.32	1.0E-129	AA625526.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
11578	20420	33882	5.01	1.0E-129	11420850	NT	MITOGEN INDUCIBLE GENE MIG-2;
12387	25273		4.28	1.0E-129	H83155.1	EST_HUMAN	q140408.x1 NCI_CGAP_Bim25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TR:Q14840 Q14840
12817	25544		1.97	1.0E-129	AL120739.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIG-2;
78	13314	26341	1.01	1.0E-130	7705530	NT	MITOGEN INDUCIBLE GENE MIG-2;
1197	14359	27418	0.64	1.0E-130	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1700	14852	27939	22.97	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1700	14852	27940	22.97	1.0E-130	BE275192.1	EST_HUMAN	6011211995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345366 5'
2040	15181		2.63	1.0E-130	X04092.1	NT	6011211995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345366 5'
2830	15944		7.23	1.0E-130	AJ010230.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2943	16120	29132	1.36	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2943	16120	29133	1.36	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3668	16831	28942	1.03	1.0E-130	AF240698.1	NT	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3864	16120	29132	6.31	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH), mRNA, complete cds
3864	16120	29133	6.31	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4047	17203	30213	1.8	1.0E-130	AW503580.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4184	17334	30328	0.91	1.0E-130	MB7710.1	NT	UI-HF-BNO-akv-g-06-Q-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4660	17796	30782	9.77	1.0E-130	AW543993.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPKM4265-variant, C alpha 1) mRNA
							CM4-CN0045-180200-511-102 CN0045 Homo sapiens cDNA

Page 479 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5208	18328	31300	1.49	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-at11 CT0318 Homo sapiens cDNA
5208	18328	31301	1.49	1.0E-130	AW363298.1	EST_HUMAN	RCO-CT0318-201199-031-at11 CT0318 Homo sapiens cDNA
6960	20188	33812	1.03	1.0E-130	AW843875.1	EST_HUMAN	GMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6960	20188	33813	1.03	1.0E-130	AW843875.1	EST_HUMAN	GMO-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6976	20203	33630	0.85	1.0E-130	11425448	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7404	20482	33949	1.85	1.0E-130		NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7606	20680	34062	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
7506	20590	34053	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
8881	21960		0.53	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARIK1), mRNA, complete cds
9019	22098	35638	2.06	1.0E-130	AW856242.1	EST_HUMAN	EST368312 IMAGE resourcess, MAGD Homo sapiens cDNA
8419	22489	36054	1.82	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	AW103454.1	EST_HUMAN	x336e06.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:288587.4 3'
4	13243	26243	2.52	0.0E+00	AA228126.1	EST_HUMAN	zr58e04.r1 Soares NIHMP4_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	13243	26244	2.52	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13246	26248	1.14	0.0E+00	4895130	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
16	13264	26254	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
16	13254	26255	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26262	3.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
23	13261	26263	3.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
27	13265	26267	9	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
35	13273	26277	0.62	0.0E+00	5802997	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
37	13275	26280	0.89	0.0E+00	M59600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
41	13279	26285	4.6	0.0E+00	8857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
68	13296	26312	1.77	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
68	13296	26313	1.77	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13298	26317	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-516H08 5'
60	13298	26318	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	13299	26319	9.89	0.0E+00	L16558.1	NT	Human ribosomal protein L7 (RPL7), mRNA, complete cds
63	13301	26322	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
63	13301	26323	16.36	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07 3'
67	13304	26327	2.48	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34

Page 480 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
69	13309		23.72	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
77	13313	26339	2.1	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	13313	26340	2.1	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26339	1.06	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26340	1.06	0.0E+00	4768977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
83	13318	26346	0.62	0.0E+00	AA953770.1	EST_HUMAN	SW:TMOD_HUMAN P28289 TROPOMODULIN ;
84	13319	26347	16.99	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amilox oxidase (copper-containing)) (ABP-1), nuclear gene encoding mitochondrial protein, mRNA
85	13320	26356	12.3	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
94	13329	26359	23.92	0.0E+00	5018088	NT	Homo sapiens actin, beta (ACTB) mRNA
97	13332	26359	40.86	0.0E+00	U89277.1	NT	Human polyomine 1 homolog (HPH1) mRNA, partial cds
103	13339	26366	2.4	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
104	13340	26367	0.9	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
110	13343	26371	0.68	0.0E+00	X91213.1	NT	H sapiens ncx1 gene (exon 2)
118	13350	26377	0.68	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
119	13350	26377	1.58	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:230833 3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
120	15980	26378	1.92	0.0E+00	N36040.1	EST_HUMAN	y01h09.t1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270017 5'
120	15980	26379	1.92	0.0E+00	N36040.1	EST_HUMAN	y01h09.t1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270017 5'
123	13353	26384	1.63	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
133	13359	26392	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
133	13359	26393	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
141	13609	26847	1.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
143	13607	26840	0.7	0.0E+00	T56945.1	EST_HUMAN	y83g04.2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
143	13607	26840	0.7	0.0E+00	T56945.1	EST_HUMAN	y83g04.2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
143	13367	26401	0.7	0.0E+00	T56945.1	EST_HUMAN	y83g04.2 Stratagene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:68310 5'
157	13382	26416	12.8	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
161	13386	26416	2.06	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3529864 5'
163	13386	26419	38.39	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
168	13391	26419	12.6	0.0E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit I gene, complete cds; and unknown genes
168	13393	26420	1.03	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
169	13393	26420	0.79	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
170	13394	26421	2.4	0.0E+00	W73973.1	EST_HUMAN	z62265.t Soares_fetal_heart_NDHH18W Homo sapiens cDNA clone IMAGE:346201 5' similar to gb-X16282_cds1 ZINC FINGER PROTEIN CLONE 847 (HUMAN);
171	13395	26422	0.78	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
171	13395	26423	0.78	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-404 HT0457 Homo sapiens cDNA
172	13396	26424	4.73	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
175	13399	26427	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
175	13399	26428	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	13407	26435	6.75	0.0E+00	BE018970.1	EST_HUMAN	b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z
185	13407	26436	6.75	0.0E+00	BE018970.1	EST_HUMAN	b524e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z
180	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
180	13412	26440	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26441	1.86	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26442	1.86	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	13422	26453	57.89	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
208	13428	26461	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome XMSL3-2 protein mRNA, complete cds
208	13428	26462	7.71	0.0E+00	AF167174.1	NT	Homo sapiens chromosome XMSL3-2 protein mRNA, complete cds
216	16007	26469	12	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb-J03181 PROFILIN1 (HUMAN);
216	16007	26470	12	0.0E+00	AI587308.1	EST_HUMAN	tq04f08.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb-J03181 PROFILIN1 (HUMAN);
218	13440	26472	1.93	0.0E+00	AF196588.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
221	13443		11.48	0.0E+00	4508632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
222	13444		6.53	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
228	13450	26478	1.48	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	13450	26478	1.34	0.0E+00	AB018294.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	13451	26478	2.02	0.0E+00	6678444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspv), mRNA
237	13459	26483	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466
237	13459	26484	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
237	13458	26485	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E-4486 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens
245	13497	26496	1.17	0.0E+00	AB018301.1	NT	cDNA clone TC8AP4466
245	13497	26497	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
248	13498	26501	7.54	0.0E+00	5453805	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
250	13471	26507	3.79	0.0E+00	AL163201.2	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
257	13478	26507	4.66	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 segment HS21C001
259	13478	26510	1.22	0.0E+00	X89772.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	13488	26510	5.95	0.0E+00	AF231919.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
280	13498	26528	1.37	0.0E+00	4507500	NT	Homo sapiens chromosome 21 unknown mRNA
280	13498	26530	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	13500	26532	1.9	0.0E+00	7706028	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
293	13510	26545	0.96	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein (LOC51260), mRNA
294	13511	26545	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
294	13511	26546	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
295	13512	26553	1.41	0.0E+00	AW945293.1	EST_HUMAN	Homo sapiens DCRR1 mRNA, partial cds
304	13520	26553	5.65	0.0E+00	4557029	NT	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
304	13520	26554	6.66	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	13531	26564	6.16	0.0E+00	AB028942.1	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
316	13532	26565	4.28	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
317	16010	26565	8.13	0.0E+00	4506728	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
318	13533	26566	1.42	0.0E+00	AA480002.1	EST_HUMAN	Homo sapiens ribosomal protein S5 (RPS5) mRNA
319	13534	26566	19.55	0.0E+00	4507152	NT	zr18c06.r1 Soares NIH/MPu S1 Homo sapiens cDNA clone IMAGE:753994 5'
320	13534	26566	24.65	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	13538	26570	1.59	0.0E+00	AF114488.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
337	13560	26579	1.15	0.0E+00	G14867	SWISSPROT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
337	13560	26580	1.15	0.0E+00	G14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
338	13551	26581	4.14	0.0E+00	7657213	NT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
339	13551	26581	1.82	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
354	13555	26593	4.38	0.0E+00	5174574	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
355	13566	26594	0.74	0.0E+00	4505256	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLL4) mRNA
358	13569	26598	4.58	0.0E+00	4827057	NT	Homo sapiens moesh (MSN), mRNA
361	13572	26603	0.96	0.0E+00	U71600.1	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
							Human zinc finger protein zfp31 (zfp31) mRNA, partial cds

Page 483 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
366	13576	26607	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13576	26608	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
367	16011	26609	2.53	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
369	13578	26611	1.01	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
372	13581	26615	1.59	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA
373	13582	26616	2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
374	13582	26616	1.43	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
376	13584	26618	0.66	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
387	13593	26629	3.37	0.0E+00	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
398	13635	26673	7.56	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
399	13636	26674	1.08	0.0E+00	AB363014.1	EST_HUMAN	q61h05.x1 NCL CGAP Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:XB4189
404	13601	26636	1.32	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
407	13603	26639	2.24	0.0E+00	4503680	NT	RC2-CT0320-300100-018-a09 CT0320 Homo sapiens cDNA
408	13604	26640	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13604	26641	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
408	13605	26642	2.18	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26643	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
410	13606	26644	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
411	13607	26645	1.68	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
412	13608	26646	2.56	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
413	13609	26647	2.14	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
414	13610	26648	0.96	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
414	13610	26649	0.96	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26648	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26649	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
419	13614		18.46	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
433	13233	26233	1.49	0.0E+00	R17786.1	EST_HUMAN	yg09a02.r1 Scabies infant brain IN1B Homo sapiens cDNA clone IMAGE:31682 5'
441	13637	26675	1.39	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
442	13638		3.85	0.0E+00	4506728	NT	phosphoribosylaminimidazole synthetase (GART) mRNA
443	13639	26678	2.82	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
444	13640	26677	17.7	0.0E+00	4507152	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
444	13640	26678	17.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
445	13641	26679	4.23	0.0E+00	AF193607.1	NT	Mus musculus truncated SCN protein (Scn) mRNA, complete cds
457	13652		1.45	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
459	13654	26692	4.44	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
464	13659		0.75	0.0E+00	BE254447.1	EST_HUMAN	601111820F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
480	13675	26706	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	13675	26707	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
488	13680	26715	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
488	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
488	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
496	13691	26722	4.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26723	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
508	13700	26729	4.25	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
508	13702	26731	1.81	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
516	13710	26737	1.66	0.0E+00	BE385144.1	EST_HUMAN	601274631F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
517	16014	26738	1.7	0.0E+00	AW938825.1	EST_HUMAN	PMO-DTD065-130400-002-008 DT0068 Homo sapiens cDNA
520	13713	26740	1.82	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
521	13714	26741	0.95	0.0E+00	8923955	NT	Homo sapiens PC326 protein (PC326), mRNA
525	13718		1.9	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0169-070800-120-F07 FT0169 Homo sapiens cDNA
532	13725	26751	4.43	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
539	16015	26755	1.57	0.0E+00	BE061527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
544	13737	26761	1.15	0.0E+00	BF028005.1	EST_HUMAN	601764858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3906988 5'
550	13743	26763	1.57	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
553	13746	26771	8.39	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
554	13747	26772	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
556	13749	26775	0.73	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
557	13750	26777	0.63	0.0E+00	8923831	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
562	13754		4.82	0.0E+00	AF003528.1	NT	regions
570	13762	26786	1.39	0.0E+00	AW136324.1	EST_HUMAN	U1-H-B1T-acb-H-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
580	13772		5.31	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
						NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene
596	13789	26810	1.85	0.0E+00	5174742	NT	encoding mitochondrial protein, mRNA

Page 485 of 550

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612	13801		7.14	0.0E+00	J04068.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
615	13804	26824	1.87	0.0E+00	BF104898.1	EST_HUMAN	801922627F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4045447 5'
617	13806	26826	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
617	13806	26827	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26828	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26827	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26828	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
624	13809	26830	0.64	0.0E+00	4501854	NT	Homo sapiens acetyl-CoA:CoA carboxylase beta (ACACB), mRNA
629	13814	26837	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
639	13824	26847	2.19	0.0E+00	AF149773.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
641	13826	26850	0.93	0.0E+00	AB037807.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
643	13826	26851	1.99	0.0E+00	6806918	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
644	13826	26852	2.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13826	26853	2.34	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
646	13830	26854	0.98	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
646	13830	26855	0.98	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13838	26863	1.42	0.0E+00	AA359488.1	EST_HUMAN	z60c07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728732 5'
656	13842	26869	6.57	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
660	13846	26872	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
660	13846	26873	4.28	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
663	13849	26876	3.58	0.0E+00	4885526	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
670	13856	26886	2.16	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
672	13858	26888	1.25	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
675	13861	26892	1.88	0.0E+00	U05235.1	NT	Homo sapiens neutral amino acid transporter (ASCT1) gene, exon 8
679	13865	26895	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
679	13865	26896	1.07	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
685	13870	26901	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
685	13870	26902	5.11	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
691	13878	26916	1.8	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
700	13883	26916	3.92	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMGT1) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
706	13888	26920	4.94	0.0E+00	AB029012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
715	13897	26935	3.83	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
727	13909	26949	13.13	0.0E+00	AA614537.1	EST_HUMAN	np49d01.s1 NCI_CGAP Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gb:X57352
731	13913	26953	6.4	0.0E+00	M60875.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
731	13913	26954	6.4	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
741	13923	26963	1.35	0.0E+00	5032182	NT	Human von Willebrand factor gene, exons 23 through 34
747	13928	26969	4.62	0.0E+00	AF264750.1	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
747	13928	26970	4.62	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13930	26973	9.17	0.0E+00	11545800	NT	Homo sapiens ALR-like protein mRNA, partial cds
755	13938	26981	2.26	0.0E+00	BE241577.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
776	13955	27005	1.19	0.0E+00	AF226990.2	NT	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
775	13955	27008	1.19	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27009	8.92	0.0E+00	J03764.1	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
778	13958	27010	8.92	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
781	13961	27011	0.96	0.0E+00	AB037760.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
782	13962	27012	2.07	0.0E+00	6912749	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
784	16022	27014	2.36	0.0E+00	D30612.1	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
785	13964	27015	3.58	0.0E+00	BE869735.1	EST_HUMAN	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
790	13969	27021	4.04	0.0E+00	R48915.1	EST_HUMAN	601446647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
791	13970	27022	2.86	0.0E+00	5032088	NT	y69908.r1 Soares breast 2Nb1Bst Homo sapiens cDNA clone IMAGE:154046 5'
800	13979	27031	1.64	0.0E+00	AB011399.1	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
803	13983	27035	3.01	0.0E+00	7661966	NT	Homo sapiens gene for AF-6, complete cds
815	13984	27048	1.24	0.0E+00	D80008.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
815	13994	27049	1.24	0.0E+00	D80008.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13999	27053	2.74	0.0E+00	X89712.1	NT	Human mRNA for KIAA0184 gene, partial cds
824	14003	27057	3.25	0.0E+00	AB020717.1	NT	H sapiens mRNA for Interferon alpha/beta receptor (long form)
824	14003	27058	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
829	14007	27064	13.47	0.0E+00	5174479	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
830	14008	27085	11.09	0.0E+00	4507500	NT	Homo sapiens pericentrin (PCNT) mRNA
847	14025	27085	1.65	0.0E+00	7657213	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
848	14028	27086	2.46	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	14028	27088	1.84	0.0E+00	4557696	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
850	14028	27088	1.84	0.0E+00	4557696	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNIE1), mRNA

Page 487 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
858	14033	27094	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
858	14033	27095	2.19	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
857	14034	27098	1.45	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MINBH) mRNA, complete cds
862	14039	27101	2.86	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
868	14042	27108	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
868	14042	27107	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
873	14048		2.07	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC8A3) gene, complete cds
877	14053	27118	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
877	14053	27119	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	14054	27120	11.32	0.0E+00	AB028942.1	NT	Homo sapiens SON DNA binding protein (SON) mRNA
879	14055	27121	4.03	0.0E+00	4507162	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	14056	27122	3.87	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
884	14060	27125	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
884	14060	27126	1.54	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
885	14061	27127	1.82	0.0E+00	AA53272.1	EST_HUMAN	U66d07.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:987453
885	14061	27128	1.82	0.0E+00	AA53272.1	EST_HUMAN	U66d07.s1 NCJ_CGAP_P10 Homo sapiens cDNA clone IMAGE:987453
888	14062		8.41	0.0E+00	BF677894.1	EST_HUMAN	602085570F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248916 5'
890	14066	27129	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
890	14066	27130	1.4	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27131	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
891	14067	27132	2.54	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
914	14089	27155	0.98	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
921	14096	27160	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 B10703 Homo sapiens cDNA
921	14096	27161	1.93	0.0E+00	BE089592.1	EST_HUMAN	QV0-BT0703-280400-211-g11 B10703 Homo sapiens cDNA
931	14106	27170	2.7	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
941	14115		9.06	0.0E+00	4504958	NT	Homo sapiens lamelin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
943	14115		9.09	0.0E+00	4504958	NT	Homo sapiens lamelin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
944	14117	27176	1.42	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
945	14118	27177	0.89	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27178	0.89	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
945	14118	27179	0.89	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
948	14119	27180	1.82	0.0E+00	L2810.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
949	14122	27183	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
949	14122	27184	0.71	0.0E+00	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
973	14146	27205	0.93	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
974	14147	27206	9.11	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
975	14148	27207	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
976	14149	27208	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
976	14149	27209	1.24	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
984	16027	27216	3.95	0.0E+00	A1001948.1	EST_HUMAN	es98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
984	16027	27217	3.85	0.0E+00	A1001948.1	EST_HUMAN	es98e03.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
996	14158	27219	14.34	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Msa2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
997	14168	27229	1.76	0.0E+00	AB030668.1	NT	Homo sapiens mRNA for PSP24, complete cds
1006	14177	27236	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27237	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1006	14177	27238	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
1008	14179	27241	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1008	14179	27242	2.02	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1017	14188	27249	3.97	0.0E+00	4757869	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
1029	14199	27257	1.07	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1030	14200	27258	5.81	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1031	14200	27258	9.09	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14203		4	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1035	14203		29.56	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1039	14207	27284	0.96	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1040	14207	27284	4.66	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1041	14207	27284	1.3	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14208	27265	1.18	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1045	14211	27268	2.11	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1049	14216	27272	1.27	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1051	14217		1.39	0.0E+00	A4459880.1	EST_HUMAN	aa86g07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8 ;
1054	14220	27277	2.43	0.0E+00	N43182.1	EST_HUMAN	EST1124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1054	14220	27278	2.43	0.0E+00	N43182.1	EST_HUMAN	EST1124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1066	14221	27279	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1055	14221	27280		0.97	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1058	14224		3.27	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
1072	14238	27285		1.51	4758669	NT	Homo sapiens heat shock 70kD protein 8B (mortalin-2) (HSPA9B) mRNA
1080	14255	27310		1.51	4926672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (GDH6) mRNA
1080	14255	27311		1.51	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (GDH6) mRNA
1094	14259	27315		2.74	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1094	14259	27316		2.74	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1095	14260	27317		13.67	AJ246922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1097	14262			0.92	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1098	14264	27321		2.81	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1105	14271	27330		2.04	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1120	14285	27340		1.91	BE005208.1	EST_HUMAN	MRO-BN0116-200300-003-h08 BN0116 Homo sapiens cDNA
1143	14308	27364		3.82	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9) mRNA
1143	14308	27365		3.82	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9) mRNA
1155	14319	27373		0.82	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1155	14319	27374		0.82	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1156	14320	27375		9.36	4508712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1158	14322	27377		1.2	8923260	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1161	14325	27380		3.98	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1163	14327	27381		19.6	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1164	14328	27382		4.52	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1164	14328	27383		4.52	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1168	14331	27386		1.44	7708500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
1169	14332	27387		0.71	X96826.1	NT	H. sapiens ART4 gene
1169	14332	27388		0.71	X96826.1	NT	H. sapiens ART4 gene
1169	14332	27389		1.15	0.0E+00	AI147850.1	q522d10x1 Scores_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE1697011 3'
1170	14335	27391		1.62	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1181	14344	27400		1.22	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1181	14344	27401		1.22	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1182	14345	27402		1.32	5966844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1185	14357	27415		2.19	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1195	14357	27416		2.19	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1198	14360	27419		1.09	AB037836.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1205	14367	27428		8.64	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1238	14395		1.28	0.0E+00	7657336	NT	Homo sapiens muLL (E. coli) homolog 3 (MLH3), mRNA
1250	14409	27471	0.94	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1254	14413	27475	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1254	14413	27476	2.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1255	14414	27477	3.33	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1256	16032	27478	2.46	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1275	14432	27503	4.88	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1276	14433	27504	1.87	0.0E+00	4503088	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1286	14442	27510	0.89	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4) mRNA
1295	14451		1.38	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1303	14459	27525	29.96	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1310	14466	27534	2.96	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSChr9) mRNA, complete cds
1316	14472	27538	1.53	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1316	14472	27539	1.63	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1328	14485	27552	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27553	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1328	14485	27554	3.28	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1329	14486		2.16	0.0E+00	AF096156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1339	16034	27566	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1346	16991	27567	1.2	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1346	16991	27573	1.4	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1346	16991	27574	1.86	0.0E+00	5803149	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1347	14502	27575	0.83	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1348	14504	27576	1.7	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1350	14505	27577	1.55	0.0E+00	5803149	NT	Homo sapiens ring finger protein 173 (ZNF173) mRNA
1351	14506	27578	0.71	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 9 (RNF9), mRNA
1353	14508	27680	4.44	0.0E+00	AB011149.1	NT	Homo sapiens RFB30 gene for RING finger protein
1354	14509	27681	1.34	0.0E+00	7661966	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1355	14510	27682	4.99	0.0E+00	7661966	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27683	3.83	0.0E+00	8667387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1356	14511	27684	3.83	0.0E+00	8667387	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1368	14522	27697	1.36	0.0E+00	M14123.1	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1426	14583	27656	1.02	0.0E+00	BE257855.1	EST_HUMAN	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1426	14583	27657	1.02	0.0E+00	BE257855.1	EST_HUMAN	Human endogenous retrovirus HERV-K10
1426	14583	27657	1.02	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1426	14583	27657	1.02	0.0E+00	BE257855.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'

Page 491 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1440	14653	27868	1.03	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyld gene
1449	14602	27880	13.57	0.0E+00	6042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	14810	27880	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1457	14810	27891	0.97	0.0E+00	4505646	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1466	14812	27864	1.99	0.0E+00	7705665	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	14812	27865	1.99	0.0E+00	7705665	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1462	14815	27897	29.09	0.0E+00	AJ238093.1	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1471	14625	27709	4.63	0.0E+00	AF038280.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1490	14643	27724	4.2	0.0E+00	AF038280.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1491	14644	27725	1.37	0.0E+00	AL137764.1	NT	Novel human gene on chromosome 20
1495	14648	27730	1.73	0.0E+00	D87077.1	NT	Novel human gene mapping to chromosome 1
1498	14651	27733	8.24	0.0E+00	6912457	NT	Human mRNA for KIAA0240 gene, partial cds
1500	14653	27735	2.28	0.0E+00	7661965	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1500	14653	27736	2.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14654	27736	3.74	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1507	14660	27742	6.62	0.0E+00	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1507	14660	27743	6.62	0.0E+00	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1541	14693	27772	2.61	0.0E+00	7706434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1555	14708	27788	2.66	0.0E+00	AA481172.1	EST_HUMAN	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51696), mRNA
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	es34a03.r1 NC1 CGAP_GOB1 Homo sapiens cDNA clone IMAGE:818116 5'
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1562	14716	27793	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1564	14717	27796	1.55	0.0E+00	AW976087.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1564	14717	27797	1.55	0.0E+00	AW976087.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1565	14718	27798	1.03	0.0E+00	D10864.1	NT	Bovine mRNA for neurocalcin
1597	14720		3.2	0.0E+00	U78027.1	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
1568	14721	27801	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1568	14721	27802	26.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1570	14723	27804	3.85	0.0E+00	7662405	NT	Homo sapiens KIAA0857 protein (KIAA0857), mRNA
1571	14724		9.78	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1576	14729	27810	64.77	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1578	14731	27811	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA

Page 492 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1579	16042		32.23	0.0E+00	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0E+00	M14199.1	NT	Human laminin receptor (2.15 epitope) mRNA, 5' end
1592	14746	27828	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1592	14745	27829	1.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1594	14747	27830	13.85	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1602	14755		3.25	0.0E+00	D00333.1	NT	human c-yes-2 gene
1611	14764	27844	11.38	0.0E+00	Z63738.1	NT	H. sapiens HH2B/e gene
1612	14765	27845	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14765	27846	2.55	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14766	27847	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKc Homo sapiens cDNA clone GKCB0F02 5'
1613	14766	27848	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKc Homo sapiens cDNA clone GKCB0F02 5'
1616	16043	27851	2.1	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1618	14770	27852	1.88	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1620	14772	27855	6.83	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1620	14772	27856	6.83	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1622	14774	27857	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1622	14774	27858	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1639	14791	27876	6.29	0.0E+00	H26973.1	EST_HUMAN	yo78c05.e1 Soares adult brain N2b4HB5Y Homo sapiens cDNA clone IMAGE:163848 3'
1648	14801	27887	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1688	14820	27903	1.68	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-gjw-c-04-0-UL.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
1698	14850	27936	2.12	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191189-004-b11 HT0168 Homo sapiens cDNA
1698	14850	27937	2.12	0.0E+00	BE144364.1	EST_HUMAN	MRO-HT0166-191189-004-b11 HT0168 Homo sapiens cDNA
1702	14864	27941	1.3	0.0E+00	A1768104.1	EST_HUMAN	wg81b07.x1 Soares NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN ;
1703	14855	27942	1.71	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1704	14866	27943	2.8	0.0E+00	AF037177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1708	14859	27947	2.1	0.0E+00	M29560.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1708	14859	27948	2.1	0.0E+00	M29560.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	64.4	0.0E+00	4557867	NT	Homo sapiens keratin 18 (KRT18) mRNA
1711	14862	27951	2.42	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1714	14865	27954	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1714	14895	27955	1.08	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:085147 O85147
1716	14896	27957	3.2	0.0E+00	4557610	NT	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1719	14898	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1719	14899	27961	4.3	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
1721	14871		0.97	0.0E+00	A149880.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1722	14872	27963	10.28	0.0E+00	Z80760.1	EST_HUMAN	yo59e08.r1 Soares breast 3NBHst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64089
1722	14872	27964	10.28	0.0E+00	Z80760.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1725	14875		21.3	0.0E+00	6031743	NT	qf43f09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1762809 3'
1734	14883	27978	6.13	0.0E+00	8923841	NT	Human H2B/h gene
1737	14886	27979	1.63	0.0E+00	5453855	NT	Human H2B/h gene
1741	14890	27983	1.96	0.0E+00	M75980.1	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1741	14890	27984	1.96	0.0E+00	M75980.1	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1744	14893	27988	1.11	0.0E+00	M75980.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1751	14900	27997	6.57	0.0E+00	AB026542.1	NT	Human hepatocyte growth factor gene, exon 15
1753	14902		2.64	0.0E+00	S94400.1	NT	Human hepatocyte growth factor gene, exon 15
1762	14911	28006	5.29	0.0E+00	4557638	NT	Human hepatocyte growth factor gene, exon 15
1784	14933	28027	3.33	0.0E+00	AF273841.1	NT	Human hepatocyte growth factor gene, exon 15
1828	15047		41.88	0.0E+00	4506718	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28073	3.2	0.0E+00	4557556	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28074	3.2	0.0E+00	4557556	NT	Human hepatocyte growth factor gene, exon 15
1833	14980	28078	2.47	0.0E+00	U63863.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1837	15048	28083	7.55	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1839	14995	28085	1.7	0.0E+00	AA113030.1	EST_HUMAN	z166c09.s1 Strategene HeLa cell c3 937216 Homo sapiens cDNA clone IMAGE:563058 3'
1850	14996	28098	24.06	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
1852	14996	28102	9	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1863	14999	28103	24.99	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1863	14999	28104	24.99	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1853	14999	28105	24.99	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1870	15015	28124	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1870	15015	28125	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	15025	28131	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1881	15025	28132	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1892	15036	28143	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1892	15036	28144	1.84	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1895	15038	28146	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1895	15038	28147	3.59	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1896	15039	28148	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1896	15039	28149	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1899	15042	28152	2.3	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn4-07-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1899	15042	28153	2.3	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn4-07-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1924	15067	28171	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1924	15067	28172	3.22	0.0E+00	BE277466.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1943	15068	28187	1.04	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-534 BN0126 Homo sapiens cDNA
1972	15115	28215	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1972	15115	28216	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1975	15118	28218	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	15118	28219	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1981	15124	28228	1.28	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1985	15128		1.64	0.0E+00	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1986	16051	28230	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1986	16051	28231	57.92	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1991	15133	28238	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1991	15133	28239	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1994	15135	28241	2.41	0.0E+00	7657038	NT	Homo sapiens cloath receptor 6 (DR6), mRNA
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1996	15137		6.39	0.0E+00	AF240786.1	NT	Human topoisomerase I pseudogene 1
2001	15142		5.28	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
2003	16052	28248	1.84	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2005	15145	28260	1.3	0.0E+00	BE018068.1	EST_HUMAN	bb73f11.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048046 5'
2011	15151	28255	1.89	0.0E+00	4809282	NT	Homo sapiens histidine aminomethylase (HAL) mRNA
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine aminomethylase (HAL) mRNA
2024	15165		1.04	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C082
2026	15167	28272	1.41	0.0E+00	8400718	NT	Homo sapiens nebulin (NEB), mRNA
2026	15167	28273	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2027	15168	28274	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2027	15168	28275	12.98	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2037	15178	28288	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2037	15178	28289	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2043	15184	28293	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2043	15184	28294	1.93	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2045	15186	28296	3.24	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2876913 3'
2045	15186	28298	3.24	0.0E+00	AW193024.1	EST_HUMAN	x69b01.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2876913 3'
2046	15187	28297	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2046	15187	28298	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2048	15189	28300	1.53	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2048	15189	28301	1.08	0.0E+00	Z47555.1	NT	H sapiens genes for semenogelin I and semenogelin II
2049	15190	28302	1.09	0.0E+00	Z47555.1	NT	H sapiens genes for semenogelin I and semenogelin II
2056	15197	28311	5.04	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2078	15218	28337	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2078	15218	28338	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2109	15247	28368	1.53	0.0E+00	8394546	NT	Homo sapiens chromosome 21 open reading frame 7 (YGB1), mRNA
2112	15250	28370	0.98	0.0E+00	7706742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2117	15255	28374	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2117	15255	28375	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2119	15257	28376	1.02	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9) mRNA
2121	15258	28378	57.63	0.0E+00	AU140831	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2122	14812	27694	0.97	0.0E+00	AU140831.1	EST_HUMAN	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2122	14812	27695	0.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2124	15260	28380	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2124	15260	28381	2.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2126	16262		3.79	0.0E+00	7687468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

Page 496 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2128	15264		1.48	0.0E+00	4985963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2129	15265	28384	2.9	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c01c02
2131	15267		2.38	0.0E+00	A1244247.1	EST_HUMAN	q980R08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2136	15272	28393	4.37	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2138	15274	28395	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2138	15274	28396	2.25	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2144	15280	28404	3.8	0.0E+00	BE687125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	15280	28405	3.6	0.0E+00	BE687125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2182	15288	28414	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2182	15288	28415	3.43	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2183	15289	28416	1.11	0.0E+00	AJ297709.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2188	15294	28420	1.16	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2182	15298	28423	1.94	0.0E+00	BE500995.1	EST_HUMAN	7634c02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER
2182	15317		3.17	0.0E+00	BE787864.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2183	15318		1.28	0.0E+00	AF018953.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR51) gene, exon 6 and complete cds
2185	15320	28446	4.84	0.0E+00	BF027952.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2186	15321	28447	1.5	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2188	15323	28448	1.29	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2180	15325	28450	3.41	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0218-271099-022-G10 CT0219 Homo sapiens cDNA
2182	15327	28452	6.48	0.0E+00	A1904640.1	EST_HUMAN	QV-BT066-020399-082 BT065 Homo sapiens cDNA
2182	15327	28453	6.48	0.0E+00	A1904640.1	EST_HUMAN	QV-BT066-020399-082 BT065 Homo sapiens cDNA
2225	15350		1.08	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNNB3L), mRNA
2249	15382		1.52	0.0E+00	L14781.1	NT	Human DNA-binding protein mRNA, 3' end
2259	15392	28518	1.28	0.0E+00	BE274696.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2261	15394	28521	0.94	0.0E+00	D87685.1	NT	Human mRNA for KIAA0244 gene, partial cds
2262	15395	28522	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBD08 5'
2262	15395	28523	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBD08 5'
2264	15397	28525	2.57	0.0E+00	AA931591.1	EST_HUMAN	cc32e01.st NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2268	15401	28529	24.38	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI_CGAP_Br64 Homo sapiens cDNA clone IMAGE:4150734 5'
2269	15402	28530	40.14	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2272	19405	28533	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2272	19405	28534	5.56	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2276	19059	28539	4.06	0.0E+00	BF313617.1	EST_HUMAN	601900281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129822 5'
2278	15411	28542	3.13	0.0E+00	BE018750.1	EST_HUMAN	b84402.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q16170 Q16170 TRANSCRIPTION FACTOR S-I-RELATED PROTEIN;
2281	15413	28544	1.88	0.0E+00	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2281	15413	28545	1.88	0.0E+00	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2289	15421	28553	3.05	0.0E+00	AL163204.2	NT	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2289	15421	28554	3.06	0.0E+00	AL163204.2	NT	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2290	15422	28555	3.72	0.0E+00	7682401	NT	Homo sapiens chromosome 21 segment HS21C004
2290	15422	28556	3.72	0.0E+00	7682401	NT	Homo sapiens chromosome 21 segment HS21C004
2295	15427	28561	2.34	0.0E+00	U36294.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2296	15428	28561	1.02	0.0E+00	AA282281.1	EST_HUMAN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2313	15445	28579	7.92	0.0E+00	4557556	NT	Human beta-prime-adaptin (BAM22) gene, exon 18
2320	15452	28584	2.63	0.0E+00	7682401	NT	z12b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2327	15459	28592	3.44	0.0E+00	BE895281.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
2331	15463	28596	1.51	0.0E+00	BE805563.1	EST_HUMAN	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2331	15463	28597	1.51	0.0E+00	BE905563.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918007 5'
2333	15464	28599	1.83	0.0E+00	AB037784.1	NT	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2333	15464	28599	1.83	0.0E+00	AB037784.1	NT	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2375	15506	28632	4.35	0.0E+00	11545748	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2375	15506	28633	4.35	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2376	15507	28634	2.67	0.0E+00	AI076404.1	EST_HUMAN	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2378	15509	28636	2.95	0.0E+00	AA428001.1	EST_HUMAN	ox09007.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2378	15509	28637	2.95	0.0E+00	AA428001.1	EST_HUMAN	z178a11.r1 Soares_fetal_liver_spleen_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2380	15511	28639	1.82	0.0E+00	BF347039.1	EST_HUMAN	z178a11.r1 Soares_fetal_liver_spleen_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2385	15516	28645	1.33	0.0E+00	AB020717.1	NT	602021846F1 NCI_CGAP_Bln67 Homo sapiens cDNA clone IMAGE:4157339 5'
2385	15516	28646	1.33	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2386	15517	28647	2.34	0.0E+00	6326466	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2386	15517	28647	2.34	0.0E+00	6326466	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2383	15524	28653	2.36	0.0E+00	BE878095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94839 O94839
2386	15527	28655	5.46	0.0E+00	AF044571.1	NT	KIAA0857 PROTEIN
2387	15528	28656	2.6	0.0E+00	AI625542.1	EST_HUMAN	Homo sapiens phosphotyrosine kinase alpha subunit (PHK2) gene, exon 32

Page 498 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	15530	28657	1.5	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2402	15533	28659	2.22	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2402	15533	28660	2.22	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2405	15536	28663	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2405	15536	28664	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2424	15553	28679	3.04	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2428	15556	28683	3.56	0.0E+00	AU131142.1	EST_HUMAN	Homo sapiens cDNA clone NT2RF302064 5'
2429	15557	28684	9.82	0.0E+00	BE794028.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2430	15558	28684	3.96	0.0E+00	7652017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2431	15559	28685	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2431	15559	28686	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2432	15560						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2432	15560		7.14	0.0E+00	AF280107.1	NT	
2434	15562	28688	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28689	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28690	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2432	15560		1.03	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 EN0070 Homo sapiens cDNA
2485	15612	28735	1.14	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2487	15614		4.63	0.0E+00	A042035.1	EST_HUMAN	α60502.x1 Sceres_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1660683 3' similar to TR:O08662
2489	15616	28737	0.94	0.0E+00	8923620	NT	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ;
2492	15619		1.35	0.0E+00	BE895035.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2503	15630		2.22	0.0E+00	AB005622.1	EST_HUMAN	601432809F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2505	15632	28752	8.05	0.0E+00	6006002	NT	AB005622 Hela cDNA (T.Nome) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2510	15636	28756	1.99	0.0E+00	D85606.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2510	15636	28757	1.98	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2520	15646	28769	2.42	0.0E+00	AF106275.1	NT	Homo sapiens gene for cholesteryltransferin type-A receptor, complete cds
2524	15649	28773	0.96	0.0E+00	BF345274.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2530	15655	28780	3.64	0.0E+00	5729777	NT	602018058F1 NCI_CGAP_Brim7 Homo sapiens cDNA clone IMAGE:4153670 5'
2538	15663	28786	1.02	0.0E+00	U13666.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2538	15663	28787	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2539	15664	28788	28.11	0.0E+00	BF569144.1	EST_HUMAN	Human G protein-coupled receptor (GPR1) gene, complete cds
2547	15672	28796	4.18	0.0E+00	AW466922.1	EST_HUMAN	60218458F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
							h040404.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	15776	28768	3.03	0.0E+00	AW601010.1	EST_HUMAN	U1-HF-BPOp-als-c-07-0-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2575	15700		2.02	0.0E+00	AW613853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2578	15704	28824	7.28	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948518 5'
2579	15135	28241	1.12	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2580	15705	28825	1.44	0.0E+00	BF509482.1	EST_HUMAN	U1-H-BL4-acc-b-08-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2583	15708	28827	2.21	0.0E+00	Z32884.2	NT	Homo sapiens mRNA for membrane transport protein (Xk gene)
2585	15710		5.17	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2587	15712	28830	1.07	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2588	15713	28831	2.39	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2589	15714	28832	3.08	0.0E+00	U93238.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2595	15720	28838	1.96	0.0E+00	BE886490.1	EST_HUMAN	60150821F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908866 5'
2598	15722	28842	13.07	0.0E+00	BE876511.1	EST_HUMAN	60148924F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2598	15722	28843	13.07	0.0E+00	BE876511.1	EST_HUMAN	60148924F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2599	15723	28844	1.12	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2616	15740	28852	1.83	0.0E+00	BE638821.1	EST_HUMAN	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2623	15746	28860	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2623	15746	28861	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2624	15747	28862	1.25	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2624	15747	28863	1.25	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887955 5'
2625	15748	28864	1.04	0.0E+00	BF223041.1	EST_HUMAN	7q27h12.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE: 3' similar to TR-000246 000246
2628	15761	28866	8.3	0.0E+00	AF245505.1	NT	HYPOTHETICAL 9.3 KD PROTEIN ;
2664	15000	28901	2.18	0.0E+00	AB037835.1	NT	Homo sapiens adican mRNA, complete cds
2664	15000	28902	2.18	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2665	15786		2.35	0.0E+00	BF513835.1	EST_HUMAN	Homo sapiens mRNA for KIAA1416 protein, partial cds
2675	15795	28912	32.6	0.0E+00	BF204131.1	EST_HUMAN	U1-H-BW1-amp-4-12-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070831 3'
2675	15795	28913	32.6	0.0E+00	BF204131.1	EST_HUMAN	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2678	15798	28915	2.15	0.0E+00	AB037742.1	NT	601869073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2679	15799	28916	2.52	0.0E+00	5032150	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2681	15801	28918	8.53	0.0E+00	AB037859.1	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF21)
2682	15802	28919	1.16	0.0E+00	BE795446.1	EST_HUMAN	mRNA
2682	15802	28920	1.16	0.0E+00	BE795445.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
2680	15810		2.75	0.0E+00	BE792472.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
							601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
							601594930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'

Page 500 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	15819	28935	2.52	0.0E+00	4504886	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2710	15828		1.16	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2711	15829	28942	5.67	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2715	15833	28943	1.07	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2718	15836	28946	0.96	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2721	15839	28949	1.15	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28950	1.16	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2721	15839	28953	1.66	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-d07 OT0086 Homo sapiens cDNA
2724	15842	28953	4.83	0.0E+00	BE383165.1	EST_HUMAN	501298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2727	15845	28956	2.8	0.0E+00	BE531263.1	EST_HUMAN	501278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
2728	15846		1	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2763	15878	28987	11.99	0.0E+00	AA316723.1	EST_HUMAN	EST189414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2785	15901		4.04	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2789	15905	29013	3.72	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2791	15907	29015	2.32	0.0E+00	AB051828.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2792	15908	29016	11.38	0.0E+00	BE796376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2797	15912	29020	17.3	0.0E+00	BE563433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2800	16072	29024	3.28	0.0E+00	AV721947.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE09 5'
2801	15915		2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29027	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29028	2.21	0.0E+00	AF290195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2804	15918	29029	47.74	0.0E+00	AF651056.1	EST_HUMAN	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2805	15919		5.84	0.0E+00	BF377897.1	EST_HUMAN	AV651056 GLC Homo sapiens cDNA clone GLCCLD07 3'
2806	15920	29030	5.84	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2806	15920	29031	5.84	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2810	15924	29034	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kd) (CDR1) mRNA
2810	15924	29035	1.15	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kd) (CDR1) mRNA
2813	15927	29039	21.96	0.0E+00	BE747193.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
2814	15928	29040	1.05	0.0E+00	N44974.1	EST_HUMAN	W35H10.11 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
2816	15930	29042	1.15	0.0E+00	BE176836.1	EST_HUMAN	A45773 kelch protein, long form - fruit fly
2827	15941		1.13	0.0E+00	AL163201.2	NT	RC4-HT0587-170300-012-d11 HT0587 Homo sapiens cDNA
2828	15942	29052	3.19	0.0E+00	BF514110.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001

Page 501 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	15949		1.67	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15955	29082	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2841	15935	29063	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2842	15956	29064	5.05	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249816 5'
2848	15962	29072	1.33	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2852	15968	29075	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCGA03 5'
2852	15968	29076	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCGA03 5'
2854	15968		14.75	0.0E+00	AI879163.1	EST_HUMAN	au55404.Y1 Schneider field brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A;
2857	15971	29081	2.14	0.0E+00	BF630661.1	EST_HUMAN	602071937F1 NCL_GAP_Brn87 Homo sapiens cDNA clone IMAGE:4214879 5'
2858	15972	29082	71.97	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2860	15974	29083	2.42	0.0E+00	AI131494.1	EST_HUMAN	AI131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2860	15974	29084	2.42	0.0E+00	AI131494.1	EST_HUMAN	AI131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2861	15975	29085	64.06	0.0E+00	BE300344.1	EST_HUMAN	500944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2861	15975	29086	64.06	0.0E+00	BE300344.1	EST_HUMAN	500944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2867	13415	28444	5.26	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2870	15982		1.64	0.0E+00	AB033281.1	NT	Homo sapiens BTCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2878	13933	28978	1.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2878	13933	28979	1.89	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2880	14230	27287	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2880	14230	27288	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2897	16076	29094	3.73	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2898	16077		1.26	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
2900	16079		1.91	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1627 protein, partial cds
2907	16085	29099	4.25	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2911	16089	29102	6.5	0.0E+00	M80902.1	NT	Human AHNAC nucleoprotein mRNA, 5' end
2914	16082	29104	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2914	16092	29105	0.93	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281289-003-e02 HT0343 Homo sapiens cDNA
2916	16094		2.05	0.0E+00	X73428.1	NT	H. sapiens l33 gene for HLH type transcription factor
2918	16096		2.6	0.0E+00	AL163266.2	NT	Homo sapiens chromosome 21 segment HS21C068
2919	16097	29108	1.3	0.0E+00	7019594	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2919	16097	29109	1.3	0.0E+00	7019594	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	16087	29110	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2921	16099	29111	15.64	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2926	16103	29117	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2926	16103	29118	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2929	16106	29121	3.42	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2930	16107		6.12	0.0E+00	Y10658.1	NT	H sapiens mRNA for nuclear DNA helicase II
2931	16108		1.13	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2932	16109	29122	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2932	16109	29123	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2944	16121	29134	2.54	0.0E+00	4607280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2947	16124	29138	1.19	0.0E+00	AL047599.1	EST_HUMAN	DKFZp596G0621_r1 586 (synonym: hufc1) Homo sapiens cDNA clone DKFZp596G0621
2948	16125	29139	0.66	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2948	16125	29140	0.98	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2949	16126		2.44	0.0E+00	4503088	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2952	16129	29142	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2952	16129	29143	5.16	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2958	16135	29151	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2958	16135	29152	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2961	16138	29156	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2961	16138	29157	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2962	16139	29158	1.3	0.0E+00	AA215578.1	EST_HUMAN	z96b11.s1 NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:583517 3' similar to contains Alu repetitive element;
2969	16145		3.99	0.0E+00	Y19210.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
2972	16148	29167	1.05	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2974	16150	29170	26.98	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2975	16151	29171	1.15	0.0E+00	AI561002.1	EST_HUMAN	In18407.x1 NC1 CGAP Bn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2975	16151	29172	1.15	0.0E+00	AI561002.1	EST_HUMAN	In18407.x1 NC1 CGAP Bn25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2977	16153	29174	1.18	0.0E+00	P62740	SWISSPROT	ZINC FINGER PROTEIN 132
2978	16154	29175	1.04	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2984	16170	29187	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2984	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2995	16171	29189	6.2	0.0E+00	AD040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	16171	28190	6.2	0.0E+00	AB040841.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2898	16174	29193	3.31	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2898	16174	28194	3.31	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2899	16175	28195	4.83	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2899	16175	28196	4.83	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
3003	16178	28199	1.29	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
3003	16178	28200	1.29	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17283 PROTEIN. ;
3011	16187	28211	3.91	0.0E+00	4505084	NT	7n40d03.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
3011	16187	28212	3.91	0.0E+00	4505084	NT	Q9VLN1 CG17283 PROTEIN. ;
3018	16185	28218	1.51	0.0E+00	4738827	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3022	16198	28221	0.98	0.0E+00	AB030304.1	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3024	16200	28223	9.6	0.0E+00	AF108275.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
3038	16214	28242	1.44	0.0E+00	AI149880.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3045	16221	28243	0.71	0.0E+00	AF281074.1	NT	q4309.x1 Soares_testes_NHT Homo sapiens cDNA clone IMAGE:1782868 3'
3046	16221	28243	0.71	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3046	16222	28244	0.92	0.0E+00	4506118	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3047	16223	28245	2.81	0.0E+00	AB004884.1	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3057	16233	28252	1.85	0.0E+00	7682273	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3058	16234	28253	1.92	0.0E+00	AW612526.1	EST_HUMAN	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3059	16235	28254	2.4	0.0E+00	5729755	NT	h0308.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2854055 3' similar to TR:O60407 O60407
3059	16235	28255	2.4	0.0E+00	5729755	NT	PAC CLONE DJ1168D11 FROM 7P21-P22, COMPLETE SEQUENCE ;
3067	16243	28263	1.17	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3067	16243	28264	1.17	0.0E+00	AF114488.1	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3081	16267	28285	0.61	0.0E+00	AL183246.2	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3083	16269	28286	1.29	0.0E+00	M74098.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3102	16278	28282	0.88	0.0E+00	4505882	NT	Homo sapiens chromosome 21 segment HS21C046
3109	16285	28285	3.33	0.0E+00	AF195953.1	NT	Human displacement protein (CCAAT) mRNA
3112	16288	28303	4.9	0.0E+00	5579469	NT	Homo sapiens semaphorin I (SEMG1) mRNA
3112	16288	28303	4.9	0.0E+00	5579469	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3112	16288	28303	4.9	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3112	16288	28304	4.9	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3114	16280		7.27	0.0E+00	AL359403.1	NT	isoform 2 of a novel human mRNA from chromosome 22
3119	16295	29309	1.88	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
							Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3122	16298		2.21	0.0E+00	AF196779.1	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3124	16300	29313	3.78	0.0E+00	4504664	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgL-C16.1)
3145	16321	29333	3.23	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3151	16326		1.92	0.0E+00	AF199355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3155	16330	29340	1.75	0.0E+00	AF064588.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3175	16350	29356	4.71	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3176	16351	29357	10.17	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3181	16356	29361	3.92	0.0E+00	7662139	NT	Homo sapiens diffractory/receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3182	16357	29362	1.29	0.0E+00	AF042075.1	NT	x92h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2684733 3' similar to SW:RNP_HYDHY P00677 RIBONUCLEASE PANCREATIC;
3187	16362	29368	1.19	0.0E+00	AW188148.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3210	16384	29395	3.61	0.0E+00	4828783	NT	Human ferritin heavy chain mRNA, complete cds
3218	16393	29404	20.63	0.0E+00	L20941.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16396	29407	1.05	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3222	16396	29408	1.05	0.0E+00	AB011121.1	NT	ye3203.e1 Stratagene lung (#37210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP-S28539
3229	16403	29415	25.61	0.0E+00	T94870.1	EST_HUMAN	S28539 BASIC PROTEIN, 23K -;
3244	16416	29433	0.93	0.0E+00	BF243336.1	EST_HUMAN	601878607F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3245	16419	29434	1.22	0.0E+00	A1988086.1	EST_HUMAN	wu12h10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2516903 3'
3250	16424	29441	5.36	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3250	16424	29442	5.36	0.0E+00	X98922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
3252	16426	29444	1.01	0.0E+00	A1655950.1	EST_HUMAN	tu38g09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICD1
3262	16436	29455	1.39	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3262	16436	29456	1.38	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3270	16444	29464	9.68	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3288	16462	29482	4.54	0.0E+00	M26699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPMT) mRNA, complete cds
3292	16466	29485	1.92	0.0E+00	4502098	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA

Page 505 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3298	16472	29493	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3298	16472	29494	0.76	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3300	16474	29495	28.49	0.0E+00	AA774783.1	EST_HUMAN	aa87b1.1 st.1 Strigene echizo brain 311 Homo sapiens cDNA clone IMAGE:971133 3'
3308	16482	29503	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3308	16482	29504	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3320	16493	29610	3.04	0.0E+00	4557580	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3328	16499	29617	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3334	16507		10.18	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3335	16508	29624	0.95	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
3338	16511	29527	4.08	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3348	18464	29635	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3348	18484	29536	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3363	16535	29649	3.56	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3364	16536	29580	0.95	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20895 (FLJ20895), mRNA
3377	16549	29593	1.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3388	16558	29573	0.72	0.0E+00	4885312	NT	Homo sapiens G-protein-coupled receptor 24 (GPR24), mRNA
3401	16571	29589	3.14	0.0E+00	AI589294.1	EST_HUMAN	tr58908.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222635 3' similar to SW:RL11_RAT
3404	16574	29589	9.94	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3412	16581	29598	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3412	16581	29597	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
3413	16582	29598	1.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3413	16582	29599	1.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3416	16585	29601	1.29	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3416	16585	29602	1.29	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3419	16588	29604	11.92	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3421	16590	29606	1.02	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3428	16598	29612	0.79	0.0E+00	BE770039.1	EST_HUMAN	60145495F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3868248 5'
3441	16609	29627	0.87	0.0E+00	AI632569.1	EST_HUMAN	wb10704.x1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q81829 Q81829
3483	16651	29667	10	0.0E+00	AU123664	EST_HUMAN	ZINC FINGER PROTEIN ;
3492	16659	29671	1.16	0.0E+00	7706239	NT	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
							Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	16680	29672	1.26	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
3498	16665		0.94	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3511	16677	29687	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3511	16677	29688	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3512	16678	29689	0.92	0.0E+00	4602398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3514	16680	29690	2.35	0.0E+00	5803087	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3523	15807	29015	3.08	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3528	16693	29703	2.46	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3532	16697	29708	5.5	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, para, and parB genes and IncA, IncB, and IncC incompatibility determinants
3535	16700	29711	1.38	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR-T), mRNA
3538	16703	29714	1.83	0.0E+00	4557748	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3544	16709	29719	4.17	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE. ;
3544	16709	29720	4.17	0.0E+00	A1935159.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634 NEURAL CELL ADHESION MOLECULE. ;
3548	16713	29725	1.91	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3555	16720	29734	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	29735	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3560	16725	29741	1.41	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3568	16731	29747	5.78	0.0E+00	U43283.1	NT	Human MDS1A (AML1/MDST fusion) mRNA, partial cds
3574	16739	29755	2.57	0.0E+00	AF046452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3574	16739	29756	2.57	0.0E+00	AF046452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3582	16747	29765	1.18	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3584	16758	29773	3.29	0.0E+00	BE304791.1	EST_HUMAN	60114353F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3081373 5'
3594	16758	29774	3.29	0.0E+00	BE304791.1	EST_HUMAN	60114353F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3081373 5'
3597	16761	29777	1.04	0.0E+00	4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3600	16764	29780	0.8	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2309)
3603	16767	29782	0.89	0.0E+00	A1984007.1	EST_HUMAN	la55g12.x1 Scores_NihMIPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498
3621	16785	29801	0.6	0.0E+00	AB032979.1	NT	DD0498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ;
3621	16785	29802	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3621	16785	29802	0.6	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds

Page 507 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16787	29803	0.88	0.0E+00	AA456282.1	EST_HUMAN	z088h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3623	16787	29804	0.88	0.0E+00	AA456282.1	EST_HUMAN	z088h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3630	16794	29811	1.45	0.0E+00	AV7071869.1	EST_HUMAN	AY701869 ADB Homo sapiens cDNA clone ADBAH06 6'
3631	16795	29812	4.48	0.0E+00	4506884	NT	Homo sapiens semogelin II (SEMG2) mRNA
3633	16797	29812	1.17	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3642	16806	29820	1.34	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3644	16807	29821	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3665	16828	29837	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3665	16828	29838	0.97	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3667	16830	29841	1.09	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3672	16835	29841	4.28	0.0E+00	AW852217.1	EST_HUMAN	QV0-CT0225-230300-168-e01 CT0225 Homo sapiens cDNA
3679	16842	29841	1.28	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase cDNA
3680	16843	29850	7.65	0.0E+00	BF670393.1	EST_HUMAN	602084563F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 6'
3704	16865	29868	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3704	16865	29869	0.59	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293645 5'
3705	16866	29869	0.99	0.0E+00	4828967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3707	16868	29871	0.76	0.0E+00	AW684693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3707	16868	29872	0.76	0.0E+00	AW684693.1	EST_HUMAN	h84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878024 3'
3711	16872	29875	0.89	0.0E+00	4828763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3713	16874	29879	0.93	0.0E+00	7662319	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3720	16881	29886	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3720	16881	29887	0.74	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3737	16898	29901	2.36	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3741	16902	29901	6.20	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3757	16918	29920	3.98	0.0E+00	AB020542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3759	16920	29922	1.06	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3761	16922	29923	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29924	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3767	16928	29932	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3767	16928	29933	32.49	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3770	16931	29935	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3770	16931	29936	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3771	16932	29937	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3771	16932	29938	0.99	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
3774	16935	29941	2.4	0.0E+00	AW851744.1	EST_HUMAN	MR2-CT0222-281099-005-005 CT0222 Homo sapiens cDNA
3776	16937	29943	2.37	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3778	16939	29945	1.15	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3780	16941	29947	0.74	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3782	16943	29949	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3782	16943	29950	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3794	16955	29959	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-qls-e-12-O-UI.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3794	16955	29960	5.42	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BWO-qls-e-12-O-UI.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'
3823	16983	29986	1.04	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 6
3824	16984	29987	1.17	0.0E+00	AA463659.1	EST_HUMAN	ae0901.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIB4. [1];
3831	16991	29993	3.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3841	17000	30003	0.83	0.0E+00	AB037635.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3856	17015	30015	5.72	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3859	17019	30018	18.03	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3866	17025	30023	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3866	17025	30024	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3889	17028	30027	8.94	0.0E+00	4505594	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2) mRNA
3922	17081	30077	1.96	0.0E+00	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3924	17083		0.73	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3925	17084	30079	2.36	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3928	17087	30083	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17087	30084	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3929	17088	30085	1.74	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3935	17094	30092	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3935	17094	30093	1.05	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGO71) gene, partial cds
3936	17095	30094	1.29	0.0E+00	A1377699.1	EST_HUMAN	te0210.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3937	17096		1	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3) mRNA, complete cds
3938	17097	30095	2.6	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP) mRNA
3940	17099	30096	15.6	0.0E+00	S78665.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6(BIR1) gene, complete cds
3942	17101	30098	2.14	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	17102	30089	1.78	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3948	17105	30101	1.62	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3946	17105	30102	1.62	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3951	17109	30107	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3951	17109	30108	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3952	17110	30109	0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115	30117	6.98	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3957	17115	30118	6.98	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5), mRNA
3959	17117	30121	4.85	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3960	17118	30122	1.12	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3963	17121	30124	1.23	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3968	17124	30127	1.44	0.0E+00	AF012619.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	30128	2.87	0.0E+00	4758171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
3969	17127	30130	0.77	0.0E+00	AF089117.1	NT	Homo sapiens amphiphysin gene, partial cds
3979	17138	30140	3.22	0.0E+00	AB64727.1	EST_HUMAN	w401601.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411085 3' similar to TR:O43340
3980	17137	30141	1.03	0.0E+00	AL163248.2	NT	O43340 R28830_2; contains element PTR7 repetitive element;
3983	17140	30145	18.17	0.0E+00	4506742	NT	Homo sapiens chromosome 21 segment HS21C048
3988	17145	30151	1.33	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3994	17151	30158	1.9	0.0E+00	6005887	NT	DKFZp434N0413_11 434 (synonym: hta33) Homo sapiens cDNA clone DKFZp434N0413 5'
3994	17151	30159	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17153	30161	3.94	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3997	17154	30162	2.26	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
4001	17158	30164	0.97	0.0E+00	AF149412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4013	17170	30178	2.65	0.0E+00	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4017	17174	30182	1.9	0.0E+00	4585842	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4026	17182	30191	6.14	0.0E+00	BF355295.1	EST_HUMAN	RC3-HT0860-170800-011-a12 HT0860 Homo sapiens cDNA
4028	17184	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1896728 similar to MXRA5
4028	17184	30194	1.37	0.0E+00	AW888221.1	EST_HUMAN	Matrix remodelling associated gene 5
4035	17191	30201	3.05	0.0E+00	AF129533.1	NT	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1896728 similar to MXRA5
4038	17194	30204	1.14	0.0E+00	U96281.1	NT	Matrix remodelling associated gene 5
							Homo sapiens F-box protein Fb35 (FBL35) mRNA, partial cds
							Homo sapiens olfactory receptor (OR7-141) gene, partial cds

Page 510 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4038	17194	30205	1.14	0.0E+00	U86281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4042	17198	30209	3.47	0.0E+00	BE378802.1	EST_HUMAN	60123696F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4043	17199	30210	1.2	0.0E+00	BE313146.1	EST_HUMAN	601153727F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508743 5'
4051	17207	30217	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-L T0031-100-100-003-H09 L10031 Homo sapiens cDNA
4052	17208	30218	1.03	0.0E+00	5360215	NT	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
4077	17233	30238	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30239	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30240	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4084	17239	30244	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4084	17239	30245	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4093	17248		3.51	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4095	17250		7.25	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4104	17258	30258	2.93	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4112	17266	30266	2.13	0.0E+00	AL163268.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4127	17281		111.8	0.0E+00	4503470	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4134	17287		0.99	0.0E+00	AI657076.1	EST_HUMAN	KIAA0563 PROTEIN ;
4137	17289	30284	1.81	0.0E+00	7662183	NT	Human zinc finger protein ZNF133
4138	17290	30285	2.85	0.0E+00	U09366.1	NT	Chlorobacillus aethiops mRNA for ribosomal protein S4X, complete cds
4157	17308	30304	6	0.0E+00	AB015610.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4168	17316		3.22	0.0E+00	AJ238617.1	NT	Homo sapiens chromosome 21 segment HS21C003
4177	17327	30318	1.58	0.0E+00	AL163203.2	NT	Homo sapiens mRNA for rape-2 (rape gene)
4178	17328	30319	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4178	17328	30320	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4185	17335	30327	8.33	0.0E+00	5032026	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase (GART) mRNA
4185	17335	30328	8.33	0.0E+00	5032026	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylglycinamide synthetase (GART) mRNA
4194	17344	30337	0.64	0.0E+00	4503914	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4202	17351	30343	6.02	0.0E+00	4885306	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4203	17352	30344	11.98	0.0E+00	AB006625.1	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4206	17355	30345	1.28	0.0E+00	4758807	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4207	17356	30346	7.08	0.0E+00	11419297	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4208	17357	30347	4.33	0.0E+00	AL086857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4209	17358		0.98	0.0E+00	AA018975.1	EST_HUMAN	ze55e09.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:382820 5' similar to contains Alu repetitive element;
4218	17367	30358	5.32	0.0E+00	AF165527.1	NT	Homo sapiens DGC8 (DGC8) mRNA, complete cds
4227	14319	27373	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase X-linked (PRKX) mRNA
4227	14319	27374	0.7	0.0E+00	4826947	NT	Homo sapiens protein kinase X-linked (PRKX) mRNA
4234	17381	30369	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4234	17381	30370	1.32	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4238	17384	30372	0.81	0.0E+00	4506884	NT	Homo sapiens semogelin II (SEM2) mRNA
4238	17384	30373	0.81	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4244	17390	30377	0.85	0.0E+00	AB020702.1	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4252	17398	30388	5.57	0.0E+00	AI982597.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
4252	17398	30387	5.57	0.0E+00	AI982597.1	EST_HUMAN	wu04404.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4266	17400	30386	1	0.0E+00	BE184856.1	EST_HUMAN	wu04404.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4266	17400	30389	1	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4259	17404		5.89	0.0E+00	BE274217.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4265	17410	30398	2.07	0.0E+00	5729725	NT	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987690 5'
							Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4272	17417		5.78	0.0E+00	AW875599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4277	17422	30410	1.12	0.0E+00	AW408788.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR ;
4278	17423	30411	1.55	0.0E+00	8922468	NT	ULHF-BM0-80x-c-02-0-UJ.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4278	17423	30412	1.55	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
							Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
4287	17432		2.35	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ), mRNA
4300	17443	30428	1.07	0.0E+00	AB037339.1	EST_HUMAN	Homo sapiens mRNA for KIAA1318 protein, partial cds
4309	17452	30438	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4309	17452	30439	11.47	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element ;
4312	17455	30443	1.2	0.0E+00	AF187475.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4338	17481	30461	8.09	0.0E+00	4758193	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
4338	17481	30462	8.09	0.0E+00	4758193	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
4345	17488		0.86	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4388	17531	30512	5.01	0.0E+00	J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4402	17545	30529	0.81	0.0E+00	AW936889.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4406	16596	29612	0.65	0.0E+00	BE779039.1	EST_HUMAN	60146495F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868246 5'
4410	17552	30537	5	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein FBX4 (FBX4) mRNA, partial cds
4419	17660	30544	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4419	17560	30545	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4420	17561		2.25	0.0E+00	AI189844.1	EST_HUMAN	q23106.x1 Soares_placenta_869weeks_2NHP869W Homo sapiens cDNA clone IMAGE:1724579 3'
4424	17564		4.68	0.0E+00	U14520.1	NT	similar to contains MER20.b2 MER20 repetitive element ;
4428	17568	30550	0.96	0.0E+00	5174574	NT	Human CBFA3 (Cbfa3) gene, partial cds
4445	17585	30565	0.72	0.0E+00	6563384	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11;16)(p13;p11) (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4445	17585	30566	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4451	17591	30572	1.08	0.0E+00	U10991.1	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4451	17591	30573	1.08	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4460	17600	30578	10.33	0.0E+00	6912281	NT	Human G2 protein mRNA, partial cds
4480	17620		1.06	0.0E+00	AF163047.2	NT	Homo sapiens GTPase domain of GTPase 1 (GTPase 1) gene, complete cds
4490	17630	30611	3.62	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4494	17634	30616	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4494	17634	30617	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4500	17640	30623	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4500	17640	30624	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4505	17644	30630	10.05	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4505	17644	30631	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4517	17656	30645	14.1	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4518	17657	30648	1.16	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4519	17658		1.24	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4522	17661	30648	1.2	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4533	17691	30671	1.9	0.0E+00	7018456	NT	Homo sapiens myosin regulatory light chain interacting protein (MLR), mRNA
4564	17702		6.61	0.0E+00	AF195963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4570	17708	30687	2.78	0.0E+00	AJ249786.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4570	17708	30688	2.78	0.0E+00	AJ249786.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4574	17711	30694	0.69	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4574	17711	30695	0.69	0.0E+00	W26179.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Page 513 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4591	17728		2.29	0.0E+00	AF200629.1	NT	Homo sapiens HPS1 gene, Intron 5
4610	17747	30726	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4610	17747	30727	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA Cc8-HAP-F1 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F205 5'
4613	17750		0.89	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4823	17760	30742	27.37	0.0E+00	AW084964.1	EST_HUMAN	xc88608.x1 NC1_CGAP_E602 Homo sapiens cDNA clone IMAGE:2588448 3' similar to SW:AHNK_HUMAN Q09668 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4825	18470		2.97	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
4827	17763	30745	1.48	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4831	17767		8.47	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4833	17769	30750	0.97	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101189-002-403 HT0305 Homo sapiens cDNA
4840	17776	30757	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4840	17776	30758	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4842	17778	30760	1.08	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 60 (GPR60) mRNA
4843	17779	30761	2.07	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4851	17787	30770	1.02	0.0E+00	S78884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
4852	17788	30771	1.2	0.0E+00	AF111163.1	NT	Homo sapiens p7rin (MEFV) gene, complete cds
4852	17788	30772	1.2	0.0E+00	AF111163.1	NT	Homo sapiens p7rin (MEFV) gene, complete cds
4861	18471	30783	3.19	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 185 (ZNF185), mRNA
4866	17801	30788	20.18	0.0E+00	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4871	17806	30795	2.17	0.0E+00	AF16237.1	NT	Homo sapiens protodactherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4874	17809	30799	2.17	0.0E+00	5464175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4885	17820	30808	59.97	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4893	17828	30814	0.73	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4897	17832	30817	1.84	0.0E+00	4503090	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4702	17837	30823	1.03	0.0E+00	4502556	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4707	17842		3.19	0.0E+00	L35465.1	NT	Homo sapiens thionate sulphate sulphatase (IDS) gene, complete cds
4709	17844	30826	15.03	0.0E+00	7662097	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4709	17844	30827	15.03	0.0E+00	7662097	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4724	17859	30841	2.87	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4727	17862	30844	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)

Page 514 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	17892	30846	11.57	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4746	17891		1.68	0.0E+00	AA174072.1	EST_HUMAN	zr18g05.e1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4749	17894		1.96	0.0E+00	7857410	NT	Homo sapiens cdz (odd Ozler-m, Drosophila) homolog 1 (ODZ1), mRNA
4751	17896		3.31	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4762	17887	30868	1.33	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4763	17888	30869	4.83	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4764	17889		1.95	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4766	17891	30870	0.69	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4761	17896	30876	1.06	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4764	17899	30879	31.32	0.0E+00	4557887	NT	Homo sapiens keralin 18 (KRT18), mRNA
4764	17899	30880	31.32	0.0E+00	4557887	NT	Homo sapiens keralin 18 (KRT18), mRNA
4765	17900	30881	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4765	17900	30882	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4766	17901	30883	2.62	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4776	17911	30895	0.98	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4776	17911	30896	0.96	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4781	17916	30902	17.22	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4787	17922	30910	1.93	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0935-160400-142-r05 BT0635 Homo sapiens cDNA
4788	17923	30911	1.37	0.0E+00	AA418246.1	EST_HUMAN	z99607.s1 Soares_NIHMP01_ST Homo sapiens cDNA clone IMAGE:767605 3'
4794	17928		1.9	0.0E+00	AF086641.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4799	17934	30921	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4799	17934	30922	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4800	17935	30923	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4800	17935	30924	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4801	17936	30925	3.06	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4804	17939	30927	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4804	17939	30928	2.06	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4806	13367	26400	2.93	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4806	13367	26401	2.93	0.0E+00	T56945.1	EST_HUMAN	ya83g04.r2 Stralagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310 5'
4810	17843		1.18	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'

Page 515 of 550
Table 4
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4814	17947	30932	1.13	0.0E+00	BE390050.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607087 5'
4830	17963	30951	0.95	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4830	17963	30952	0.95	0.0E+00	6729817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4835	17968	30956	50.79	0.0E+00	M80802.1	NT	Human AHNK nucleoprotein mRNA, 5' and
4838	17971	30959	3.07	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4838	17971	30960	3.07	0.0E+00	M69197.1	NT	Human heptoglobin and heptoglobin-related protein (HP and HPR) genes, complete cds
4842	17975	30965	2.07	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4844	17977	30967	1.05	0.0E+00	7652479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4846	17979	30968	1.73	0.0E+00	7652181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17984	30972	1.15	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exon 2-10, complete cds
4856	17989	30977	1.29	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4872	18005	30987	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4872	18005	30988	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4882	18012	30995	1.25	0.0E+00	AF028501.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4886	18016	31000	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4886	18016	31001	0.82	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (ADO13), mRNA
4907	18037	31025	1.29	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-OJL1 NCI CGAP Sub55 Homo sapiens cDNA clone IMAGE:2733264 3'
4911	18041	31031	1.18	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4913	18043		2.07	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4924	18054		1.33	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
4925	18055		0.64	0.0E+00	AW338253.1	EST_HUMAN	X289006x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4966	18095		2.87	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4967	18096	31072	1.95	0.0E+00	4505394	NT	Homo sapiens nicotinic (enacin) (NID) mRNA
4970	18099	31076	1.09	0.0E+00	X87205.1	NT	M.fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4972	18101	31077	0.99	0.0E+00	AF084476.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCE9) mRNA, complete cds
4973	18102	31078	1.04	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds
4974	18103	31079	4.54	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4976	18105	31081	9.88	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4977	18106	31082	1	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4982	18111	31088	3.41	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4985	18114	31091	1.35	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J8 J81 segments; and Tor-C-alpha gene, exons 1-4

Page 516 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4985	18114	31092	1.35	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tr-alpha) gene, J1-
4987	18116	31094	1.3	0.0E+00	X94628.1	NT	J61 segments; and Tcr-C-alpha gene, exons 1-4
4987	18116	31094	1.3	0.0E+00	X94628.1	NT	Hi.sapiens MeCP-2 gene
4987	18116	31095	1.3	0.0E+00	X94628.1	NT	Hi.sapiens MeCP-2 gene
4990	18119	31098	1.46	0.0E+00	M55582.1	NT	Human collagenase type IV (CLCA) gene, exon 2
4991	18120	31099	2.55	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5000	18129	31104	1.08	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I) mRNA
5007	18136	31110	1.19	0.0E+00	X92841.1	NT	Hi.sapiens MICA gene
5008	18138	31112	1.32	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
5010	18139	31113	1.39	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5011	18140	31114	2.74	0.0E+00	6677848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
5012	18141	31115	1.02	0.0E+00	5174580	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5013	18142	31116	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5014	18143	31117	0.94	0.0E+00	BE007935.1	EST_HUMAN	QV0-BN0147-280400-213-g11 BN0147 Homo sapiens cDNA
5014	18143	31118	4.26	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP1), mRNA
5016	18145	31120	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5016	18145	31121	1.79	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-coil proline-rich) (MGEA6), mRNA
5017	18146	31122	0.98	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HJMHOXY1), mRNA
5020	18149	31127	11.02	0.0E+00	AF055066.1	NT	Homo sapiens MHC class 1 region
5022	18151		2.46	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA
5023	18152	31130	2.77	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5036	18164	31140	1.55	0.0E+00	4503694	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDPs) mRNA
5040	18168		1.17	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5042	18170	31145	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5042	18170	31146	1.14	0.0E+00	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
5043	18171	31147	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5043	18171	31148	7.67	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5049	18177	31154	1.39	0.0E+00	4504032	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
5049	18177	31155	1.39	0.0E+00	4504032	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
5049	18177	31155	1.39	0.0E+00	4504032	NT	Homo sapiens glycocalyx 4 (GPC4) mRNA
5057	18185	31169	1.28	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5073	18201	31173	0.71	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
5082	18210	31182	1.15	0.0E+00	8922928	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5087	18215		7.86	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
5097	18225	31197	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5099	18227		2.97	0.0E+00	BE408663.1	EST_HUMAN	601303728F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:363818.6'
5102	18230	31201	4.85	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
5110	18238	31205	1.43	0.0E+00	AB028663.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5121	18247	31212	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5121	18247	31213	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5135	18259	31225	0.72	0.0E+00	AA801246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3' similar to TR:E239140
5135	18259	31226	0.72	0.0E+00	AA801246.1	EST_HUMAN	E239140 SPALT PROTEIN
5135	18259	31227	0.72	0.0E+00	AA801246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3' similar to TR:E239140
5139	18282	31228	2.09	0.0E+00	U82871.2	NT	E239140 SPALT PROTEIN
5139	18282	31230	2.09	0.0E+00	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
5148	18270	26472	0.72	0.0E+00	AF195658.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
5148	18270		1.09	0.0E+00	4758225	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5160	18282	31247	0.84	0.0E+00	U53588.1	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5167	18299		1.89	0.0E+00	AL183209.2	NT	Homo sapiens MHC class 1 region
5170	18292		18.98	0.0E+00	D50657.1	NT	Homo sapiens chromosome 21 segment HS21C009
5182	18304	31268	0.92	0.0E+00	4507720	NT	Homo sapiens gamma-cytoplasmic actin (ACTGAP3) pseudogene
5186	18318	31287	3.55	0.0E+00	Xc2988.1	NT	Homo sapiens titin (TTN) mRNA
5197	18319	31288	0.61	0.0E+00	X72791.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5213	18334	31305	1.82	0.0E+00	AF240636.1	NT	Human endogenous retrovirus mRNA for gag protein
5213	18334	31306	1.82	0.0E+00	AF240636.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5214	18335	31307	1.18	0.0E+00	5454159	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5232	18354	31322	0.82	0.0E+00	5902056	NT	Homo sapiens ring finger protein (RNF), mRNA
5234	18356	31323	4.58	0.0E+00	M10906.1	NT	Human cellular fibronectin mRNA
5234	18356	31324	4.58	0.0E+00	M10906.1	NT	Human cellular fibronectin mRNA
5236	18358	31327	0.8	0.0E+00	708032.1	NT	Human endogenous retrovirus-K, LTR US and gag gene

Page 518 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5250	18371	31338	0.65	0.0E+00	5902091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5253	18373	31339	1.91	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5256	18385	31351	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5266	18385	31352	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
5267	18386	31353	0.69	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5267	18386	31364	0.69	0.0E+00	7708245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5274	18393	31362	1.89	0.0E+00	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
5278	18397	31364	1.03	0.0E+00	AA425183.1	EST_HUMAN	zw44f12.1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:772943 5'
5278	18397	31365	1.03	0.0E+00	AA425183.1	EST_HUMAN	zw44f12.1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:772943 5'
5280	18408	31375	0.93	0.0E+00	7857442	NT	Homo sapiens protocadherin 11 (PCDH11), mRNA
5284	18412	31378	1.47	0.0E+00	AF155682.1	NT	Homo sapiens core1 UDP-galactose 4-epimerase (GALACT1) mRNA, complete cds
5287	18472	31382	1.84	0.0E+00	AF167336.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4
5300	18417	31386	0.94	0.0E+00	S69002.1	NT	AVL1-EV1-1-AM11-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
5301	18418	31387	1.93	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5301	18418	31388	1.93	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
5303	18420	31390	24.36	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
5306	18423	31393	1.07	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU16552), mRNA
5319	18435	31405	0.79	0.0E+00	X78060.1	NT	H. sapiens mRNA for YRRM2
6321	18426	28444	0.85	0.0E+00	AB685950.1	EST_HUMAN	tu35g09.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICDI
5328	18441	31410	0.96	0.0E+00	AF245703.1	NT	P03967 RAS-LIKE PROTEIN RASD
5328	18441	31411	0.96	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5333	18446	31414	0.96	0.0E+00	AL163208.2	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5336	18451	31419	110.9	0.0E+00	AF006061.1	NT	Homo sapiens chromosome 21 segment HS21C006
5340	18453	31421	1.06	0.0E+00	AV726632.1	EST_HUMAN	Homo sapiens placental growth hormone isoform hGH-V3 (hGH-V) mRNA, complete cds
5344	18457	31423	1.29	0.0E+00	5174632	NT	AV726632 HTC Homo sapiens cDNA clone HTCCCEA03 5'
5346	18459	31424	1.18	0.0E+00	4902582	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
5355	18482	31436	2.45	0.0E+00	AF093093.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
5366	18569	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens acylase (ACD) gene, nuclear gene encoding mitochondrial protein, exon 15
5366	18569	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5388	18590	31662	1.21	0.0E+00	AB34964.1	EST_HUMAN	Homo sapiens keratin 12 (KRT12) gene, complete cds
5388	18590	31662	1.21	0.0E+00	AB34964.1	EST_HUMAN	wp06g09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'

Page 519 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5391	18593	31565	1.2	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
5406	18608	31580	3.52	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-b03 GN0076 Homo sapiens cDNA
5410	18612	31584	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5418	18619	31594	8.57	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5418	18619	31594	8.57	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5418	18619	31594	8.57	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5498	18598	31714	6.41	0.0E+00	BE676498.1	EST_HUMAN	710c06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294250 3'
5500	18599	31715	1.7	0.0E+00	BE220763.1	EST_HUMAN	189a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3185194 3' similar to SW:Y054_HUMAN
5501	18700	31716	1.57	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0084 ;
5501	18700	31717	1.67	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5502	18701	31718	0.72	0.0E+00	AI189142.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5506	18705	31721	5.23	0.0E+00	M28908.1	NT	q004d04.x1 Scoreo_placenta_8to9weeks_2NHP8to9W Homo sapiens cDNA clone IMAGE:1722702 3' similar to SW:T2D3_DROME P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 85 KD SUBUNIT ;
5510	18709	31724	1.3	0.0E+00	AI791383.1	EST_HUMAN	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
5520	25906	31732	4.52	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V-J REGION (HUMAN);
5530	18727		4	0.0E+00	BF665932.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5531	18728	31743	0.78	0.0E+00	AU134406.1	EST_HUMAN	602118628F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276284 5'
5531	18728	31744	0.78	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5537	18734	31751	0.67	0.0E+00	BE538857.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894 5'
5548	18743	31777	1.63	0.0E+00	BE292784.1	EST_HUMAN	601061489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5551	18748	31783	1.95	0.0E+00	BF526328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5551	18748	31784	1.95	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214272 5'
5570	20121	33535	1.71	0.0E+00	4657384	NT	602071372F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4214272 5'
5573	18769	31811	1.29	0.0E+00	AB007835.1	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5573	18769	31812	1.29	0.0E+00	AB007835.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5577	18772	31816	8.96	0.0E+00	AF267737.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
5577	18772	31817	8.95	0.0E+00	AF267737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31831	1.34	0.0E+00	D26535.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31832	1.34	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5608	18801	31897	2.01	0.0E+00	11420819	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5612	18806	31873	0.79	0.0E+00	Z38133.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5612	18806	31873	0.79	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5630	18924	31898	0.73	0.0E+00	D61564.1	EST_HUMAN	HUM418D058 Clontech human fetal brain polyA+ mRNA (#6536) Homo sapiens cDNA clone GEN-418D05
5630	18924	31899		0.0E+00	D61564.1	EST_HUMAN	5'
5633	18927	31903	2.92	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCL CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4179888 5'
5633	18927	31904	2.92	0.0E+00	BF529831.1	EST_HUMAN	602042322F1 NCL CGAP_Bin67 Homo sapiens cDNA clone IMAGE:4179888 5'
5638	18932	31908	2.62	0.0E+00	BF313139.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5648	18943	32124	4.23	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5664	18958	32141	0.59	0.0E+00	A1928181.1	EST_HUMAN	wc95b02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5664	18958	32142	0.59	0.0E+00	A1928181.1	EST_HUMAN	075064 KIAA0466 PROTEIN ;
5682	18976	32165	1.3	0.0E+00	BE260777.1	EST_HUMAN	wc95b02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5691	18985		3.95	0.0E+00	AW867316.1	EST_HUMAN	075064 KIAA0466 PROTEIN ;
5705	18988	32190	2.49	0.0E+00	BE292889.1	EST_HUMAN	MRO-SN037-030400-001-h07 SN037 Homo sapiens cDNA
5705	18988	32191	2.49	0.0E+00	BE292889.1	EST_HUMAN	MRO-SN037-030400-001-h07 SN037 Homo sapiens cDNA
5725	18918	32212	1.7	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887603 5'
5725	18918	32213	1.7	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887603 5'
5733	18926	32222	4.16	0.0E+00	AF064254.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5733	18926	32222	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32232	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32233	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5769	18961	32262	1	0.0E+00	A198515.1	EST_HUMAN	Homo sapiens Surf-5 and Surf-6 genes
5773	18955	32268	7.55	0.0E+00	M85719.1	EST_HUMAN	q194g10.x1 Soares_placenta_86c9weeks_2Nhp80a9W Homo sapiens cDNA clone IMAGE:1757730 3' similar to SW:CADC_HUMAN P55289 BRAIN-CADHERIN PRECURSOR ;
5780	18972	32277	4.52	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Striatum (cap636206) Homo sapiens cDNA clone HFBGM48
5793	18984	32287	1.12	0.0E+00	Z86289.1	NT	UIHF-BLO-adj-d-02-0-UI,r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5804	18994	32297	1.85	0.0E+00	AW361877.1	EST_HUMAN	H.sapiens isoform 1 gene for L-type calcium channel, exon 14 and 15
5804	18994	32298	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5804	18994	32299	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5807	18997	32302	0.59	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neuritin II, complete cds
5807	18997	32303	0.59	0.0E+00	AB035266.1	NT	Homo sapiens mRNA for neuritin II, complete cds
5809	18999	32306	1.87	0.0E+00	U36281.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5840	19030	32336	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds

Page 521 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5893	18088	32400	1.49	0.0E+00	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5898	18088	32401	1.49	0.0E+00	AJ008345.1	NT	Homo sapiens KVLQT1 gene
5906	18085	32410	1.23	0.0E+00	AJ207816.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5928	19114	32427	4.63	0.0E+00	11416801	EST	Homo sapiens protocadherin beta 2 (PCDH2B2), mRNA
5933	18119	32430	1.19	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938951 5'
5942	18128	32441	1.1	0.0E+00	9898943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5943	18129	32442	7.24	0.0E+00	BE60082.1	EST_HUMAN	601345141F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3677843 5'
5944	18130	32443	2.46	0.0E+00	10048478	NT	Mus musculus ezrin (Acz), mRNA
5945	18131	32444	3.06	0.0E+00	U66981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5946	18131	32445	3.06	0.0E+00	U66981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5965	18151	32466	2.96	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Bri64 Homo sapiens cDNA clone IMAGE:4184321 5'
5968	18154	32469	0.92	0.0E+00	AF142821.1	NT	Homo sapiens calcium channel gamma 5 subunit (CAGNG5) gene, exon 4 and complete cds
5969	18155	32470	3.07	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
5979	18164	32484	1.12	0.0E+00	BE503086.1	EST_HUMAN	h23d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214881 3' similar to TR:Q62084 Q62084
5984	18169	32491	2.09	0.0E+00	BF569905.1	EST_HUMAN	PHOSPHOLIPASE C NEIGHBORING
5989	18174	32495	0.99	0.0E+00	AA454042.1	EST_HUMAN	602185652F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6021	19204	32524	2.15	0.0E+00	AF217289.1	NT	z69d06.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:3827775 5'
6023	19206	32526	4.69	0.0E+00	BE828144.1	EST_HUMAN	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6028	19211	32531	1.19	0.0E+00	BE696836.1	EST_HUMAN	RC6-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6044	19227	32550	0.58	0.0E+00	BE673988.1	EST_HUMAN	601945287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930463 5'
6044	19227	32551	0.58	0.0E+00	BE673988.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278640 3' similar to SW:DAX1_HUMAN, P91843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6048	19231	32555	0.8	0.0E+00	AW278760.1	EST_HUMAN	7d72e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278640 3' similar to SW:DAX1_HUMAN, P91843 ORPHAN NUCLEAR RECEPTOR DAX-1, [1];
6056	19240	32565	0.96	0.0E+00	BF031742.1	EST_HUMAN	x66f03.x1 NCI_CGAP_Ox39 Homo sapiens cDNA clone IMAGE:2743245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN;
6056	19240	32566	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6070	19252	32581	0.65	0.0E+00	AW470846.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6082	19264	32592	1.09	0.0E+00	BF155670.1	EST_HUMAN	h23d11.x1 NCI_CGAP_Ku112 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q821N3 Q821N3 MYOSIN-RHO GAP PROTEIN, MYR 7;
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-280900-398-a10 HT0894 Homo sapiens cDNA
6082	19264	32593	1.09	0.0E+00	BF155670.1	EST_HUMAN	QV4-HT0894-280900-398-a10 HT0894 Homo sapiens cDNA

Page 522 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6080	19271	32589	1.67	0.0E+00	W33089.1	EST_HUMAN	zc08h06.r1 Soares_parrathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6090	19271	32800	1.67	0.0E+00	W33089.1	EST_HUMAN	zc08h06.r1 Soares_parrathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6091	19272		2.3	0.0E+00	AF012018.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6094	19275	32804	3.37	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:350323 5'
6100	19280	32812	2.43	0.0E+00	BE889610.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6102	19282	32815	0.58	0.0E+00	BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6117	19287	32833	0.65	0.0E+00	AW752848.1	EST_HUMAN	IL3-CT0220-111199-028-ED4 CT0220 Homo sapiens cDNA
6120	19299	32835	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6120	19299	32836	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6121	19300	32837	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32838	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32839	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6137	25819	32656	10.17	0.0E+00	9789986	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2), mRNA
6140	19318	32659	1.28	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6140	19318	32660	1.28	0.0E+00	AA193506.1	EST_HUMAN	zr40h01.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42894 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6163	19339	32885	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6163	19339	32886	10.44	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6203	19378	32729	1.06	0.0E+00	BE288330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
6213	19388	32737	1.15	0.0E+00	BE156561.1	EST_HUMAN	QVO-HT0368-090200-099-e09 HT0368 Homo sapiens cDNA
6223	19398	32747	0.86	0.0E+00	M88107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6259	19433	32780	1.6	0.0E+00	BE379007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6285	19439	32786	1.35	0.0E+00	AU137772.1	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone IMAGE:1007201 5'
6287	19480	32812	3.33	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-9 gene, complete cds
6316	19488	32844	4.34	0.0E+00	AA204740.1	EST_HUMAN	zr41d03.r1 Stragene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6317	19489	32845	3.89	0.0E+00	11545613	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6317	19489	32846	3.89	0.0E+00	11545613	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6353	19523	32890	2.23	0.0E+00	11428367	NT	Homo sapiens carcembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6357	19527	32885	3.15	0.0E+00	BE25173.1	EST_HUMAN	601109532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350922 5'
6371	19540		0.98	0.0E+00	A1685048.1	EST_HUMAN	189110.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839 MI-2 PROTEIN. ;

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6375	19544	32902	1.32	0.0E+00	U35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6383	19552	32908	0.96	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942328 5'
6383	19552	32909	0.96	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942328 5'
6393	19562	32922	0.71	0.0E+00	A1198025.1	EST_HUMAN	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1659801 3' similar to TR:Q12838 Q12838
6393	19562	32923	0.71	0.0E+00	A1198025.1	EST_HUMAN	q150b11.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1659801 3' similar to TR:Q12838 Q12838
6396	19564	32924	1.11	0.0E+00	BF357123.1	EST_HUMAN	TFIIC ALPHA SUBUNIT ;
6403	19572	32934	1.3	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51298), mRNA
6413	19582	32943	0.59	0.0E+00	D55949.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6429	19597	32963	1.07	0.0E+00	AW178142.1	EST_HUMAN	U3-HIT0082-010989-014-A04 HT0062 Homo sapiens cDNA
6450	19617	32980	0.6	0.0E+00	BE874544.1	EST_HUMAN	7e02c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302.3' similar to SW:Y176_HUMAN
6464	19621	32985	0.77	0.0E+00	7662039	NT	Q14881 HYPOTHETICAL PROTEIN KIAA0176 ;
6468	19636	33006	9.28	0.0E+00	AV650020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6477	19644	33006	3.46	0.0E+00	AW675598.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCCAD09 3'
6480	19647	33009	4.63	0.0E+00	H01265.1	EST_HUMAN	UJ-HF-BL0-acc-g-12-Q-UJ.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058761 3'
6488	19656	33018	0.71	0.0E+00	11426293	NT	y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933 5'
6492	19658	33021	1.67	0.0E+00	X15377.1	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerate) (ACCN1), mRNA
6494	19660	33023	1.17	0.0E+00	AA456375.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6495	19661	33024	1.04	0.0E+00	AI612841.1	EST_HUMAN	aat14907.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:813252 5'
6501	19667	33030	4.27	0.0E+00	BE735696.1	EST_HUMAN	t257d08.x1 NCL CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282687 3' similar to SW:NTCS_HUMAN
6501	19667	33031	4.27	0.0E+00	BE735696.1	EST_HUMAN	P53786 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6505	19671	33037	0.86	0.0E+00	AW748596.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6505	19671	33038	0.86	0.0E+00	AW748596.1	EST_HUMAN	601305388F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6507	19673	33040	52.21	0.0E+00	AU119245.1	EST_HUMAN	MFO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6507	19673	33041	52.21	0.0E+00	AU119245.1	EST_HUMAN	MFO-BT0264-221199-002-f11 BT0264 Homo sapiens cDNA
6512	19677	33047	0.8	0.0E+00	BE760463.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6513	19678	33048	0.84	0.0E+00	X92217.1	NT	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6527	19691	33065	1.71	0.0E+00	AI089483.1	EST_HUMAN	601488712F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871899 5'
6541	19704	33076	4.06	0.0E+00	BE293163.1	EST_HUMAN	H.sapiens germ-line immunoglobulin heavy chain, variable region, (13-2)
6541	19704	33077	4.06	0.0E+00	BE293163.1	EST_HUMAN	ws25c07.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2498220 3'
6573	19735	33114	1.07	0.0E+00	BE887657.1	EST_HUMAN	601105344F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2687863 5'
6573	19735	33114	1.07	0.0E+00	BE887657.1	EST_HUMAN	601105344F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2687863 5'

Page 524 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6609	19799	33158	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6609	19799	33159	1.81	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BLO-acc-h-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931 5'
6640	19798	33168	0.94	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLOEHC06 5'
6649	19808	33195	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6649	19808	33196	0.74	0.0E+00	BE898340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6652	19811	33199	2.13	0.0E+00	AF190860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6655	19814	33202	0.64	0.0E+00	L48546.1	NT	Homo sapiens tuberin (TSC2) gene, exons 38, 39, 40 and 41
6657	19816	33203	0.99	0.0E+00	11420658	NT	Homo sapiens transcription/transcription domain-associated protein (TRRAP), mRNA
6664	19823	33210	3.5	0.0E+00	AW163940.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2764159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206
6664	19823	33211	3.5	0.0E+00	AW163940.1	EST_HUMAN	au96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2764159 5' similar to TR:O15390 O15390 GT24. [3] TR:O43840 TR:O43206
6668	19827	33214	1.06	0.0E+00	W37163.1	EST_HUMAN	z20e06.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZNA45_HUMAN Q02386 ZINC FINGER PROTEIN 45
6668	19827	33215	1.06	0.0E+00	W37163.1	EST_HUMAN	z20e06.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZNA45_HUMAN Q02386 ZINC FINGER PROTEIN 45
6684	19842	33232	1.21	0.0E+00	BE794893.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6691	19849	33239	5.1	0.0E+00	BE79873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6692	19850	33240	1.38	0.0E+00	BE787855.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6692	19850	33241	1.38	0.0E+00	BE787855.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6696	19854	33244	6.83	0.0E+00	BE889813.1	EST_HUMAN	601572058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6696	19854	33245	6.83	0.0E+00	BE889813.1	EST_HUMAN	601572058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6705	19863	33253	4.51	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6710	19868	33257	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6710	19868	33258	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6716	19874	33265	3.68	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6720	19877	33268	4.12	0.0E+00	A1638412.1	EST_HUMAN	tb31f11.x1 NCI_CGAP GC8 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6722	19879	33270	1.46	0.0E+00	L32832.1	NT	P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR.
6735	19891	33283	0.82	0.0E+00	AW505430.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6737	19893	33284	4.11	0.0E+00	AA434594.1	EST_HUMAN	zw52c03.r1 Soares_fetal_lung_Nb21F8_9w Homo sapiens cDNA clone IMAGE:3081217 5'
6751	19907		1.13	0.0E+00	BF217200.1	EST_HUMAN	601886317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
6756	19912	33307	1.63	0.0E+00	BE926876.1	EST_HUMAN	QV3-BN0047-300800-278-c06 BN0047 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6789	19944	33342	0.76	0.0E+00	11428768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A8), mRNA
6789	19944	33343	0.76	0.0E+00	11428768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A8), mRNA
6790	19945	33345	0.58	0.0E+00	AW611864.1	EST_HUMAN	hg82a04.x1 NCL_CGAP_K011 Homo sapiens cDNA clone IMAGE:2952128 3'
6808	19962	33368	1.64	0.0E+00	AU126928.1	EST_HUMAN	AU126928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6810	19964	33368	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6810	19964	33369	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6832	19985	33383	1.27	0.0E+00	BE142383.1	EST_HUMAN	CM0-HT0143-270899-082-e08 HT0143 Homo sapiens cDNA
6854	20007	33416	2.43	0.0E+00	BE008012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6854	20007	33417	2.43	0.0E+00	BE008012.1	EST_HUMAN	RC0-BN0121-280300-032-e04 BN0121 Homo sapiens cDNA
6876	20028	33438	7.79	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6876	20030	33440	2.04	0.0E+00	BF085687.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6915	20230	33663	3.33	0.0E+00	AA190755.1	EST_HUMAN	zp89e03.r1 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:627292 5'
6928	20241	33678	0.83	0.0E+00	U39573.1	NT	Human salivary peroxidase mRNA, complete cds
6930	20245	33678	0.76	0.0E+00	BE871987.1	EST_HUMAN	7a49b07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285
6940	20263	33889	6.73	0.0E+00	A1940621.1	EST_HUMAN	TEKTIN. ;
6940	20253	33890	6.73	0.0E+00	A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6951	20284	33703	2.15	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
6963	20191	33617	0.73	0.0E+00	AL042443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6964	20192	33618	11.05	0.0E+00	X56163.1	NT	H sapiens Immunoglobulin heavy chain gene, variable region
6967	20195	33621	0.92	0.0E+00	A1168270.1	EST_HUMAN	cc10d01.x1 Scores_NSF_Fa_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1665761 3' similar to
6972	20200	33626	0.85	0.0E+00	BE734087.1	EST_HUMAN	TR:Q26623 Q26623 TEKTIN C1. ;
6991	18510	31502	1.28	0.0E+00	BE666381.1	EST_HUMAN	601697370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6998	18517	31509	13.83	0.0E+00	BE867889.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3882287 5'
6998	18517	31510	13.83	0.0E+00	BE867889.1	EST_HUMAN	601443967F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7004	20140	33558	1.74	0.0E+00	BE550162.1	EST_HUMAN	601443967F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
7004	20140	33559	1.74	0.0E+00	BE550162.1	EST_HUMAN	7b49b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231981 3' similar to SW:G685_HUMAN
7030	20166	33588	1.66	0.0E+00	BF088376.1	EST_HUMAN	7b49b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231981 3' similar to SW:G685_HUMAN
7038	20172	33694	1.4	0.0E+00	AA198106.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
							zr34g03.r1 Scores_NHIMPu_S1 Homo sapiens cDNA clone IMAGE:665332 5'

Page 526 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7044	20087		11.81	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7046	20099	33515	1.11	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7061	20114	33529	2.69	0.0E+00	BF569005.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7068	20121	33636	0.66	0.0E+00	4587384	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7078	20129		2.08	0.0E+00	J03069.1	NT	Human MYCL2 gene, complete cds
7083	20177	33569	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7083	20177	33600	2.56	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7084	20178	33601	1.07	0.0E+00	M38113.1	NT	Human neurofibromatosis type 1 gene, exon x6
7095	18522	31515	3.59	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7099	18526	31518	0.7	0.0E+00	BE256708.1	EST_HUMAN	601115515F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356330 5'
7111	18537	31493	0.62	0.0E+00	AI600911.1	EST_HUMAN	w21c09.x1 Soares_Dickgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element;
7111	18537	31493	0.62	0.0E+00	AI600911.1	EST_HUMAN	w21c09.x1 Soares_Dickgraefe_colon_NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-A4 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element;
7120	18548	31494	0.62	0.0E+00	AI600911.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003679 5'
7123	18549	31461	7.52	0.0E+00	BE262841.1	EST_HUMAN	601148954F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3501829 5'
7124	18550	31462	2.72	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31463	2.72	0.0E+00	Z37976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7125	18551	31464	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31465	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7132	18558	31472	1.26	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7137	20272	33711	0.61	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-140600-223-f01 NT0022 Homo sapiens cDNA
7142	20277	33717	2.56	0.0E+00	BF569005.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7144	20279	33719	0.78	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7144	20279	33720	0.78	0.0E+00	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7148	20283	33725	3.25	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7153	20287	33729	0.72	0.0E+00	AW502362.1	EST_HUMAN	UHF-BR0p-ata-d-10-0-JL1.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7153	20287	33730	0.72	0.0E+00	AW502362.1	EST_HUMAN	UHF-BR0p-ata-d-10-0-JL1.1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076290 5'
7162	20296	33738	0.87	0.0E+00	AL039591.1	EST_HUMAN	DKFZp343D221.1 J1 434 (synonym: hss3) Homo sapiens cDNA clone DKFZp343D221.1 5'
7162	20296	33739	0.87	0.0E+00	AL039591.1	EST_HUMAN	DKFZp343D221.1 J1 434 (synonym: hss3) Homo sapiens cDNA clone DKFZp343D221.1 5'
7171	20304	33747	5.81	0.0E+00	BF306998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

Page 527 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7177	20309	33752	2.13	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7219	20384	33499	1.15	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7225	20089	33506	0.84	0.0E+00	AW513069.1	EST_HUMAN	xc04002.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2708468 3' similar to TR:094895 094895
7257	20340	33780	0.62	0.0E+00	AB028893.1	NT	KIAA0803 PROTEIN ;
7257	20340	33791	0.62	0.0E+00	AB028893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7262	20345	33797	0.84	0.0E+00	AU137738.1	EST_HUMAN	Homo sapiens mRNA for vascular cadherin-2, complete cds
7262	20345	33798	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7268	20351	33804	1.16	0.0E+00	AW654806.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7269	20352	33805	0.72	0.0E+00	BE254103.1	EST_HUMAN	EST366876 MAGC resequences, MAGC Homo sapiens cDNA
7283	20368	33819	1	0.0E+00	L01973.1	NT	607113968F1 NIH_MGC 16 Homo sapiens cDNA clone IMAGE:3354588 5'
7281	20373	33829	1.03	0.0E+00	AB007935.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7291	20373	33830	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7297	20379	33837	1.47	0.0E+00	AU133213.1	EST_HUMAN	Homo sapiens mRNA for KIAA0468 protein, partial cds
7313	20395	33857	1.06	0.0E+00	11428081	NT	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001566 5'
7319	20401		2.82	0.0E+00	AU143706.1	EST_HUMAN	Homo sapiens membrane protein GH1 (GH1), mRNA
7320	20402	33864	0.71	0.0E+00	4738839	NT	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002385 5'
7329	20411	33872	1.25	0.0E+00	BE891286.1	EST_HUMAN	Homo sapiens netrin 1 (NTN1), mRNA
7329	20411	33873	1.25	0.0E+00	BE891286.1	EST_HUMAN	607431819F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3917184 5'
7350	18599	31436	2.43	0.0E+00	AF137286.1	NT	607431819F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3917164 5'
7350	18599	31437	2.43	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7361	20440	33901	0.67	0.0E+00	BE747231.1	EST_HUMAN	Homo sapiens keratin 12 (KRT12) gene, complete cds
7361	20440	33902	0.67	0.0E+00	BE747231.1	EST_HUMAN	607580948F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928722 5'
7371	20460	33913	4.07	0.0E+00		NT	607580948F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928722 5'
7371	20450	33914	4.07	0.0E+00	11438699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7385	20463	33927	0.63	0.0E+00	AF227744.1	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
						NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform ae (CACNA1G) mRNA, complete cds
7408	20484	33962	36.37	0.0E+00	A1128344.1	EST_HUMAN	q67a07.x1 Soares_placenta_8tc0weeks_2NbhP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR
7408	20484	33963	36.37	0.0E+00	A1128344.1	EST_HUMAN	q67a07.x1 Soares_placenta_8tc0weeks_2NbhP8b9W Homo sapiens cDNA clone IMAGE:1714844 3' similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR ; contains element HGR

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7408	20486	33955	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor 12R9 gene, complete cds
7408	20486	33958	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor 12R9 gene, complete cds
7410	20488	33958	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7410	20488	33959	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7413	20491		13.11	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4182839 5'
						EST_HUMAN	zmf008.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562
7415	20493	33961	3.49	0.0E+00	AA128453.1	EST_HUMAN	G806562 NEBULIN, ;
7420	20497	33967	0.77	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7420	20497	33968	0.77	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7431	20508	33980	0.69	0.0E+00	AJ270996.1	NT	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7461	20538	34011	1.13	0.0E+00	BE286489.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7463	20538	34012	0.91	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
7466	20541		1.33	0.0E+00	AU118607	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7467	20542	34015	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7467	20542	34016	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7479	20554	34026	0.83	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
7487	20562	34031	6.47	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7489	20564	34033	5.81	0.0E+00	U45448.1	NT	Human P2X1 receptor mRNA, complete cds
7489	20564	34034	5.81	0.0E+00	U45448.1	NT	Human P2X1 receptor mRNA, complete cds
7502	20577	34049	0.89	0.0E+00	AW959503.1	EST_HUMAN	EST368573 MAGe sequences, MAGD Homo sapiens cDNA
7504	20579	34051	2.31	0.0E+00	AW950516.1	EST_HUMAN	EST362566 MAGe sequences, MAGA Homo sapiens cDNA
7531	20604	34078	1.03	0.0E+00	AF001643.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34079	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7531	20604	34080	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7552	20624		0.58	0.0E+00	M80354.1	NT	Human BTIF3 protein homologue gene, complete cds
7553	20625	34101	0.8	0.0E+00	BE408293.1	EST_HUMAN	601302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7580	20652		1.09	0.0E+00	R87430.1	EST_HUMAN	ym8810.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:166051 5'
						EST_HUMAN	x839a05.y1 NCI_CGAP_Lu37 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7581	20653	34129	1.81	0.0E+00	AW236328.1	EST_HUMAN	HNF3/FH TRANSCRIPTION FACTOR GENESIS ;
7600	20670		1.5	0.0E+00	AU117593.1	EST_HUMAN	AU117593 HEMBA1 Homo sapiens cDNA clone HEMBA1001661 5'
7602	20672	34146	3.8	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7622	20692	34168	0.62	0.0E+00	AA211663.1	EST_HUMAN	zmf56102.r1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7629	20698	34174	0.63	0.0E+00	BF229235.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
						EST_HUMAN	VR0-AN00883-270900-004-007 AND0883 Homo sapiens cDNA

Page 529 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7634	20703	34182	0.67	0.0E+00	AW405627.1	EST_HUMAN	UJHF-BLO-abs-d-07-q-UJ1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 8'
7641	20710	34189	0.8	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7667	20733	34209	0.9	0.0E+00	BF306996.1	EST_HUMAN	601899823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7667	20733	34210	0.9	0.0E+00	BF306996.1	EST_HUMAN	601899823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7675	20740	34220	1.09	0.0E+00	AU118767.1	EST_HUMAN	AU118767 HEMBAT1 Homo sapiens cDNA clone HEMBA1004314 5'
7733	20784	34281	4.41	0.0E+00	A1762561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7733	20784	34282	4.41	0.0E+00	A1762561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7768	20852	34344	0.6	0.0E+00	AL046347.2	EST_HUMAN	DKFZp434J087_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J087 5'
7813	20868	34363	1.78	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7813	20868	34364	1.79	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7821	20876	34375	1.34	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7835	20890	34392	1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7863	20917	34422	0.7	0.0E+00	A1825504.1	EST_HUMAN	wb17g05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O76363 O76363 ABC1.1
7863	20917	34423	0.7	0.0E+00	A1825504.1	EST_HUMAN	wb17g05.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:O76363 O76363 ABC1.1
7871	20925	34432	1.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7877	20929	34435	0.88	0.0E+00	N76126.1	EST_HUMAN	za86e05.s1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:298459 3'
7881	20933	34438	6.1	0.0E+00	BF217805.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103728 5'
7886	20938	34444	0.62	0.0E+00	BF569892.1	EST_HUMAN	602185908F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4310266 5'
7891	20943	34449	3.62	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2006913 5'
7911	20955	34469	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42a08.x1 Jia bone marrow stroma Homo sapiens cDNA clone HEMSC_cr42a08 3'
7911	20955	34470	0.95	0.0E+00	AW069274.1	EST_HUMAN	cr42a08.x1 Jia bone marrow stroma Homo sapiens cDNA clone HEMSC_cr42a08 3'
7915	20966	34472	6.67	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7922	20973	34478	0.92	0.0E+00	A1765467.1	EST_HUMAN	A1765467 BM Homo sapiens cDNA clone BMFBGG05 5'
7924	20974	34480	5.78	0.0E+00	BE739870.1	EST_HUMAN	601563156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7924	20974	34481	5.78	0.0E+00	BE739870.1	EST_HUMAN	601563156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7925	20975	34482	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0709), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7925	20976	34483	0.78	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7926	20976	34484	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBBT Homo sapiens cDNA clone HEMBB1000655 5'
7928	20976	34485	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBBT Homo sapiens cDNA clone HEMBB1000655 5'
7948	20998	34508	12.57	0.0E+00	BF590287.1	EST_HUMAN	hnb22c04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3283214 3' similar to contains element TAR1 repetitive element;
7959	21008	34519	1.86	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884258 5'
7959	21009	34520	1.88	0.0E+00	BE787610.1	EST_HUMAN	601481713F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884258 5'
7998	21048	34561	0.63	0.0E+00	Y16795.1	NT	Homo sapiens psliHaa pseudogene
7999	21049	34562	3.86	0.0E+00	AI346148.1	EST_HUMAN	qp4305.x1 NCL_CGAP_C08 Homo sapiens cDNA clone IMAGE:1925783 3' similar to SW:EVX1_HUMAN P49640 HOMEBOX EVEN-SKIPPED HOMOLOG PROTEIN 1;
8001	21051	34564	0.68	0.0E+00	W52873.1	EST_HUMAN	z807010.1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:338443 5'
8002	21052	34565	0.58	0.0E+00	11426128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8003	21053	34566	0.59	0.0E+00	AU117333.1	EST_HUMAN	AU117333 HEMBA1 Homo sapiens cDNA clone HEMBA1001175 5'
8004	21054		0.57	0.0E+00	BE613963.1	EST_HUMAN	601504084F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3805733 5'
8018	21059	34580	0.73	0.0E+00	6995985	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8018	21069	34581	0.73	0.0E+00	6995985	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8037	21120	34640	0.49	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8083	21165		0.69	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
8096	21178	34695	0.81	0.0E+00	BE313013.1	EST_HUMAN	601160347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8108	21190	34710	1.36	0.0E+00	AA149761.1	EST_HUMAN	z001c05.1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'
8121	21203	34724	0.72	0.0E+00	BF026628.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
8135	21217	34738	0.55	0.0E+00	AA017021.1	EST_HUMAN	z633108.1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:360831 5'
8153	21235	34756	2.06	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
8170	21252	34772	3.19	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8170	21252	34773	3.19	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8200	21282	34804	0.56	0.0E+00	AW674991.1	EST_HUMAN	bb34402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN.;
8200	21282	34805	0.56	0.0E+00	AW674991.1	EST_HUMAN	bb34402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:O64652 O64652 F17K2.26 PROTEIN.;
8207	21289	34811	2.07	0.0E+00	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8209	21291	34812	0.85	0.0E+00	AW387131.1	EST_HUMAN	MRQ-ST0031-C61099-003-a11 ST0031 Homo sapiens cDNA
8212	21294		0.64	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8213	21295	34814	6.15	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
8216	21298	34818	0.86	0.0E+00	BE388421.1	EST_HUMAN	60128550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8216	21298	34819	0.88	0.0E+00	BE388421.1	EST_HUMAN	60128550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8231	21313	34833	0.59	0.0E+00	7657276	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8233	21315	34835	0.84	0.0E+00	W95278.1	EST_HUMAN	z605d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8233	21315	34836	0.84	0.0E+00	W95278.1	EST_HUMAN	z605d01.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8235	21317		4.11	0.0E+00	BF673096.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284128 5'
8239	21321		0.83	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARG1 Homo sapiens cDNA clone OVARC1001289 5'
8253	21335	34853	0.96	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4212727 5'
8253	21335	34854	0.95	0.0E+00	BF525534.1	EST_HUMAN	602069632F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4212727 5'
8255	21367	34886	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8255	21367	34887	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8328	21410		1.16	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3887773 5'
8351	21432	34956	1.27	0.0E+00	AW500549.1	EST_HUMAN	U1-HF-BN0-ak4-01-0-U1-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077498 5'
8359	21440	34982	14.12	0.0E+00	AW157233.1	EST_HUMAN	au93b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783798 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE. [1];
8378	21467	34981	0.68	0.0E+00	AW072395.1	EST_HUMAN	z607d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2587639 3' similar to contains element ORF repetitive element
8394	21475	35002	1.11	0.0E+00	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8397	21478	35005	0.67	0.0E+00	W01616.1	EST_HUMAN	z336d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284633 5'
8399	21480	35007	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8399	21480	35008	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8411	21492	35022	1.13	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8431	21512	35043	0.46	0.0E+00	D45032.1	NT	Human DNA for centodactylin, exon 5
8450	21531	35060	0.53	0.0E+00	AB367350.1	EST_HUMAN	q95c12.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:1986334 3' similar to TR:Q14673 Q14673 KIAA0184 PROTEIN.;
8462	21543	35073	2.23	0.0E+00	BE674157.1	EST_HUMAN	7d76a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3275882 3' similar to TR:O95783 O95783 STAUEN PROTEIN.;
8464	21646	35075	1.96	0.0E+00	AB85871.1	EST_HUMAN	w60b10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428273 3' similar to SW-COGT_HUMAN P60281 MATRIX METALLOPROTEINASE-14 PRECURSOR;
8477	21558	35091	1.47	0.0E+00	BE56350.1	EST_HUMAN	601334780F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:368865 5'

Page 532 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8477	21558	35092	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3686655 5'
8485	21568	35102	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8485	21568	35103	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8487	21568	35105	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66502.1 Soares_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.
8487	21568	35106	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66502.1 Soares_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD.
8528	21809		3.61	0.0E+00	AA398511.1	EST_HUMAN	z173a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S65655
8537	21818	35155	0.5	0.0E+00	BE837593.1	EST_HUMAN	PROHIBITIN (HUMAN);
8538	21819	35156	1.34	0.0E+00	AW364874.1	EST_HUMAN	RQ2-FN0094-120600-013-n07 FN0094 Homo sapiens cDNA
8538	21819	35157	1.34	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8537	21838	35176	1.24	0.0E+00	BE612585.1	EST_HUMAN	QV3-DT0045-221299-046-c07 DT0045 Homo sapiens cDNA
8537	21838	35177	1.24	0.0E+00	BE612585.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8572	21853	35194	1.16	0.0E+00	AL163209.2	NT	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856179 5'
8572	21853	35195	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8581	21862	35202	0.93	0.0E+00	AI884477.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
8588	21869	35208	0.71	0.0E+00	AA502294.1	EST_HUMAN	wn33a1.1.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457
8593	21874		0.68	0.0E+00	11416799	NT	ne25d10.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1138434
8601	21882	35220	0.52	0.0E+00	AI590780.1	EST_HUMAN	G1138434 KIAA0187 PROTEIN.
8604	21885		2.08	0.0E+00	BE860797.1	EST_HUMAN	Homo sapiens prolactin beta 3 (PQDHB3), mRNA
8630	21710	35246	0.61	0.0E+00	AW245765.1	EST_HUMAN	1a04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8630	21710	35247	0.61	0.0E+00	AW245765.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8631	21711	35248	2.13	0.0E+00	4758695	NT	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8631	21711	35249	2.13	0.0E+00	4758695	NT	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8635	21715	35252	0.61	0.0E+00	U68084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8635	21715	35253	0.61	0.0E+00	U68084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8635	21715	35254	0.61	0.0E+00	U68084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8635	21715	35255	0.61	0.0E+00	U68084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8635	21715	35256	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35257	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35258	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35259	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35260	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35261	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35262	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35263	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35264	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35265	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35266	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35267	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35268	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35269	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35270	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35271	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35272	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35273	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35274	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35275	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35276	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35277	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35278	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35279	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35280	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35281	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35282	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35283	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35284	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35285	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35286	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35287	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35288	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35289	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35290	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35291	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35292	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35293	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35294	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35295	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35296	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35297	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35298	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35299	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35300	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35301	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35302	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35303	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35304	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35305	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35306	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35307	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35308	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35309	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35310	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35311	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35312	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35313	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35314	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35315	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35316	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35317	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35318	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35319	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35320	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35321	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35322	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35323	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35324	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8635	21715	35325	0.61	0.0E+00	U68084.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8723	21803	35339	0.76	0.0E+00	U82979.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8765	21844	35385	0.81	0.0E+00	AF022855.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8765	21844	35386	0.81	0.0E+00	AF022855.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8798	21847	35388	0.87	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8784	21863	35408	0.84	0.0E+00	11428672	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8788	21867		1.35	0.0E+00	AW513513.1	EST_HUMAN	xc46a01.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:U14123_cds4
8790	21869		0.54	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
8791	21870	35409	1.82	0.0E+00	D52850.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02
8823	21902	35442	4.15	0.0E+00	BE378495.1	EST_HUMAN	5'
8828	21908	35446	2.16	0.0E+00	AA410545.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8831	21910		1.35	0.0E+00	BF313949.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8838	21917	35455	0.54	0.0E+00	11424387	NT	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8843	21922	35460	1.41	0.0E+00	AW139873.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8843	21922	35461	1.41	0.0E+00	AW139873.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8878	21958	35493	2.16	0.0E+00	BE260272.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8884	21963	35497	2.91	0.0E+00	BF700165.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8884	21963	35498	2.91	0.0E+00	BF700165.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8884	21963	35499	2.91	0.0E+00	BF700165.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8923	22002	35541	0.84	0.0E+00	AL449770.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8930	22008	35547	3.89	0.0E+00	AA962527.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8938	22015	35555	3.41	0.0E+00	10947037	NT	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8938	22015	35556	3.41	0.0E+00	10947037	NT	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8961	22040	35583	1.65	0.0E+00	Y11107.3	NT	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8963	22042	35585	1.09	0.0E+00	BE278917.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8973	22052		2.88	0.0E+00	AV718377.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8980	22059	35600	3.12	0.0E+00	AW337277.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8988	22065	35605	1.59	0.0E+00	AU124051.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
9063	22142	35687	0.98	0.0E+00	AU140704.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
9073	22152	35696	0.94	0.0E+00	AB007923.1	NT	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9078	22157	35700	0.68	0.0E+00	R17132.1	EST_HUMAN	Y09609.t1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:31674 5'
9078	22157	35701	0.68	0.0E+00	R17132.1	EST_HUMAN	Y09609.t1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:31674 5'
9082	22161	35703	4.78	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935098 3'
9082	22161	35704	4.78	0.0E+00	AW592233.1	EST_HUMAN	h48a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935098 3'
9129	22208	35751	0.93	0.0E+00	AV714764.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone DGBUA06 5'
9145	22224	35766	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9145	22224	35767	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1814 3'
9151	22229	35773	1.32	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
9153	22231	35776	2.12	0.0E+00	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9161	22239		0.61	0.0E+00	BF058289.1	EST_HUMAN	7k29503.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476892 3' similar to TR:O36448 O36448
9161	22239	35808	2.79	0.0E+00	11422857	NT	S GAG ;
9201	22278	35818	1.59	0.0E+00	K01241.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
9209	22287	35828	5.28	0.0E+00	AB020630.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
9209	22287	35829	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
9214	22292	35835	1.84	0.0E+00	AV680739.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
9220	22298	35841	3.41	0.0E+00	7706638	NT	AV680739 GLC Homo sapiens cDNA clone GLCGKG12 3'
9225	22303	35846	0.6	0.0E+00	BE793326.1	EST_HUMAN	Homo sapiens polykylin-L (PKDL), mRNA
9246	22323	35867	4.22	0.0E+00	BE315402.1	EST_HUMAN	601688304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553 5'
9246	22323	35868	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9256	22333	35883	0.8	0.0E+00	BE612721.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'
9256	22333	35884	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9259	22336		0.54	0.0E+00	M89968.1	NT	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856100 5'
9261	22338	35888	1.65	0.0E+00	K14766.1	NT	Human polymorphic loci in Xq28
9278	22355	35905	0.53	0.0E+00	AU127096.1	EST_HUMAN	Human mRNA for GABA-A receptor, alpha 1 subunit
9283	22359	35909	0.83	0.0E+00	AI061395.1	EST_HUMAN	Human mRNA for GABA-A receptor, alpha 1 subunit
9288	22364	35913	1.96	0.0E+00	AI054607.1	EST_HUMAN	AU127098 NT2RP2 Homo sapiens cDNA clone NT2RP2000579 5'
9293	22369	35919	5.69	0.0E+00	9256595	NT	en29e04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9303	22379	35930	2.73	0.0E+00	AW058311.1	EST_HUMAN	wq34e12.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MG83_HUMAN
9313	22389	35940	1.32	0.0E+00	9635487	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
9328	22404	35956	0.84	0.0E+00	AU142662.1	EST_HUMAN	Human epsilon proteobactherin alpha 8 (PCDH48), mRNA
9344	22420	35974	1.04	0.0E+00	11436995	NT	Human endogenous retrovirus, complete genome

Page 535 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9345	22421		0.76	0.0E+00	BE410783.1	EST_HUMAN	601301678F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838183 5'
9359	22434	35993	1.32	0.0E+00	BF002024.1	EST_HUMAN	7g97m12.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UH62
9373	22448	36009	1.62	0.0E+00	AB011150.1	NT	Q9UH62 HYPOTHETICAL 42.5 KD PROTEIN. ;
9374	22449	36010	3.42	0.0E+00	BE794823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9378	22453	36015	0.47	0.0E+00	BE810292.1	EST_HUMAN	601589294F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'
9378	22453	36016	0.47	0.0E+00	BE810292.1	EST_HUMAN	RC3-PT0151-290800-011-c05 PT0151 Homo sapiens cDNA
9381	22456	36019	0.97	0.0E+00	AU136228.1	EST_HUMAN	AU136228 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9386	22461	36024	1.19	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9386	22461	36025	1.19	0.0E+00	BE883843.1	EST_HUMAN	601510247F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911986 5'
9403	22477	36040	0.87	0.0E+00	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9407	22481	36044	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9407	22481	36045	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST50505 Gall bladder 1 Homo sapiens cDNA 5' end
9464	22521	36083	0.96	0.0E+00	AW873469.1	EST_HUMAN	ba64d08.x3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60276 O60276
9464	22521	36084	0.96	0.0E+00	AW873469.1	EST_HUMAN	ba64d08.x3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900387 5' similar to TR:O60276 O60276
9498	22554	36116	0.99	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9498	22554	36117	0.99	0.0E+00	BE207063.1	EST_HUMAN	ba09f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus
9509	22775	36348	1.95	0.0E+00	BF348013.1	EST_HUMAN	Bel-xL mRNA, complete cds (MOUSE);
9545	22810	36178	3.1	0.0E+00	BE712515.1	EST_HUMAN	Bel-xL mRNA, complete cds (MOUSE);
9577	22719	36287	0.49	0.0E+00	BF034377.1	EST_HUMAN	QV2-HT0668-250700-282-508 HT0668 Homo sapiens cDNA
9577	22719	36288	0.49	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9583	22725	36295	0.98	0.0E+00	A1906351.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
9588	22728	36297	0.77	0.0E+00		NT	RC-BT108-040393-032 BT108 Homo sapiens cDNA
9588	22728	36298	0.77	0.0E+00		NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9596	22631	36223	0.85	0.0E+00	AL042278.1	EST_HUMAN	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9631	22696	36257	1.3	0.0E+00	A1058043.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9636	21081	34592	0.67	0.0E+00	BF306662.1	EST_HUMAN	aw60h01.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14877 Q14877 KIAA0171 PROTEIN. ;
							601892249F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138066 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9640	21083	34595	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9640	21083	34596	2.32	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9642	21085	34599	6.52	0.0E+00	A1280909.1	EST_HUMAN	qm09a06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9642	21085	34600	6.52	0.0E+00	A1280909.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A. ;
9643	21086	34601	2.15	0.0E+00	AW593836.1	EST_HUMAN	qm09a08.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9670	22832	36201	3.85	0.0E+00	AF153456.1	NT	EST386026 MAGE resequences, MAGE Homo sapiens cDNA
9673	22835	36205	0.69	0.0E+00	BE885128.1	EST_HUMAN	Homo sapiens polyoma kidney disease 2-like protein (PKD2L) gene, exon 8
9673	22835	36206	0.69	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9683	22732	36305	5.87	0.0E+00	BE255929.1	EST_HUMAN	601103994F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9686	22735	36305	1.44	0.0E+00	BE761382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9686	22735	36306	1.44	0.0E+00	BE761382.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9688	22737	36307	5.46	0.0E+00	AW163779.1	EST_HUMAN	au68c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072
9697	22746	36315	0.58	0.0E+00	D87675.1	NT	60S RIBOSOMAL PROTEIN L7A (HUMAN);
9709	22758	36329	3.41	0.0E+00	BE263191.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9727	22762	36364	4.49	0.0E+00	C06158.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9727	22762	36365	4.49	0.0E+00	C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9728	22784	36368	3.38	0.0E+00	BE746215.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9739	22804	36378	2.03	0.0E+00	11437282	NT	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9739	22804	36379	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9759	22897	36265	1.91	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9759	22897	36265	1.91	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9776	22816	36394	1.5	0.0E+00	AV701829.1	EST_HUMAN	601873425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9778	22828	36405	2.55	0.0E+00	AF019084.1	NT	AV701828 ADB Homo sapiens cDNA clone ADBBYH01 5'
9788	22828	36405	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9821	22861	36442	1.13	0.0E+00	BE082977.1	EST_HUMAN	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9841	22881	36464	1.72	0.0E+00	AW500293.1	EST_HUMAN	RC2-BT0642-130300-017-g01 BT0642 Homo sapiens cDNA
9841	22881	36465	1.72	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BNO-ekg-b-120-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22890	36470	1.87	0.0E+00	AF026308.1	NT	UI-HF-BNO-ekg-b-120-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22890	36471	1.87	0.0E+00	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9850	22890	36471	1.87	0.0E+00	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9852	22892	36472	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9852	22892	36473	0.52	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9851	22891	36485	0.63	0.0E+00	W58829.1	EST_HUMAN	zdf6e11.1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9851	22901	36486	0.63	0.0E+00	W56629.1	EST_HUMAN	zdf6e11.1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9874	22914	36499	0.46	0.0E+00	AF206054.1	NT	Homo sapiens non-inhibitory killer-cell Ig-like receptor KIR (KIR2DS5) mRNA, complete cds
9876	22916	36500	1.04	0.0E+00	AB036356.1	NT	Homo sapiens mRNA for neurixin-Lalpha protein, complete cds
9879	22919		0.84	0.0E+00	AI124780.1	EST_HUMAN	am66a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9881	22921	36505	3	0.0E+00	AW500528.1	EST_HUMAN	UI-HF-BN0-ek-c-07-Q.U.1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9825	22865	36554	2.65	0.0E+00	AF006688.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9853	22892	36585	2.88	0.0E+00	S78468.1	NT	AGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 8 of 9]
9853	22892	36586	2.88	0.0E+00	S78468.1	NT	AGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 6 of 9]
9878	23015	36608	1.26	0.0E+00	AW363135.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3686860 5'
9897	23035	36627	0.86	0.0E+00	11438432	NT	CM2-CT0311-301189-043-h11 CT0311 Homo sapiens cDNA Homo sapiens multimerin (MVRN), mRNA
9898	23036	36628	0.62	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
1007	23045	36638	0.91	0.0E+00	BE206710.1	EST_HUMAN	b228c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2864000 3'
10024	23062	36658	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10024	23062	36659	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10033	23071	36671	0.95	0.0E+00	AW500936.1	EST_HUMAN	UI-HF-BP0p-ai-4-05-Q.U.1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
10039	23077	36677	13.28	0.0E+00	BE740490.1	EST_HUMAN	601695558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10039	23077	36678	13.28	0.0E+00	BE740490.1	EST_HUMAN	601695558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10062	23090	36692	1.66	0.0E+00	7682067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
10069	23107	36710	1.94	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
10074	23112	36716	0.57	0.0E+00	AL041094.2	EST_HUMAN	DKFZp434B2416.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2416 5'
10084	23122	36723	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10095	23123	36724	2.16	0.0E+00	AF162308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10112	23150	36751	2.84	0.0E+00	AF008220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10112	23150	36752	2.84	0.0E+00	AF008220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
10128	23166	36765	1.13	0.0E+00	BF092888.1	EST_HUMAN	MR4-TN0114-110900-101-904 TN0114 Homo sapiens cDNA
10160	23197	36793	2.75	0.0E+00	BE280793.1	EST_HUMAN	601156227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138788 5'
10169	23206	36799	6.97	0.0E+00	BE398700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10169	23208	36800	6.57	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10178	23215	36806	0.87	0.0E+00	AW236289.1	EST_HUMAN	chr72601.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2696977 3' similar to gb:U02162_cds1 L-
10179	23216	36807	0.84	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10188	23225	36819	0.69	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10208	23244	36834	0.94	0.0E+00	AW664113.1	EST_HUMAN	EST376186 MAGC resequences, MAGH Homo sapiens cDNA
10222	23258	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10222	23258	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y78AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10225	23281	36849	3.31	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10228	23263	36851	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10228	23263	36852	2.75	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10261	23286	36894	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10261	23296	36895	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10277	23312	36909	.2	0.0E+00	AJ295944.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10277	23312	36910	.2	0.0E+00	AJ295944.1	NT	Homo sapiens partial RANBP7 gene for RanBP7/importin7 and partial ZNF143 gene
10282	23317	36917	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GK Hom sapiens cDNA clone GKCDXA07 5'
10282	23317	36918	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GK Hom sapiens cDNA clone GKCDXA07 5'
10288	23323	36925	0.72	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10290	23325	36928	2.42	0.0E+00	AA198387.1	EST_HUMAN	z997h11.1 Stratiagene muscle 637206 Homo sapiens cDNA clone IMAGE:628197 5'
10317	23352	36959	0.76	0.0E+00	AA131248.1	EST_HUMAN	z81101.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10317	23352	36960	0.76	0.0E+00	AA131248.1	EST_HUMAN	z81101.1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10359	23394	37005	1.61	0.0E+00	AF179309.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10404	23439	37048	0.99	0.0E+00	BE860698.1	EST_HUMAN	601491566F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893667 5'
10417	23462	37057	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10417	23462	37058	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10422	23457	37062	0.8	0.0E+00	AU127403.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone NT2RP2001212 5'
10432	23487	37073	0.89	0.0E+00	BE868511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10432	23487	37074	0.89	0.0E+00	BE868511.1	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10450	23485	37094	0.48	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10460	23495	37107	0.91	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10461	23498	37108	0.55	0.0E+00	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
10473	23508	37121	0.64	0.0E+00	BE801113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10475	23510	37123	0.77	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10486	23521	37130	1.56	0.0E+00	AB029280.1	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10487	23522	37131	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2887918 5'
10487	23522	37132	0.5	0.0E+00	BE304522.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10484	23529	37137	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10484	23529	37138	5.8	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10502	23537	37147	0.77	0.0E+00	AA704457.1	EST_HUMAN	Z19008.s1 Soares_fetal_liver_spleen_1NFUS_S1 Homo sapiens cDNA clone IMAGE:480707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10504	23539	37148	1.08	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyltransferase mRNA, complete cds
10508	23541	37151	4.87	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184939 5'
10508	23541	37182	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184939 5'
10530	23566	37172	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10530	23566	37173	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10595	23530	37237	1.07	0.0E+00	AI531818.1	EST_HUMAN	wa38e03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10595	23530	37238	1.07	0.0E+00	AI531818.1	EST_HUMAN	Q61204 NOTCH2-LIKE ;
10610	23644	37262	1.84	0.0E+00	T03078.1	EST_HUMAN	Q61204 NOTCH2-LIKE ;
10638	23672	37292	0.87	0.0E+00	AU122426.1	EST_HUMAN	FB23A4 Fetal brain, Stragelene Homo sapiens cDNA clone FB23A4 3' end
10644	23676	37288	0.48	0.0E+00	6005921	NT	AU122428 MAMMA1 Homo sapiens cDNA clone MAMMA1002388 5'
10668	23702	37312	2.22	0.0E+00	BF436218.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10669	23703		1.71	0.0E+00	AV684765.1	EST_HUMAN	neb45612.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10689	23722	37328	3.08	0.0E+00	AW517960.1	EST_HUMAN	AV684765 GLC Homo sapiens cDNA clone GLC02C07 3'
10693	23726	37332	2.88	0.0E+00	BE548213.1	EST_HUMAN	xu74501.x1 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2867401 3' similar to gb:Ma8086 MOESIN (HUMAN);
10709	23742	37348	0.82	0.0E+00	11436005	NT	601078784F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10735	23768	37378	0.52	0.0E+00	X89893.1	NT	Homo sapiens hypothetical protein DKFZp761P1010 (DKFZp761P1010), mRNA
10736	23769	37379	3.35	0.0E+00	BE781742.1	EST_HUMAN	H.sapiens mRNA for NK receptor (183 Act)
10758	23791	37409	2.32	0.0E+00	BE082720.1	EST_HUMAN	601487419F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3870700 5'
10764	23797	37417	0.67	0.0E+00	Y08032.1	NT	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10772	23805	37428	0.77	0.0E+00	AI656890.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0642 Homo sapiens cDNA
10779	23812	37435	8.15	0.0E+00	BE743215.1	EST_HUMAN	Human endogenous retrovirus-K, LTR U5 and gag gene
10779	23812	37438	9.15	0.0E+00	BE743215.1	EST_HUMAN	tt84607.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244612 3'
10784	23817	37439	0.63	0.0E+00	BE617655.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10784	23817	37440	0.63	0.0E+00	BE617655.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10784	23817	37440	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10784	23817	37440	0.63	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'

Page 540 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10786	23819	37442	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10788	23819	37443	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10809	23842	37465	0.51	0.0E+00	H39805.1	EST_HUMAN	yp01a10.r1 Soares breast 3NBH8a1 Homo sapiens cDNA clone IMAGE:186138 5'
10835	23868	37491	0.54	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10846	23876	37499	0.59	0.0E+00	BE392276.1	EST_HUMAN	601308187F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3826128 5'
10883	23888	37518	0.52	0.0E+00	AU125996	EST_HUMAN	AU125996 NT2RM4 Homo sapiens cDNA clone NT2RM4002636 5'
10872	23957	37586	1.84	0.0E+00	AU125996	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 5'
10872	23957	37587	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CUAAG005 5'
10874	23959	37595	2.55	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10882	23968	37610	5.5	0.0E+00	AW813783.1	EST_HUMAN	EST375638 IMAGE resequences, MAGH Homo sapiens cDNA
10885	23979	37610	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10895	23978	37611	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10898	23982	37614	1.7	0.0E+00	AW057621.1	EST_HUMAN	wy61f08.x1 Soares NSF_F8_GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553085 3' similar to TRQ60568 Q60566 VDX;
10906	23989	37621	8.59	0.0E+00	BE243270.1	EST_HUMAN	TCAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project= TCAA Homo sapiens cDNA clone TCAAP0917
10907	23990	37622	2.72	0.0E+00	AB652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10907	23990	37623	2.72	0.0E+00	AB652239.1	EST_HUMAN	wb28a12.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10912	23995	37628	1.48	0.0E+00	BF306642.1	EST_HUMAN	MSR1 MSR1 repetitive element;
10913	23998	37629	1.74	0.0E+00	BE872608.1	EST_HUMAN	601888704F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122649 5'
10913	23996	37630	1.74	0.0E+00	BE872608.1	EST_HUMAN	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853289 5'
10920	24003	37637	3.59	0.0E+00	11545911	NT	601451502F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853289 5'
10920	24003	37638	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10936	24018	37651	1.52	0.0E+00	AW404785.1	EST_HUMAN	Homo sapiens NOD2 protein (NOD2), mRNA
10940	24022	37656	2.85	0.0E+00	11424829	NT	UHF-BL0-actm-d-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
10941	24023	37658	8.39	0.0E+00	4504536	NT	Homo sapiens hypothetical protein FLJ20078 (FLJ20078), mRNA
10942	24024	37659	8.39	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10946	24028	37665	3.22	0.0E+00	AB91827.1	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10950	24032	37667	6.12	0.0E+00	BE882109.1	EST_HUMAN	w32506.x1 Soares Diacylglycerol, colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
10952	24034	37668	1.55	0.0E+00	BE882109.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10952	24034	37669	1.55	0.0E+00	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

Page 541 of 550

Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10965	24046	37680	22.14	0.0E+00	BE003304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10968	19087	32389	1.85	0.0E+00	AA195905.1	EST_HUMAN	z995b11.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:927633 5' similar to gb:X03740
10990	24069	37703	4.49	0.0E+00	BE793495.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10998	24077	37710	2.4	0.0E+00	BE729705.1	EST_HUMAN	601668623F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943016 5'
10998	24077	37711	2.4	0.0E+00	BE729705.1	EST_HUMAN	601662864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932575 5'
10999	24078	37712	11.66	0.0E+00	AV727362.1	EST_HUMAN	601662864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832575 5'
10999	24078	37713	11.66	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
10999	24078	37713	11.66	0.0E+00	AV727362.1	EST_HUMAN	AV727362 HTC Homo sapiens cDNA clone HTCAQH06 5'
11003	24082	37718	1.6	0.0E+00	R17132.1	EST_HUMAN	y908a09.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31874 5'
11003	24082	37719	1.6	0.0E+00	R17132.1	EST_HUMAN	y908a09.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31874 5'
11009	24088		2.62	0.0E+00	AW139414.1	EST_HUMAN	U1-H-B1-act-e-06-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717674 3'
11014	24093	37792	11.81	0.0E+00	AW516055.1	EST_HUMAN	x04g10.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2862226 3' similar to gb:M60854 40S
11020	24098	37737	4.44	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
11026	24105	37741	2.66	0.0E+00	AW593333.1	EST_HUMAN	AU135741 PLACE1 Homo sapiens cDNA clone PLAGE1002794 5'
11026	24105	37742	2.66	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11026	24105	37743	2.66	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945476 3' similar to contains element MSR1 repetitive element;
11026	24107	37744	2.66	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSR1 repetitive element;
11029	24108	37745	2.76	0.0E+00	F13069.1	EST_HUMAN	H.sapiens mRNA for H1 histamine receptor
11037	24116	37760	2.95	0.0E+00	D10083.1	NT	HSC3C031 normalized infant brain cDNA Homo sapiens cDNA clone c-3c03
11054	24131	37767	1.71	0.0E+00	AW338094.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11055	24132	37768	3.75	0.0E+00	AW451230.1	EST_HUMAN	xv6801.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17116 IG MU
11055	24132	37769	3.75	0.0E+00	AW451230.1	EST_HUMAN	CHAIN C REGION (HUMAN);
11058	13443		9.52	0.0E+00	4506632	NT	U1-H-B13-alt-a-01-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
11060	24136	37771	1.79	0.0E+00	AB014567.1	NT	U1-H-B13-alt-a-01-0-U1.s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736849 3'
11073	24148	37767	1.92	0.0E+00	BE298449.1	EST_HUMAN	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11087	24161	37787	1.47	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0687 protein, partial cds
11092	24166	37803	1.39	0.0E+00	AA377505.1	EST_HUMAN	601119249F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11108	24178	37813	3.3	0.0E+00	BE792165.1	EST_HUMAN	Homo sapiens mRNA for KIAA0645 protein, partial cds
11107	24179		76.9	0.0E+00	BF684061.1	EST_HUMAN	ESTB0347 Synovial sarcoma Homo sapiens cDNA 5' end similar to LERK-2, placenta
							601882046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3968539 5'
							602141405F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302432 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11108	24180	37814	1.45	0.0E+00	BE269288.1	EST_HUMAN	601188342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544259 5'
11110	24182	37816	7.93	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
11111	24183		1.81	0.0E+00	AW236269.1	EST_HUMAN	xt72b01.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-
11116	24188	37820	5.71	0.0E+00	AH149809.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
11116	24188	37821	5.71	0.0E+00	AH149809.1	EST_HUMAN	qf43c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
11117	24189	37822	2.53	0.0E+00	AA7391937.1	EST_HUMAN	QVA-ST0234-121189-032-b08 ST0234 Homo sapiens cDNA
11127	24199		11.83	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11130	24202	37827	9.67	0.0E+00	11424728	NT	Homo sapiens Insulin receptor (INSR), mRNA
11132	24204	37828	2.14	0.0E+00	A1367350.1	EST_HUMAN	q95c12.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN;
11132	24204	37829	2.14	0.0E+00	A1367350.1	EST_HUMAN	q95c12.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN;
11137	24209	37835	1.63	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184976 5'
11139	24211	37837	13.91	0.0E+00	BE281209.1	EST_HUMAN	601146357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11144	24216	37843	2.19	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
11147	24219	37846	1.51	0.0E+00	AB007932.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11161	24222	37850	3.89	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
11155	24226	37855	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA
11155	24226	37856	2.43	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-07 FT0134 Homo sapiens cDNA
11177	24246	37879	51.22	0.0E+00	AA740782.1	EST_HUMAN	ob32a07.s1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1328412 3' similar to contains element MSR1 repetitive element;
11186	24255	37890	2.81	0.0E+00	AF252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11199	24268	37903	1.71	0.0E+00	BE286478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11199	24268	37904	1.71	0.0E+00	BE286478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3536867 5'
11201	24270	37906	4.9	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNAKamure) Homo sapiens cDNA clone 3NHC4817
11208	24277	37914	2.1	0.0E+00	AA746375.1	EST_HUMAN	ea56h01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11208	24277	37915	2.1	0.0E+00	AA746375.1	EST_HUMAN	ea56h01.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
11218	24287	37926	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
11218	24287	37927	2.69	0.0E+00	M78448.1	EST_HUMAN	EST00596 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBCC26
11221	24290	37930	1.76	0.0E+00	BF33625.1	EST_HUMAN	QV2-HT0698-020800-295-d07 HT0698 Homo sapiens cDNA
11222	24291	37931	6.6	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
11234	24303	37940	1.86	0.0E+00	BE562822.1	EST_HUMAN	601336530F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690390 5'
11236	24305	37942	6.05	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'

Page 543 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11250	24319	37959	1.75	0.0E+00	AV693558.1	EST_HUMAN	AV693558 GKC Homo sapiens cDNA clone GKCCN003 5'
11260	24329	37969	2.97	0.0E+00	BF386553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
11288	24354	37984	2.4	0.0E+00	BE182360.1	EST_HUMAN	PV0-H70846-060500-002-E05 HT0846 Homo sapiens cDNA
11288	24354	37985	2.4	0.0E+00	BE182360.1	EST_HUMAN	PV0-H70845-060500-002-E05 HT0845 Homo sapiens cDNA
11290	24356		1.51	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAAD06 5'
11305	24370	38011	3.02	0.0E+00	BE898423.1	EST_HUMAN	601439092F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824142 5'
11311	24375	38019	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-alkg-d-02-0-J1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11311	24375	38020	1.83	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-alkg-d-02-0-J1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							b678c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048486 5' similar to gb:Y00345_cds1
11314	24378	38023	2.49	0.0E+00	BE018293.1	EST_HUMAN	POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X55553 M.musculus mRNA for poly(A) binding protein (MOUSE);
11348	25969	38058	1.48	0.0E+00	AW387768.1	EST_HUMAN	MF4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11345	25969	38059	1.45	0.0E+00	AW387768.1	EST_HUMAN	MF4-ST0118-041099-010-A12 ST0118 Homo sapiens cDNA
11353	24415	38070	3.23	0.0E+00	BE897853.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3828403 5'
11355	24417	38073	2.24	0.0E+00	AI459545.1	EST_HUMAN	ac88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11356	24417	38074	2.24	0.0E+00	AI459545.1	EST_HUMAN	ac88g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11369	24430	38087	1.89	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434L0120 5'
11390	24451	38112	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN
							Q07854 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
11390	24451	38113	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN
							Q07854 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
11390	24451	38114	1.37	0.0E+00	AI073917.1	EST_HUMAN	ou61d04.x1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632295 3' similar to SW:LRP1_HUMAN
11404	24465	38130	3.8	0.0E+00	4758827	NT	Q07854 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR;
11405	24466	38131	24.41	0.0E+00	BF206591.1	EST_HUMAN	Homo sapiens neurexin III (NRXN3) mRNA
11411	24472	38137	11.85	0.0E+00	AW207734.1	EST_HUMAN	601870502F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11418	24477	38141	3.93	0.0E+00	AB018260.1	NT	UI-HF-BI2-agg-H-01-0-J1r1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11418	24477	38142	3.83	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11418	24479	38144	2.63	0.0E+00	BE208846.1	EST_HUMAN	Homo sapiens mRNA for KIAA0717 protein, partial cds
							ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B
							55KDA-ASSOCIATED PROTEIN;

Page 544 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11418	24479	38145	2.63	0.0E+00	BE206846.1	EST_HUMAN	ba04407.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E18
11429	24490	38155	2.37	0.0E+00	11528408	NT	55KDA-ASSOCIATED PROTEIN.
11438	24499	38166	1.98	0.0E+00	AI075915.1	EST_HUMAN	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
11445	24506	38172	1.73	0.0E+00	11024711	NT	ov46g07.x1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:1640412 3' similar to TR:Q14507
11448	24509	38176	1.98	0.0E+00	BF093687.1	EST_HUMAN	Q14507 EPIDIDYMS-SPECIFIC GENE PRODUCT, ALPHA. ;
11449	24510	38189	1.94	0.0E+00	132832.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11462	24512	38178	4.61	0.0E+00	BE148076.1	EST_HUMAN	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
11452	24512	38179	4.61	0.0E+00	BE148076.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11475	24534	38204	1.66	0.0E+00	AW673469.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11475	24534	38205	1.66	0.0E+00	AW673469.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11480	24549	38223	4.84	0.0E+00	BF507876.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11490	24549	38224	4.84	0.0E+00	BF507876.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
11498	24554	38228	4.65	0.0E+00	AU135170.1	EST_HUMAN	KIAA0522 PROTEIN ;
11501	24559	38234	2.07	0.0E+00	BF576138.1	EST_HUMAN	KIAA0522 PROTEIN ;
11501	24559	38235	2.07	0.0E+00	BF576138.1	EST_HUMAN	ba54408.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
11503	24561	38238	4.06	0.0E+00	BE976401.1	EST_HUMAN	KIAA0522 PROTEIN ;
11503	24561	38239	4.06	0.0E+00	BE976401.1	EST_HUMAN	KIAA0522 PROTEIN ;
11511	24569	38246	1.61	0.0E+00	D87682.1	NT	KIAA0522 PROTEIN ;
11516	24573	38257	3.87	0.0E+00	BF240536.1	EST_HUMAN	KIAA0522 PROTEIN ;
11531	24587	38262	1.81	0.0E+00	AB037737.1	NT	KIAA0522 PROTEIN ;
11531	24587	38263	1.81	0.0E+00	AB037737.1	NT	KIAA0522 PROTEIN ;
11535	24591	38267	3.09	0.0E+00	11430868	NT	KIAA0522 PROTEIN ;
11535	24591	38267	3.09	0.0E+00	11430868	NT	KIAA0522 PROTEIN ;
11563	24608	38287	6.13	0.0E+00	4503544	NT	KIAA0522 PROTEIN ;
11560	24615	38294	2.06	0.0E+00	BF576287.1	EST_HUMAN	KIAA0522 PROTEIN ;
11562	24617	38297	3.53	0.0E+00	AW328173.1	EST_HUMAN	KIAA0522 PROTEIN ;
11567	24622		42.5	0.0E+00	M55093.1	NT	KIAA0522 PROTEIN ;
11571	24626	38305	1.75	0.0E+00	AI660968.1	EST_HUMAN	KIAA0522 PROTEIN ;
11574	24629	38307	3.37	0.0E+00	BF306996.1	EST_HUMAN	KIAA0522 PROTEIN ;

Page 545 of 550
Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11574	24629	38308	3.37	0.0E+00	BF306966.1	EST_HUMAN	801889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123848 5'
11581	24635	38315	47.2	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-e04 NN0054 Homo sapiens cDNA
11601	24654	38338	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11601	24654	38339	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11606	24659		4.33	0.0E+00	BE897051.1	EST_HUMAN	801439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924877 5'
11607	24660		2.37	0.0E+00	4503786	NT	Homo sapiens tyrosine-related kinase (PRK) mRNA
11621	24672	38361	2.34	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11623	24674		2.07	0.0E+00	BF207662.1	EST_HUMAN	601786194F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11636	24716	38407	4.53	0.0E+00	BE206946.1	EST_HUMAN	ba04607.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O78022 O78022 ETB-55KDA-ASSOCIATED PROTEIN.
11638	24716	38408	4.53	0.0E+00	BE206946.1	EST_HUMAN	ba04607.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O78022 O78022 ETB-55KDA-ASSOCIATED PROTEIN.
11638	24718	38410	3.69	0.0E+00	AW763028.1	EST_HUMAN	QV0-GT0225-101209-071-606 CT0225 Homo sapiens cDNA
11643	24723		3.01	0.0E+00	AA559707.1	EST_HUMAN	nt42c08.e1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M85178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11644	18580	31562	2.56	0.0E+00	A1934954.1	EST_HUMAN	wp06g08.x1 NCL_CGAP_K1a12 Homo sapiens cDNA clone IMAGE:2464094 3'
11645	24724	38416	7.51	0.0E+00	AW327895.1	EST_HUMAN	dr02p08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11654	26970	38435	1.76	0.0E+00	AW292776.1	EST_HUMAN	UI-H-BWO-aj-d-07-0-UI.3.t NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729509 3'
11671	23899	37522	1.93	0.0E+00	4758827	NT	Homo sapiens neuritin III (NRXN3) mRNA
11677	24676	38367	1.35	0.0E+00	BE254058.1	EST_HUMAN	601113903F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11680	24679	38369	1.79	0.0E+00	BE965098.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11680	24679	38370	1.79	0.0E+00	BE965098.2	EST_HUMAN	601659088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11681	24680	38371	3.81	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020500-077-05 HT0731 Homo sapiens cDNA
11682	24681		1.39	0.0E+00	BF513960.1	EST_HUMAN	UIH-BW1-amv-a-05-0-UI.5.t NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11698	24693	38384	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: h1a3) Homo sapiens cDNA clone DKFZp434G178 5'
11698	24693	38386	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: h1a3) Homo sapiens cDNA clone DKFZp434G178 5'
11706	24703	38395	10.19	0.0E+00	A1923116.1	EST_HUMAN	wn83g03.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11708	24746	38440	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.a1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13668
11708	24746	38441	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.a1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13668
11713	24763	38447	2.21	0.0E+00	BE910546.1	EST_HUMAN	901501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902926 5'

Single Exon Probes Expressed in Placenta

Probes SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11723	23909	37533	11.64	0.0E+00	BE676347.1	EST_HUMAN	727112.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:000409 000409 CHECKPOINT SUPPRESSOR 1.;
11725	23911	37535	1.47	0.0E+00	AI683358.1	EST_HUMAN	b66609.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274821 3' similar to gb:M65642
11727	23913	37537	3.13	0.0E+00	BE615686.1	EST_HUMAN	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN);
11727	23913	37538	3.13	0.0E+00	BE615686.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11734	23920	37545	1.59	0.0E+00	AV717420.1	EST_HUMAN	601279335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11739	23925	37550	7.33	0.0E+00	AI037746.1	EST_HUMAN	AV76720 BM Homo sapiens cDNA clone BMFAGH03 5'
11740	23926	37551	4.2	0.0E+00	UG2769.1	NT	DKFZp564C187_r1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564C187 5'
11745	23931	37557	1.33	0.0E+00	BE883368.1	EST_HUMAN	Human oxytocinase variant 2 mRNA, complete cds
11766	24759	38454	1.75	0.0E+00	Y18890.1	EST_HUMAN	601309139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833 5'
11769	24761	38455	3.59	0.0E+00	L39891.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11769	24761	38456	3.59	0.0E+00	L39891.1	NT	Homo sapiens polykissic kidney disease-associated protein (PKD1) gene, complete cds
11784	24774	38470	2.03	0.0E+00	AI138211.1	EST_HUMAN	Homo sapiens polykissic kidney disease-associated protein (PKD1) gene, complete cds
11797	24787	38485	6.43	0.0E+00	BE622317.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11833	24822	38512	17.72	0.0E+00	BE748899.1	EST_HUMAN	601441098F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11833	24822	38513	17.72	0.0E+00	BE748899.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11845	24834	38527	4.58	0.0E+00	AU141882.1	EST_HUMAN	601672186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11845	24834	38528	4.58	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11848	24837	38531	2.7	0.0E+00	AW006022.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11853	25871	38537	2.73	0.0E+00	BF002333.1	EST_HUMAN	w291h01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP.F53H10.2
11854	24852	38548	1.32	0.0E+00	CG6264.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2 TYPE 1
11856	24856		1.56	0.0E+00	BE72781.1	EST_HUMAN	7h22b10.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO.;
11872	24860	38555	2.36	0.0E+00	AI472010.1	EST_HUMAN	C08284 Human pancreatic islet Homo sapiens cDNA similar to insulin receptor
11878	24866	38563	2.84	0.0E+00	AW387776.1	EST_HUMAN	C08284 Human pancreatic islet Homo sapiens cDNA similar to insulin receptor
11878	24866	38564	2.84	0.0E+00	AW387776.1	EST_HUMAN	601264180F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833730 5'
11889	24877		1.8	0.0E+00	AW633771.1	EST_HUMAN	ig8a10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2147802 3' similar to gb:M31681 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN);
11901	24889	38569	3.67	0.0E+00	11435244	NT	MR4-ST0118-261069-012-b03 ST0118 Homo sapiens cDNA
11901	24889	38590	3.67	0.0E+00	11435244	NT	MR4-ST0118-261069-012-b03 ST0118 Homo sapiens cDNA
11907	24894	38596	4.38	0.0E+00	U36263.1	EST_HUMAN	MR3-SN0010-310300-107-b03 SN0010 Homo sapiens cDNA
11911	24908	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11911	24908	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11911	24908	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	Human beta-prime-adaptin (BAM22) gene, exon 6
11911	24908	38600	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'

Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11911	24888	38601	20.74	0.0E+00	BE378254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609823 5'
11917	24903	38606	4.87	0.0E+00	AW500356.1	EST_HUMAN	U1HF.BNO-ak-b-03-0-UI_r1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3077332 5'
11932	24918	38621	2.06	0.0E+00	BE794788.1	EST_HUMAN	601690688F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11934	24920	38623	65.18	0.0E+00	BE878633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11935	24921	38623	1.8	0.0E+00	MG00676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11941	24927	38628	1.38	0.0E+00	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
11941	24927	38630	1.38	0.0E+00	4758827	NT	Homo sapiens neuraxin III (NRXN3) mRNA
11946	24932	38635	1.68	0.0E+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11953	24939	38642	7.29	0.0E+00	BE409893.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:362844 5'
11954	24940	38643	2.22	0.0E+00	BE148850.1	EST_HUMAN	MR0-HT0241-150500-011-02 HT0241 Homo sapiens cDNA
11955	24941	38644	2.89	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11956	24941	38645	2.89	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11956	18785	31831	1.48	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11956	18785	31832	1.48	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11958	24943	38647	11.38	0.0E+00	BF681641.1	EST_HUMAN	602166722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286725 5'
11958	24943	38648	11.38	0.0E+00	BF681641.1	EST_HUMAN	602166722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286725 5'
11964	24949	38655	1.79	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000928 5'
11967	24952	38657	4.99	0.0E+00	BE903372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658335 5'
11963	24968	38671	1.56	0.0E+00	BF312652.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11963	24968	38672	1.56	0.0E+00	BF312652.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11966	24971	38675	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11966	24971	38676	3.4	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11968	24983		1.96	0.0E+00	BE906402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'
12013	24997	38700	1.46	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12028	28872		8.57	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
12029	28912	38713	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12029	28912	38714	2.37	0.0E+00	BE698861.1	EST_HUMAN	RC4-NN0025-120600-016-b07 NN0025 Homo sapiens cDNA
12032	25015	38717	60.96	0.0E+00	BE291715.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3632968 5'
12046	25027	38733	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576625F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12046	25027	38734	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576625F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12054	25035	38741	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353376 5'
12054	25035	38742	2.02	0.0E+00	BE257612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353376 5'

Page 548 of 550
Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12084	25064	38770	2.85	0.0E+00	BE545535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5'
12087	25067	38773	1.34	0.0E+00	AA399001.1	EST_HUMAN	Z893a01.f1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728912 5' similar to SW:PMT1_SCHPO
12088	25068	38774	1.55	0.0E+00	AU117974.1	EST_HUMAN	P-40899 DNA METHYLTRANSFERASE PMT1 ;
12088	25068	38775	1.55	0.0E+00	AU117974.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
12091	25071	38778	1.72	0.0E+00	BE780463.1	EST_HUMAN	AU117974 HEMBA1 Homo sapiens cDNA clone HEMBA1002812 5'
12108	25088	38792	2.15	0.0E+00	AW269890.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12118	25098	38803	1.99	0.0E+00	AU132394.1	EST_HUMAN	xv46h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816213 3' similar to
12131	25111	38815	1.35	0.0E+00	BE292840.1	EST_HUMAN	gbl.L11706 cds1 HORMONE SENSITIVE LIPASE (HUMAN);
12147	25185	31540	9.34	0.0E+00	BE312542.1	EST_HUMAN	AU132394 NT2RP3 Homo sapiens cDNA clone NT2RP3004339 5'
12160	26005		3.02	0.0E+00	AL163246.2	NT	601105652F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988325 5'
12162	26013		5.49	0.0E+00	A190063.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
12172	25134		3.73	0.0E+00	AB011389.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
12182	25149		6.97	0.0E+00	AL163246.2	NT	qet7b12.x1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
12194	25151		1.35	0.0E+00	AB018195.1	NT	Homo sapiens chromosome 21 segment HS21C046
12201	25156		3.2	0.0E+00	11417852	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
12220	25170		4.95	0.0E+00	5802973	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12254	25973	31767	1.47	0.0E+00	AF240786.1	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
12287	25983		3.47	0.0E+00	AL041931.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12285	26146		3.39	0.0E+00	11418318	NT	genes, complete cds
12304	25222		4.77	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434K0819 5'
12317	26017		2.92	0.0E+00	A1903497.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GSTSE1), mRNA
12368	26172		1.88	0.0E+00	N54494.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434G218 5'
12371	25285		4.08	0.0E+00	AF106656.1	NT	IL-BT030-271098-001 BT030 Homo sapiens cDNA
12374	14042	27108	5.36	0.0E+00	4507500	NT	yv40e03.a1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245222 3' similar to
12374	14042	27107	5.36	0.0E+00	4607600	NT	SW:POL_BAEVM P10272 POL POLYPROTEIN ;
12383	26021		3.07	0.0E+00	10092587	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12415	13754		4.88	0.0E+00	AF035528.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
							Homo sapiens X-linked arthralgia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

Page 549 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12450	25781	31937	3.95	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12510	25950	31765	1.84	0.0E+00	AW590082.1	EST_HUMAN	hg31e06.x1 NC1_CGAP_G06 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
12542	25982		1.34	0.0E+00	L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12573	26015		2.73	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12618	25416		4.61	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12638	25429		1.19	0.0E+00	AV720878.1	EST_HUMAN	AV720878 GLC Homo sapiens cDNA clone GLCEPG09 5'
12660	26009		3.51	0.0E+00	AI204814.1	EST_HUMAN	an5h04.x1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12684	25462		1.33	0.0E+00	AB04646.1	EST_HUMAN	QV-BT065-020399-103 BT066 Homo sapiens cDNA
12702	26008		2.29	0.0E+00	BE439792.1	EST_HUMAN	HTM1-864F HTM1 Homo sapiens cDNA
12714	15187	28297	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12714	15187	28298	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12739	25460	32027	1.21	0.0E+00	AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12751	14889	27960	3.26	0.0E+00	H30132.1	EST_HUMAN	yc59d08.1 Soares breast 3Nbh18st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:MB4099
12751	14889	27961	3.26	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12755	13979	27031	1.6	0.0E+00	AB011396.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12768	25509		33.13	0.0E+00	D50859.1	NT	Homo sapiens gene for AF-6, complete cds
12771	25514	31997	5.44	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGPR) pseudogene
12771	25514	31998	5.44	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12776	25518		7.88	0.0E+00	AB028698.1	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12776	15294	28420	1.7	0.0E+00	4758489	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12837	25567		2.11	0.0E+00	AW664099.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
12847	25563	31988	1.43	0.0E+00	11430460	NT	h86a08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12892	14409	27471	1.74	0.0E+00	8922593	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12927	16658	28573	3.11	0.0E+00	4885312	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
12935	16494	31632	2.3	0.0E+00	6806918	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12938	25517		1.89	0.0E+00	AB028900.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12981	25639	31983	1.82	0.0E+00	9558724	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13010	26197		2.93	0.0E+00	AL163246.2	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
13017	13828	26861	2.46	0.0E+00	6806918	NT	Homo sapiens chromosome 21 segment HS21C048
13113	25728	31943	1.17	0.0E+00	11417882	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

Page 550 of 550
Table 4
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13116	25728		1.4	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13119	25731		3.11	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
13140	25740		5.98	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
13151	26207		1.16	0.0E+00	AW505176.1	EST_HUMAN	UI-HF-BNO-aly-g-08-0-UI.H NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081389 5'
13180	25774		1.51	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
13209	16135	29151	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13209	16135	29152	1.37	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13215	14345	27402	1.29	0.0E+00	8968944	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human placenta comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 13,233 - 26,232.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human placenta.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- 10 of SEQ ID NOs.: 26,233 - 38,837, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
- 25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human placenta, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human placenta; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the placenta of said eukaryote, said probe
is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 26,232 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 26,232.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 26,233 - 38,837.

1/10

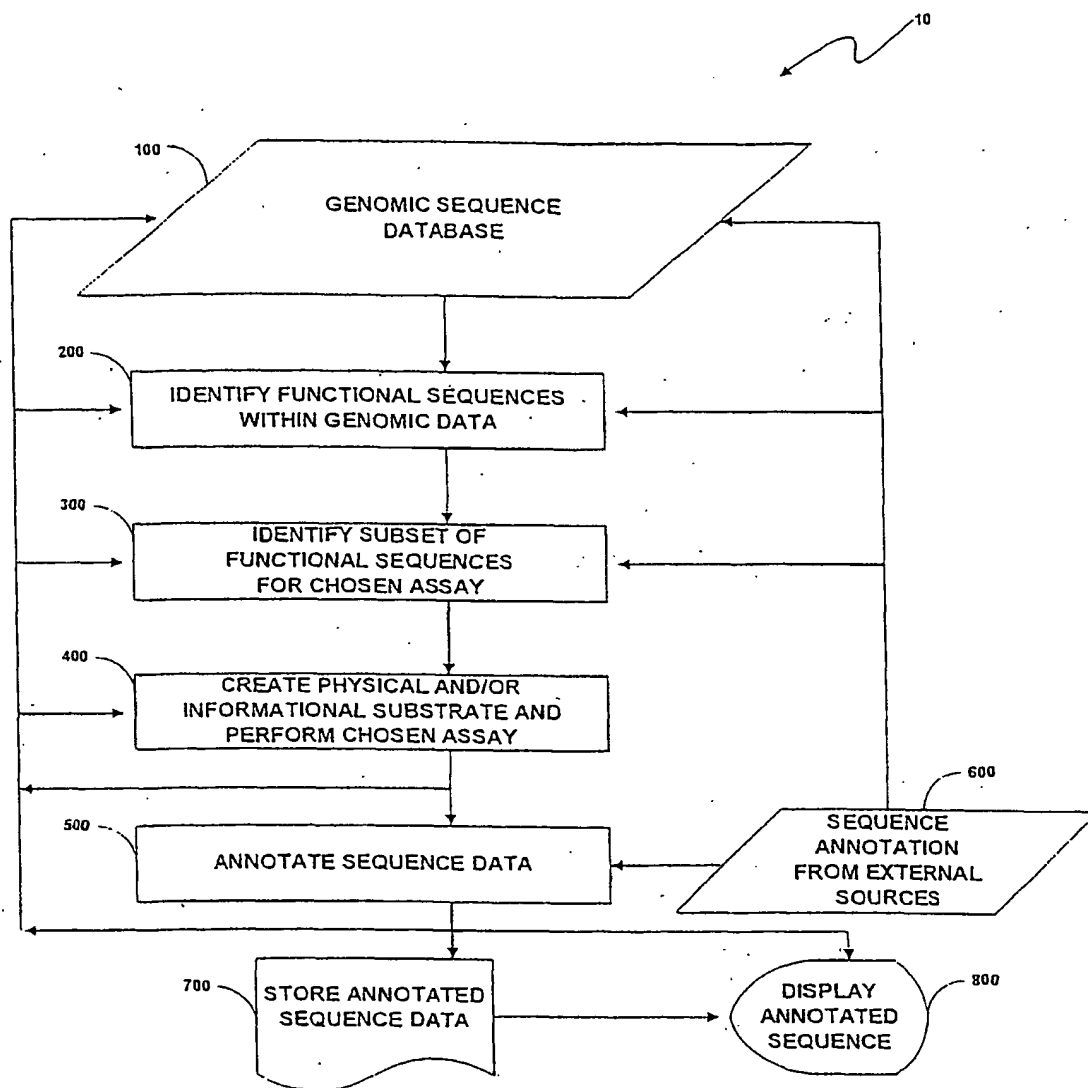


Fig. 1

2/10

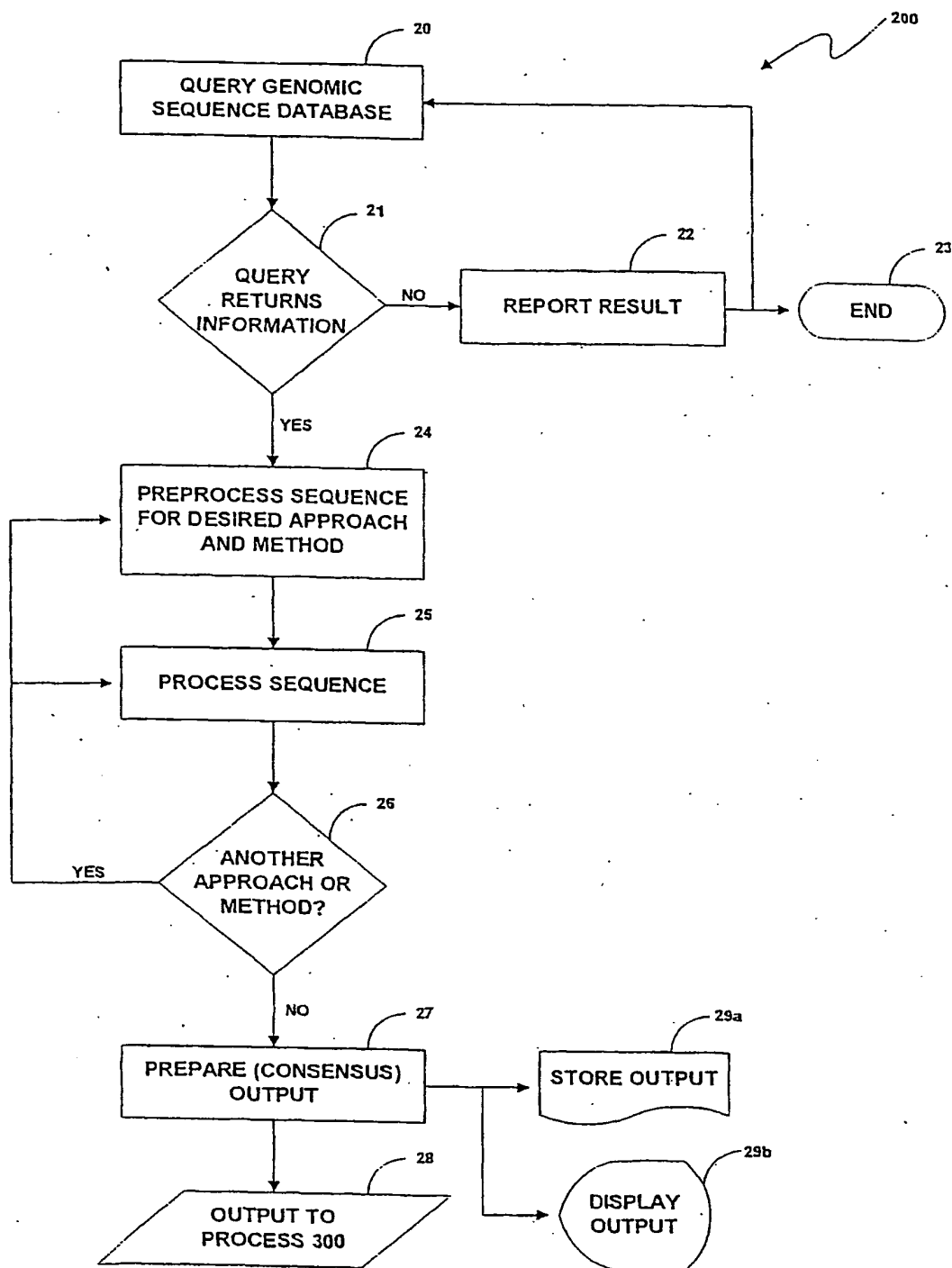


Fig. 2

3/10

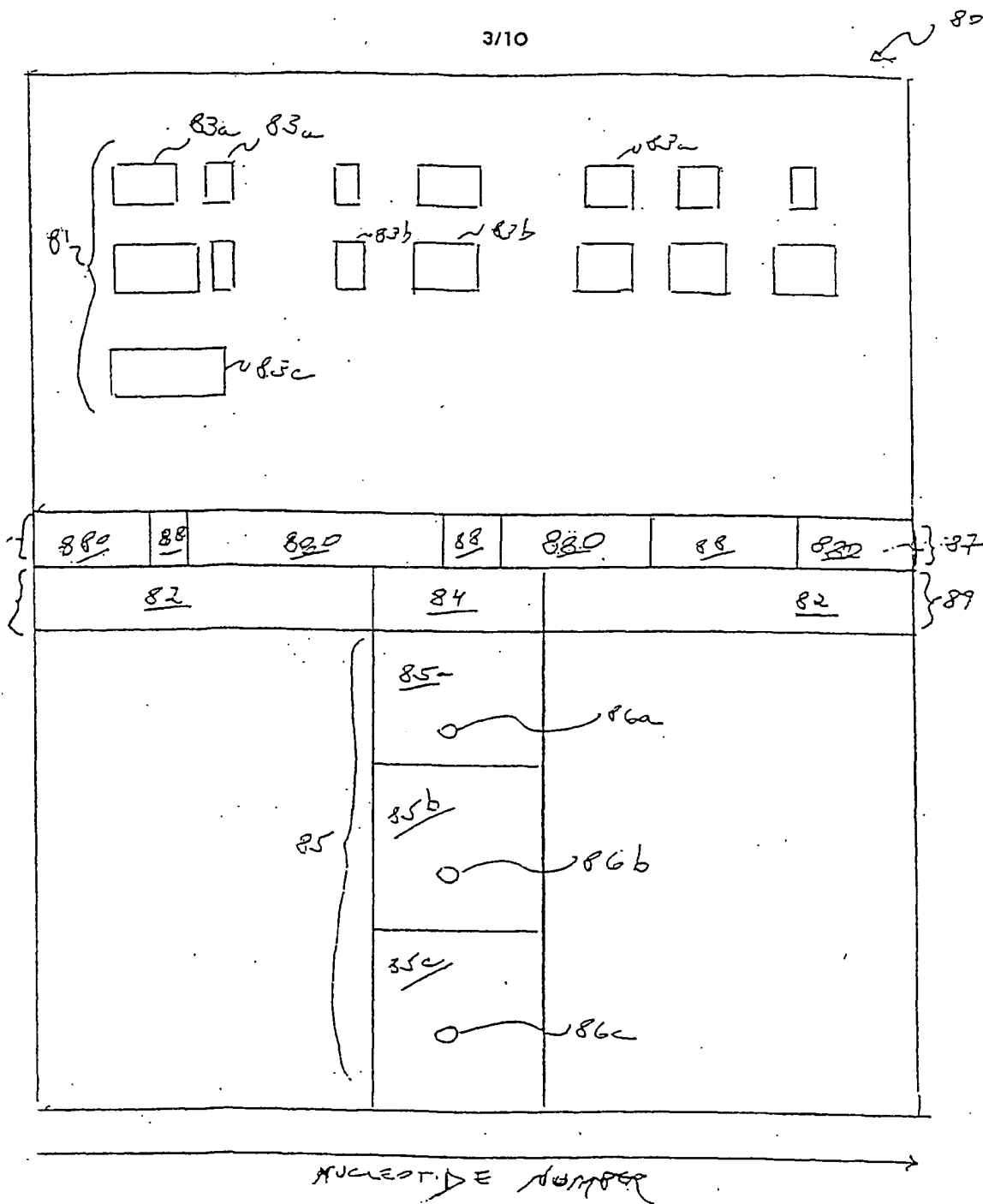


Fig. 3

4/10

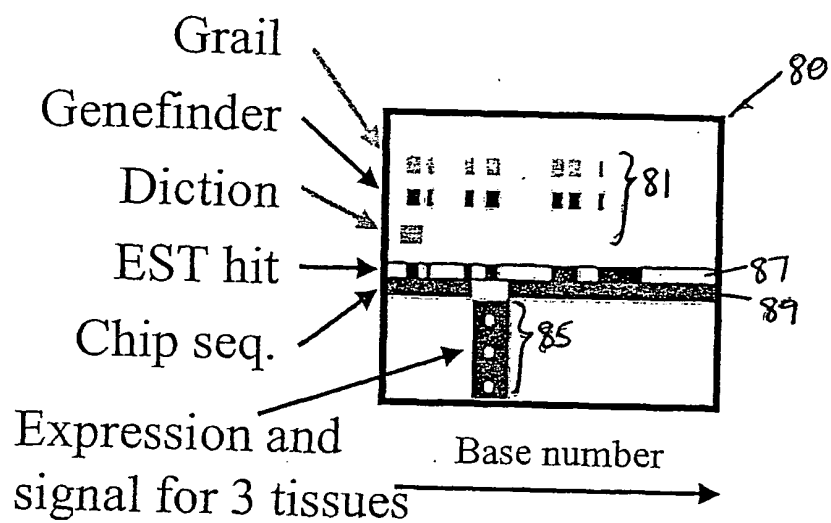


Fig. 4

5/10

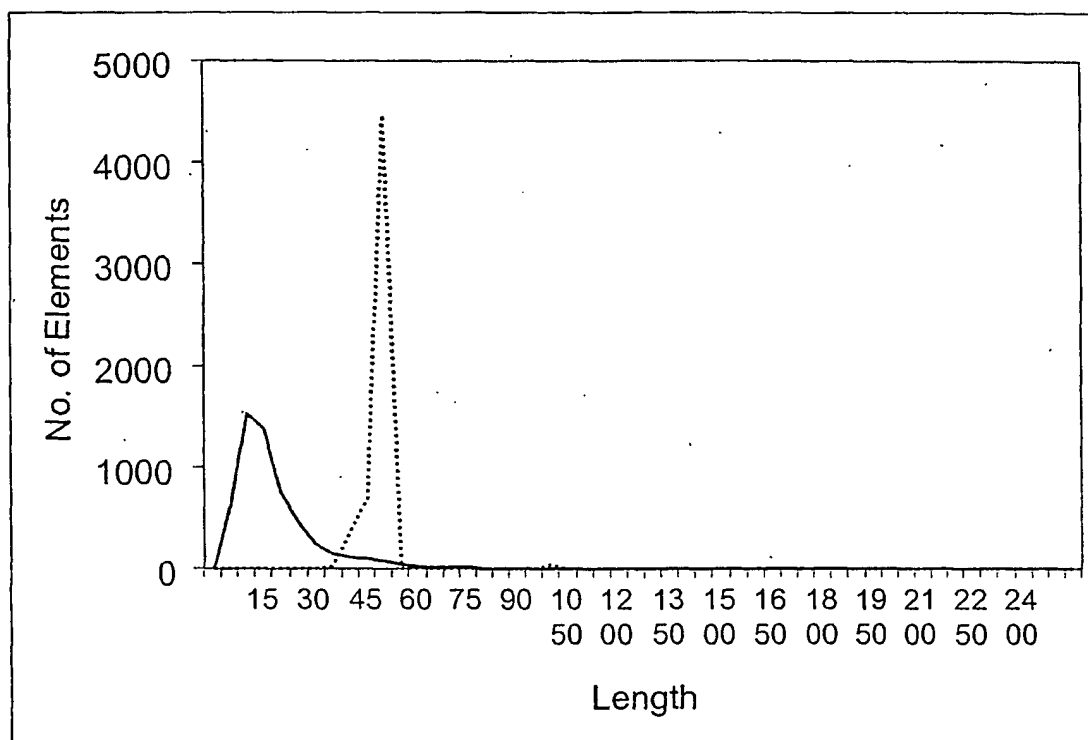


Fig. 5

6/10

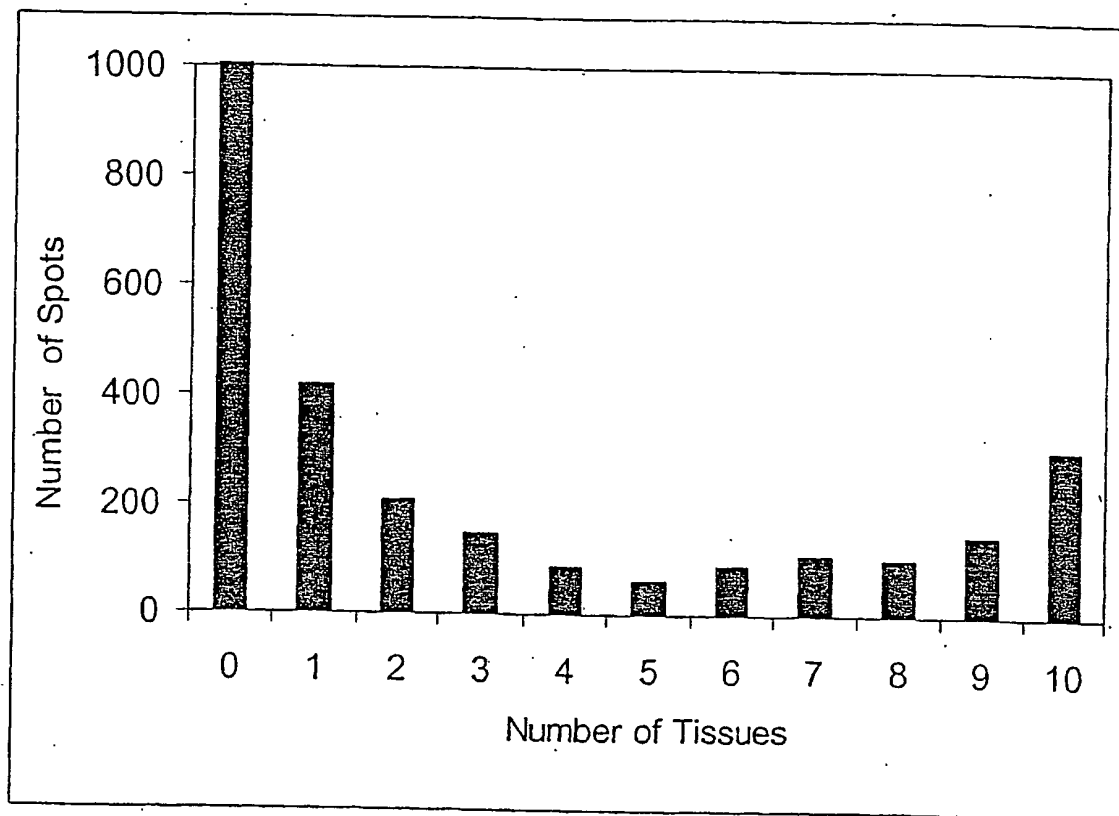


Fig. 6



Fig. 7a

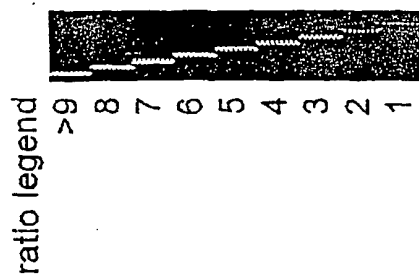


Fig. 7b

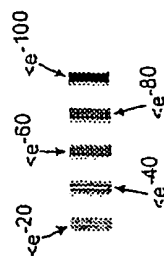


Fig. 7c

8/10

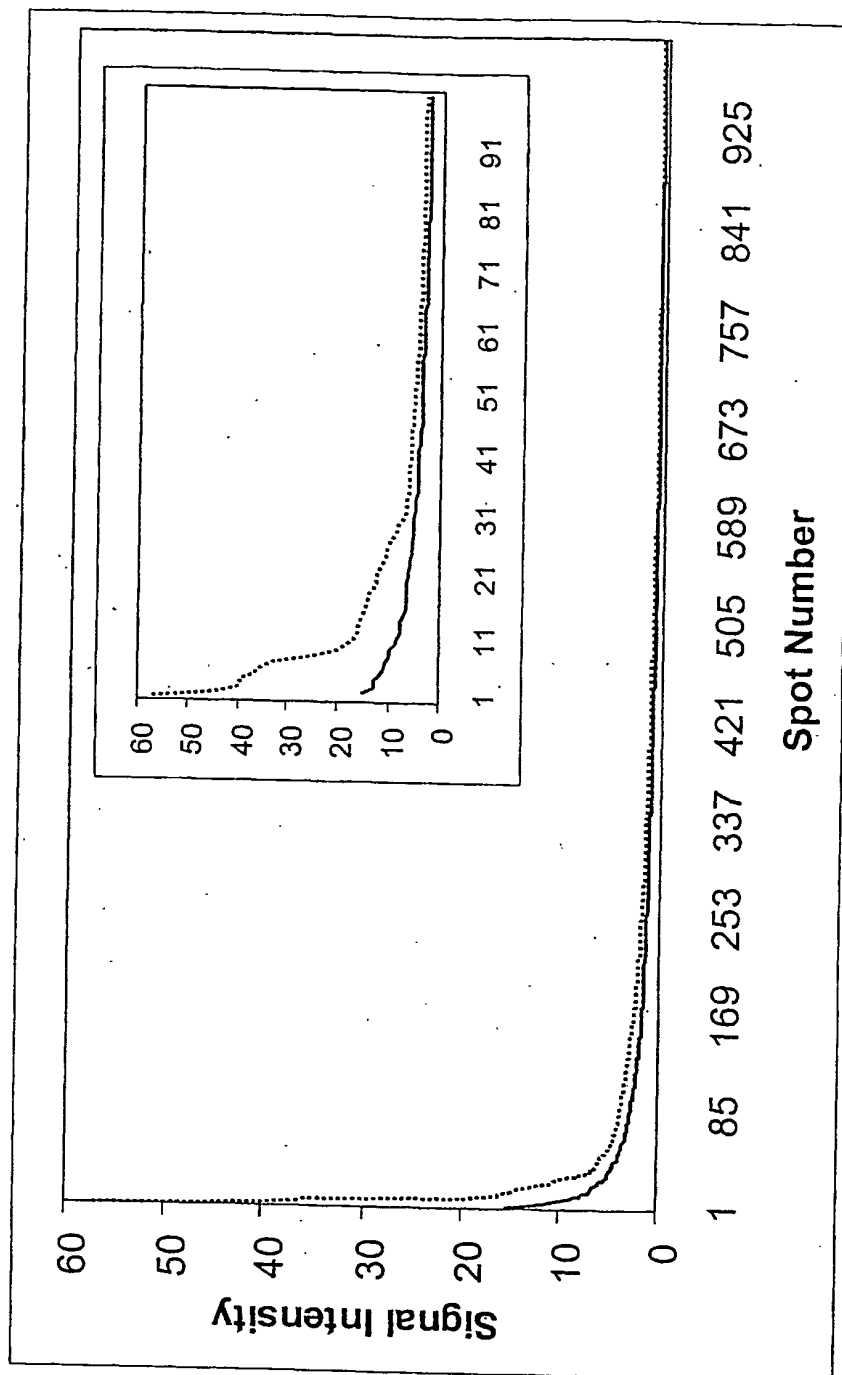


Fig. 8

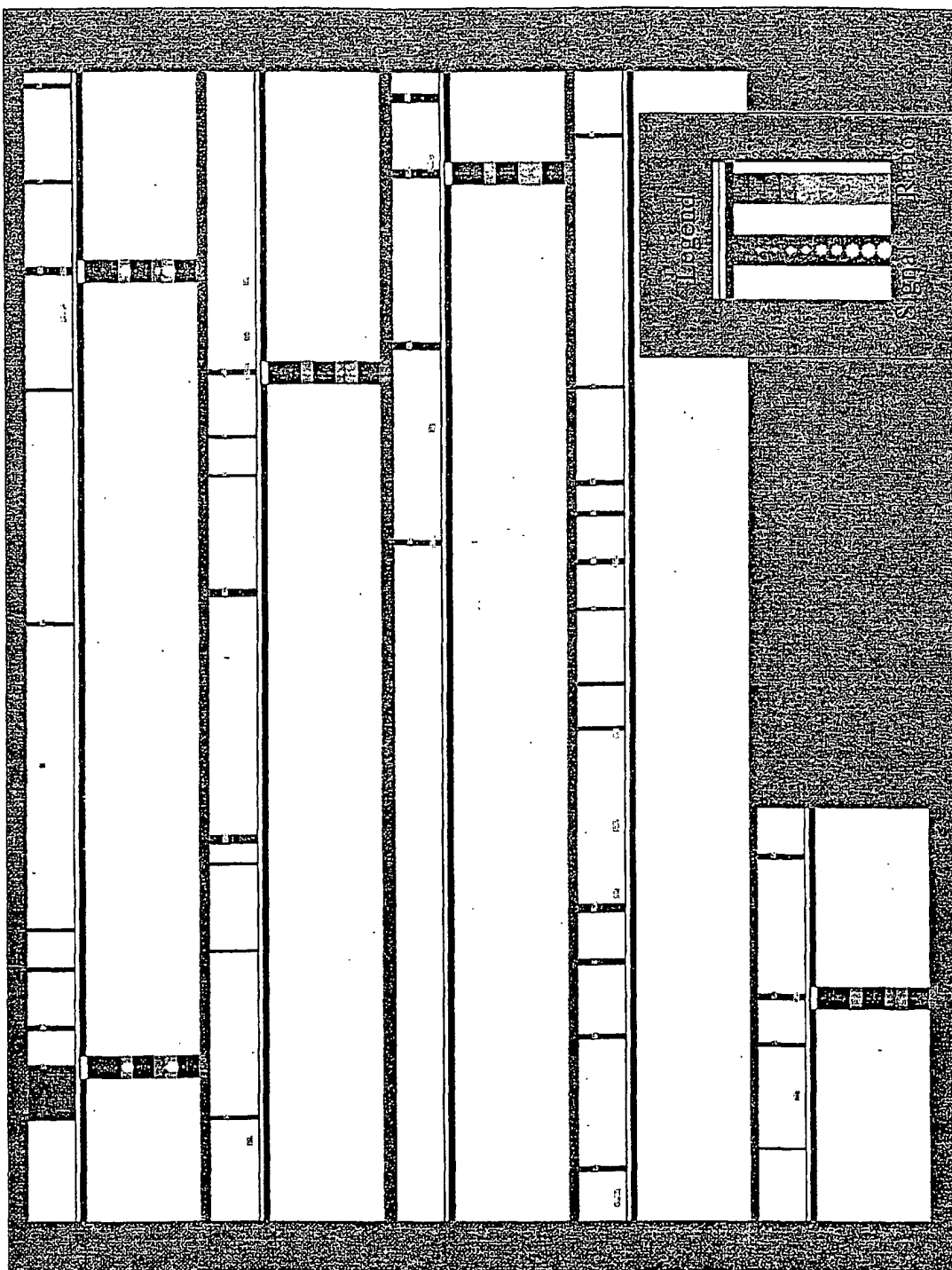


Fig. 9

10/10

Fig. 10

